

Attorney Docket No. 2750-1096P

Table 1

Client Docket No. 80142.004

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Maximum Length Sequence corresponding to clone ID 101665

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1
- Ceres seq_id 1481332

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2
- Ceres seq_id 1481333
- Location of start within SEQ ID NO 1: at 203 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 107900

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 3
- Ceres seq_id 1481342

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 4
- Ceres seq_id 1481343
- Location of start within SEQ ID NO 3: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 5
- Ceres seq_id 1481344
- Location of start within SEQ ID NO 3: at 50 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 6
- Ceres seq_id 1481345
- Location of start within SEQ ID NO 3: at 518 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 108514

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 7
- Ceres seq_id 1481346

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 8
- Ceres seq_id 1481347
- Location of start within SEQ ID NO 7: at 629 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 9

- Ceres seq_id 1481348
- Location of start within SEQ ID NO 7: at 779 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 10
- Ceres seq_id 1481349
- Location of start within SEQ ID NO 7: at 828 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 109446

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 11
- Ceres seq_id 1481357

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 12
- Ceres seq_id 1481358
- Location of start within SEQ ID NO 11: at 342 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 13
- Ceres seq_id 1481359
- Location of start within SEQ ID NO 11: at 387 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 14
- Ceres seq_id 1481360
- Location of start within SEQ ID NO 11: at 396 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 113536

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 15
- Ceres seq_id 1481372

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 16
- Ceres seq_id 1481373
- Location of start within SEQ ID NO 15: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 17
- Ceres seq_id 1481374
- Location of start within SEQ ID NO 15: at 44 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 18
- Ceres seq_id 1481375
- Location of start within SEQ ID NO 15: at 348 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 115279

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 19
- Ceres seq_id 1481388

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 20
- Ceres seq_id 1481389
- Location of start within SEQ ID NO 19: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 21
- Ceres seq_id 1481390
- Location of start within SEQ ID NO 19: at 9 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 22
- Ceres seq_id 1481391
- Location of start within SEQ ID NO 19: at 63 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 118207

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 23
- Ceres seq_id 1481423

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 24
- Ceres seq_id 1481424
- Location of start within SEQ ID NO 23: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 25
- Ceres seq_id 1481425
- Location of start within SEQ ID NO 23: at 75 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 125028

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 26
- Ceres seq_id 1481471

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 27
- Ceres seq_id 1481472
- Location of start within SEQ ID NO 26: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 28
- Ceres seq_id 1481473
- Location of start within SEQ ID NO 26: at 169 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 29
- Ceres seq_id 1481474
- Location of start within SEQ ID NO 26: at 190 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 126108

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 30
- Ceres seq_id 1481479

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 31
- Ceres seq_id 1481480
- Location of start within SEQ ID NO 30: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 32

- Ceres seq_id 1481481
- Location of start within SEQ ID NO 30: at 114 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 33
- Ceres seq_id 1481482
- Location of start within SEQ ID NO 30: at 297 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 12613

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 34
- Ceres seq_id 1481483

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 35
- Ceres seq_id 1481484
- Location of start within SEQ ID NO 34: at 184 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 36
- Ceres seq_id 1481485
- Location of start within SEQ ID NO 34: at 268 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 37
- Ceres seq_id 1481486
- Location of start within SEQ ID NO 34: at 283 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 13607

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 38
- Ceres seq_id 1481487

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 39
- Ceres seq_id 1481488
- Location of start within SEQ ID NO 38: at 124 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 40
 - Ceres seq_id 1481489
 - Location of start within SEQ ID NO 38: at 133 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 41
 - Ceres seq_id 1481490
 - Location of start within SEQ ID NO 38: at 145 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 1367

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 42
 - Ceres seq_id 1481491
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 43
 - Ceres seq_id 1481492
 - Location of start within SEQ ID NO 42: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 14568

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 44
 - Ceres seq_id 1481504
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 45
 - Ceres seq_id 1481505
 - Location of start within SEQ ID NO 44: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 46
 - Ceres seq_id 1481506
 - Location of start within SEQ ID NO 44: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 47
 - Ceres seq_id 1481507
 - Location of start within SEQ ID NO 44: at 41 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 147980

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 48
- Ceres seq_id 1481516

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 49
- Ceres seq_id 1481517
- Location of start within SEQ ID NO 48: at 90 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 50
- Ceres seq_id 1481518
- Location of start within SEQ ID NO 48: at 186 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 51
- Ceres seq_id 1481519
- Location of start within SEQ ID NO 48: at 348 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 147983

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 52
- Ceres seq_id 1481520

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 53
- Ceres seq_id 1481521
- Location of start within SEQ ID NO 52: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 54
- Ceres seq_id 1481522
- Location of start within SEQ ID NO 52: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 55

- Ceres seq_id 1481523
- Location of start within SEQ ID NO 52: at 170 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 148070

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 56
 - Ceres seq_id 1481524
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 57
 - Ceres seq_id 1481525
 - Location of start within SEQ ID NO 56: at 448 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 58
 - Ceres seq_id 1481526
 - Location of start within SEQ ID NO 56: at 1241 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 59
 - Ceres seq_id 1481527
 - Location of start within SEQ ID NO 56: at 1403 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 148232

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 60
 - Ceres seq_id 1481532
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 61
 - Ceres seq_id 1481533
 - Location of start within SEQ ID NO 60: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 62
 - Ceres seq_id 1481534
 - Location of start within SEQ ID NO 60: at 108 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 63
 - Ceres seq_id 1481535
 - Location of start within SEQ ID NO 60: at 153 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 148887

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 64
- Ceres seq_id 1481540

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 65
- Ceres seq_id 1481541
- Location of start within SEQ ID NO 64: at 163 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 66
- Ceres seq_id 1481542
- Location of start within SEQ ID NO 64: at 220 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 67
- Ceres seq_id 1481543
- Location of start within SEQ ID NO 64: at 238 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 149204

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 68
- Ceres seq_id 1481544

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 69
- Ceres seq_id 1481545
- Location of start within SEQ ID NO 68: at 124 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 70
- Ceres seq_id 1481546
- Location of start within SEQ ID NO 68: at 178 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 71
- Ceres seq_id 1481547
- Location of start within SEQ ID NO 68: at 280 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 150293

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 72
- Ceres seq_id 1481564

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 73
- Ceres seq_id 1481565
- Location of start within SEQ ID NO 72: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 74
- Ceres seq_id 1481566
- Location of start within SEQ ID NO 72: at 60 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 75
- Ceres seq_id 1481567
- Location of start within SEQ ID NO 72: at 69 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 150540

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 76
- Ceres seq_id 1481580

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 77
- Ceres seq_id 1481581
- Location of start within SEQ ID NO 76: at 594 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 78

- Ceres seq_id 1481582
- Location of start within SEQ ID NO 76: at 630 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 79
- Ceres seq_id 1481583
- Location of start within SEQ ID NO 76: at 768 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 151413

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 80
- Ceres seq_id 1481596

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 81
- Ceres seq_id 1481597
- Location of start within SEQ ID NO 80: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 82
- Ceres seq_id 1481598
- Location of start within SEQ ID NO 80: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 83
- Ceres seq_id 1481599
- Location of start within SEQ ID NO 80: at 114 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 152305

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 84
- Ceres seq_id 1481613

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 85
- Ceres seq_id 1481614
- Location of start within SEQ ID NO 84: at 403 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 86
 - Ceres seq_id 1481615
 - Location of start within SEQ ID NO 84: at 562 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 87
 - Ceres seq_id 1481616
 - Location of start within SEQ ID NO 84: at 616 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 153154

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 88
- Ceres seq_id 1481621

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 89
- Ceres seq_id 1481622
- Location of start within SEQ ID NO 88: at 180 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 90
- Ceres seq_id 1481623
- Location of start within SEQ ID NO 88: at 291 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 91
- Ceres seq_id 1481624
- Location of start within SEQ ID NO 88: at 345 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 153808

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 92
- Ceres seq_id 1481625

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 93
- Ceres seq_id 1481626
- Location of start within SEQ ID NO 92: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 94
- Ceres seq_id 1481627
- Location of start within SEQ ID NO 92: at 88 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 95
- Ceres seq_id 1481628
- Location of start within SEQ ID NO 92: at 499 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 155661

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 96
- Ceres seq_id 1481632

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 97
- Ceres seq_id 1481633
- Location of start within SEQ ID NO 96: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 98
- Ceres seq_id 1481634
- Location of start within SEQ ID NO 96: at 9 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 155696

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 99
- Ceres seq_id 1481635

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 100
- Ceres seq_id 1481636
- Location of start within SEQ ID NO 99: at 152 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 101

- Ceres seq_id 1481637
- Location of start within SEQ ID NO 99: at 409 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 102
- Ceres seq_id 1481638
- Location of start within SEQ ID NO 99: at 457 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 155707

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 103
- Ceres seq_id 1481639

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 104
- Ceres seq_id 1481640
- Location of start within SEQ ID NO 103: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 105
- Ceres seq_id 1481641
- Location of start within SEQ ID NO 103: at 142 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 106
- Ceres seq_id 1481642
- Location of start within SEQ ID NO 103: at 712 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 156573

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 107
- Ceres seq_id 1481647

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 108
- Ceres seq_id 1481648
- Location of start within SEQ ID NO 107: at 156 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 109
 - Ceres seq_id 1481649
 - Location of start within SEQ ID NO 107: at 243 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 110
 - Ceres seq_id 1481650
 - Location of start within SEQ ID NO 107: at 429 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 1939

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 111
 - Ceres seq_id 1481668
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 112
 - Ceres seq_id 1481669
 - Location of start within SEQ ID NO 111: at 201 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 113
 - Ceres seq_id 1481670
 - Location of start within SEQ ID NO 111: at 405 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 20783

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 114
 - Ceres seq_id 1481681
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 115
 - Ceres seq_id 1481682
 - Location of start within SEQ ID NO 114: at 239 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 116
 - Ceres seq_id 1481683
 - Location of start within SEQ ID NO 114: at 398 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 218721

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 117
- Ceres seq_id 1481700

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 118
- Ceres seq_id 1481701
- Location of start within SEQ ID NO 117: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 119
- Ceres seq_id 1481702
- Location of start within SEQ ID NO 117: at 268 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 120
- Ceres seq_id 1481703
- Location of start within SEQ ID NO 117: at 292 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 218758

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 121
- Ceres seq_id 1481704

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 122
- Ceres seq_id 1481705
- Location of start within SEQ ID NO 121: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 123
- Ceres seq_id 1481706
- Location of start within SEQ ID NO 121: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 124

- Ceres seq_id 1481707
- Location of start within SEQ ID NO 121: at 60 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 220633

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 125
- Ceres seq_id 1481716

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 126
- Ceres seq_id 1481717
- Location of start within SEQ ID NO 125: at 55 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 127
- Ceres seq_id 1481718
- Location of start within SEQ ID NO 125: at 320 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 128
- Ceres seq_id 1481719
- Location of start within SEQ ID NO 125: at 395 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 220825

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 129
- Ceres seq_id 1481728

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 130
- Ceres seq_id 1481729
- Location of start within SEQ ID NO 129: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 131
- Ceres seq_id 1481730
- Location of start within SEQ ID NO 129: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 132
 - Ceres seq_id 1481731
 - Location of start within SEQ ID NO 129: at 214 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 220829

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 133
 - Ceres seq_id 1481732
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 134
 - Ceres seq_id 1481733
 - Location of start within SEQ ID NO 133: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 135
 - Ceres seq_id 1481734
 - Location of start within SEQ ID NO 133: at 169 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 136
 - Ceres seq_id 1481735
 - Location of start within SEQ ID NO 133: at 405 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 220846

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 137
 - Ceres seq_id 1481740
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 138
 - Ceres seq_id 1481741
 - Location of start within SEQ ID NO 137: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 139
 - Ceres seq_id 1481742
 - Location of start within SEQ ID NO 137: at 10 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 140
- Ceres seq_id 1481743
- Location of start within SEQ ID NO 137: at 22 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 220852

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 141
- Ceres seq_id 1481744

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 142
- Ceres seq_id 1481745
- Location of start within SEQ ID NO 141: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 143
- Ceres seq_id 1481746
- Location of start within SEQ ID NO 141: at 29 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 220854

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 144
- Ceres seq_id 1481747

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 145
- Ceres seq_id 1481748
- Location of start within SEQ ID NO 144: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 146
- Ceres seq_id 1481749
- Location of start within SEQ ID NO 144: at 74 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 147

- Ceres seq_id 1481750

- Location of start within SEQ ID NO 144: at 95 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 220915

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 148

- Ceres seq_id 1481755

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 149

- Ceres seq_id 1481756

- Location of start within SEQ ID NO 148: at 178 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 220934

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 150

- Ceres seq_id 1481764

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 151

- Ceres seq_id 1481765

- Location of start within SEQ ID NO 150: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 152

- Ceres seq_id 1481766

- Location of start within SEQ ID NO 150: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 220944

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 153

- Ceres seq_id 1481770

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 154

- Ceres seq_id 1481771

- Location of start within SEQ ID NO 153: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 155

- Ceres seq_id 1481772

- Location of start within SEQ ID NO 153: at 96 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 226475

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 156
- Ceres seq_id 1481775

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 157
- Ceres seq_id 1481776
- Location of start within SEQ ID NO 156: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 158
- Ceres seq_id 1481777
- Location of start within SEQ ID NO 156: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 159
- Ceres seq_id 1481778
- Location of start within SEQ ID NO 156: at 255 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 226483

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 160
- Ceres seq_id 1481779

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 161
- Ceres seq_id 1481780
- Location of start within SEQ ID NO 160: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 226501

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 162
- Ceres seq_id 1481789

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 163
- Ceres seq_id 1481790
- Location of start within SEQ ID NO 162: at 109 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 164
- Ceres seq_id 1481791
- Location of start within SEQ ID NO 162: at 229 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 226516

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 165
- Ceres seq_id 1481792

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 166
- Ceres seq_id 1481793
- Location of start within SEQ ID NO 165: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 167
- Ceres seq_id 1481794
- Location of start within SEQ ID NO 165: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 168
- Ceres seq_id 1481795
- Location of start within SEQ ID NO 165: at 67 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 227154

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 169
- Ceres seq_id 1481796

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 170
- Ceres seq_id 1481797
- Location of start within SEQ ID NO 169: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 171

- Ceres seq_id 1481798
- Location of start within SEQ ID NO 169: at 118 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 227202

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 172
- Ceres seq_id 1481799

Maximum Length Sequence corresponding to clone ID 227468

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 173
- Ceres seq_id 1481800

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 174
- Ceres seq_id 1481801
- Location of start within SEQ ID NO 173: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 175
- Ceres seq_id 1481802
- Location of start within SEQ ID NO 173: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 176
- Ceres seq_id 1481803
- Location of start within SEQ ID NO 173: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 227480

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 177
- Ceres seq_id 1481808

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 178
- Ceres seq_id 1481809
- Location of start within SEQ ID NO 177: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 179
- Ceres seq_id 1481810
- Location of start within SEQ ID NO 177: at 15 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 180
- Ceres seq_id 1481811
- Location of start within SEQ ID NO 177: at 45 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 227719

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 181
- Ceres seq_id 1481815

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 182
- Ceres seq_id 1481816
- Location of start within SEQ ID NO 181: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 183
- Ceres seq_id 1481817
- Location of start within SEQ ID NO 181: at 40 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 184
- Ceres seq_id 1481818
- Location of start within SEQ ID NO 181: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 227812

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 185
- Ceres seq_id 1481819

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 186
- Ceres seq_id 1481820
- Location of start within SEQ ID NO 185: at 51 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 187
- Ceres seq_id 1481821
- Location of start within SEQ ID NO 185: at 57 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 188
- Ceres seq_id 1481822
- Location of start within SEQ ID NO 185: at 66 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 227814

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 189
- Ceres seq_id 1481823

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 190
- Ceres seq_id 1481824
- Location of start within SEQ ID NO 189: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 191
- Ceres seq_id 1481825
- Location of start within SEQ ID NO 189: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 192
- Ceres seq_id 1481826
- Location of start within SEQ ID NO 189: at 70 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 227825

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 193
- Ceres seq_id 1481827

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 194
- Ceres seq_id 1481828
- Location of start within SEQ ID NO 193: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 195
- Ceres seq_id 1481829
- Location of start within SEQ ID NO 193: at 167 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 196
- Ceres seq_id 1481830
- Location of start within SEQ ID NO 193: at 215 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 229883

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 197
- Ceres seq_id 1481831

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 198
- Ceres seq_id 1481832
- Location of start within SEQ ID NO 197: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 199
- Ceres seq_id 1481833
- Location of start within SEQ ID NO 197: at 69 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 200
- Ceres seq_id 1481834
- Location of start within SEQ ID NO 197: at 96 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 231825

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 201
- Ceres seq_id 1481839

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 202
- Ceres seq_id 1481840
- Location of start within SEQ ID NO 201: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 203
- Ceres seq_id 1481841
- Location of start within SEQ ID NO 201: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 204
- Ceres seq_id 1481842
- Location of start within SEQ ID NO 201: at 272 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 232410

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 205
- Ceres seq_id 1481847

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 206
- Ceres seq_id 1481848
- Location of start within SEQ ID NO 205: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 207
- Ceres seq_id 1481849
- Location of start within SEQ ID NO 205: at 44 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 208
- Ceres seq_id 1481850
- Location of start within SEQ ID NO 205: at 128 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 232492

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 209
- Ceres seq_id 1481851

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 210
- Ceres seq_id 1481852
- Location of start within SEQ ID NO 209: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 211
- Ceres seq_id 1481853
- Location of start within SEQ ID NO 209: at 62 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 212
- Ceres seq_id 1481854
- Location of start within SEQ ID NO 209: at 122 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 237301

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 213
- Ceres seq_id 1481859

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 214
- Ceres seq_id 1481860
- Location of start within SEQ ID NO 213: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 215
- Ceres seq_id 1481861
- Location of start within SEQ ID NO 213: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 216
- Ceres seq_id 1481862
- Location of start within SEQ ID NO 213: at 5 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 237328

(A) Polynucleotide Sequence

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- Pat. Appln. SEQ ID NO 217

- Ceres seq_id 1481863

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 218

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- Ceres seq_id 1481864
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- Location of start within SEQ ID NO 217: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 219

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- Ceres seq_id 1481865
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- Location of start within SEQ ID NO 217: at 71 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 246496

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 220

- Ceres seq_id 1481873

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 221

- Ceres seq id 1481874

- Location of start within SEQ ID NO 220: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 222

- Ceres seq id 1481875

- Location of start within SEQ ID NO 220: at 379 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 246936

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 223

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- Ceres seq id 1481885
```

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 224

- Ceres seq id 1481886

- Location of start within SEQ ID NO 223: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 225

- Ceres seq id 1481887

- Location of start within SEQ ID NO 223: at 48 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 226
- Ceres seq_id 1481888
- Location of start within SEQ ID NO 223: at 109 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247196

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 227
- Ceres seq_id 1481893

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 228
- Ceres seq_id 1481894
- Location of start within SEQ ID NO 227: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 229
- Ceres seq_id 1481895
- Location of start within SEQ ID NO 227: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 230
- Ceres seq_id 1481896
- Location of start within SEQ ID NO 227: at 271 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247299

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 231
- Ceres seq_id 1481897

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 232
- Ceres seq_id 1481898
- Location of start within SEQ ID NO 231: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 233
- Ceres seq_id 1481899
- Location of start within SEQ ID NO 231: at 37 nt.
```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

#### (D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 234
- Ceres seq_id 1481900
- Location of start within SEQ ID NO 231: at 70 nt.
```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 250561

(A) Polynucleotide Sequence

- ```

- Pat. Appln. SEQ ID NO 235
- Ceres seq_id 1481901
(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 236
- Ceres seq_id 1481902
- Location of start within

```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 250647

(A) Polynucleotide Sequence

- ```

- Pat. Appln. SEQ ID NO 237
- Ceres seq_id 1481903
(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 238
- Ceres seq_id 1481904
- Location of start within SEQ ID NO 237: at 2 nt.

```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 239
- Ceres seq_id 1481905
- Location of start within SEQ ID NO 237: at 68 nt.
```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 240
- Ceres seq_id 1481906
- Location of start within SEQ ID NO 237: at 116 nt.
```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

Maximum Length Sequence corresponding to clone ID 250663

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 241
- Ceres seq_id 1481907

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 242
- Ceres seq_id 1481908
- Location of start within SEQ ID NO 241: at 165 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 250775

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 243
- Ceres seq_id 1481913

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 244
- Ceres seq_id 1481914
- Location of start within SEQ ID NO 243: at 126 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 245
- Ceres seq_id 1481915
- Location of start within SEQ ID NO 243: at 291 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 251921

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 246
- Ceres seq_id 1481916

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 247
- Ceres seq_id 1481917
- Location of start within SEQ ID NO 246: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 248
- Ceres seq_id 1481918
- Location of start within SEQ ID NO 246: at 231 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

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Table 1

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Maximum Length Sequence corresponding to clone ID 252000

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 249
- Ceres seq_id 1481919

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 250
- Ceres seq_id 1481920
- Location of start within SEQ ID NO 249: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 251
- Ceres seq_id 1481921
- Location of start within SEQ ID NO 249: at 48 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 252
- Ceres seq_id 1481922
- Location of start within SEQ ID NO 249: at 198 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 252002

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 253
- Ceres seq_id 1481923

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 254
- Ceres seq_id 1481924
- Location of start within SEQ ID NO 253: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 255
- Ceres seq_id 1481925
- Location of start within SEQ ID NO 253: at 424 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 257043

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 256
- Ceres seq_id 1481941

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 257

- Ceres seq_id 1481942
- Location of start within SEQ ID NO 256: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 258
- Ceres seq_id 1481943
- Location of start within SEQ ID NO 256: at 71 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 259
- Ceres seq_id 1481944
- Location of start within SEQ ID NO 256: at 74 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 257207

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 260
- Ceres seq_id 1481949

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 261
- Ceres seq_id 1481950
- Location of start within SEQ ID NO 260: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 262
- Ceres seq_id 1481951
- Location of start within SEQ ID NO 260: at 276 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 263
- Ceres seq_id 1481952
- Location of start within SEQ ID NO 260: at 454 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 265955

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 264

- Ceres seq_id 1481965
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 265
 - Ceres seq_id 1481966
 - Location of start within SEQ ID NO 264: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 266
 - Ceres seq_id 1481967
 - Location of start within SEQ ID NO 264: at 103 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 267
 - Ceres seq_id 1481968
 - Location of start within SEQ ID NO 264: at 327 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 266374

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 268
 - Ceres seq_id 1481973
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 269
 - Ceres seq_id 1481974
 - Location of start within SEQ ID NO 268: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 270
 - Ceres seq_id 1481975
 - Location of start within SEQ ID NO 268: at 113 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 266934

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 271
 - Ceres seq_id 1481976
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 272
 - Ceres seq_id 1481977
 - Location of start within SEQ ID NO 271: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 273
- Ceres seq_id 1481978
- Location of start within SEQ ID NO 271: at 5 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 274
- Ceres seq_id 1481979
- Location of start within SEQ ID NO 271: at 65 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 266951

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 275
- Ceres seq_id 1481980

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 276
- Ceres seq_id 1481981
- Location of start within SEQ ID NO 275: at 54 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 277
- Ceres seq_id 1481982
- Location of start within SEQ ID NO 275: at 307 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 267031

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 278
- Ceres seq_id 1481983

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 279
- Ceres seq_id 1481984
- Location of start within SEQ ID NO 278: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 280

- Ceres seq_id 1481985
- Location of start within SEQ ID NO 278: at 31 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 267032

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 281
- Ceres seq_id 1481986

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 282
- Ceres seq_id 1481987
- Location of start within SEQ ID NO 281: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 283
- Ceres seq_id 1481988
- Location of start within SEQ ID NO 281: at 38 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 284
- Ceres seq_id 1481989
- Location of start within SEQ ID NO 281: at 131 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 267296

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 285
- Ceres seq_id 1481990

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 286
- Ceres seq_id 1481991
- Location of start within SEQ ID NO 285: at 157 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 287
- Ceres seq_id 1481992
- Location of start within SEQ ID NO 285: at 163 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 288
 - Ceres seq_id 1481993
 - Location of start within SEQ ID NO 285: at 412 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 267626

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 289
- Ceres seq_id 1481994

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 290
 - Ceres seq_id 1481995
 - Location of start within SEQ ID NO 289: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 291
 - Ceres seq_id 1481996
 - Location of start within SEQ ID NO 289: at 157 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 292
 - Ceres seq_id 1481997
 - Location of start within SEQ ID NO 289: at 175 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 268353

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 293
- Ceres seq_id 1482009

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 294
 - Ceres seq_id 1482010
 - Location of start within SEQ ID NO 293: at 72 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 295
 - Ceres seq_id 1482011
 - Location of start within SEQ ID NO 293: at 144 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 296
- Ceres seq_id 1482012
- Location of start within SEQ ID NO 293: at 321 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 268652

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 297
- Ceres seq_id 1482013

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 298
- Ceres seq_id 1482014
- Location of start within SEQ ID NO 297: at 33 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 299
- Ceres seq_id 1482015
- Location of start within SEQ ID NO 297: at 156 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 268680

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 300
- Ceres seq_id 1482016

Maximum Length Sequence corresponding to clone ID 269248

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 301
- Ceres seq_id 1482021

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 302
- Ceres seq_id 1482022
- Location of start within SEQ ID NO 301: at 175 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 303
- Ceres seq_id 1482023
- Location of start within SEQ ID NO 301: at 190 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 304
 - Ceres seq_id 1482024
 - Location of start within SEQ ID NO 301: at 262 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 270513

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 305
 - Ceres seq_id 1482029
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 306
 - Ceres seq_id 1482030
 - Location of start within SEQ ID NO 305: at 86 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 307
 - Ceres seq_id 1482031
 - Location of start within SEQ ID NO 305: at 194 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 308
 - Ceres seq_id 1482032
 - Location of start within SEQ ID NO 305: at 203 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 270518

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 309
 - Ceres seq_id 1482033
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 310
 - Ceres seq_id 1482034
 - Location of start within SEQ ID NO 309: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 311
 - Ceres seq_id 1482035
 - Location of start within SEQ ID NO 309: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 312
 - Ceres seq_id 1482036
 - Location of start within SEQ ID NO 309: at 119 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 271717

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 313
 - Ceres seq_id 1482041

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 314
 - Ceres seq_id 1482042
 - Location of start within SEQ ID NO 313: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 315
 - Ceres seq_id 1482043
 - Location of start within SEQ ID NO 313: at 491 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 316
 - Ceres seq_id 1482044
 - Location of start within SEQ ID NO 313: at 518 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 271756

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 317
 - Ceres seq_id 1482045

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 318
 - Ceres seq_id 1482046
 - Location of start within SEQ ID NO 317: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 319
- Ceres seq_id 1482047
- Location of start within SEQ ID NO 317: at 71 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 320
- Ceres seq_id 1482048
- Location of start within SEQ ID NO 317: at 149 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 271765

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 321
- Ceres seq_id 1482049

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 322
- Ceres seq_id 1482050
- Location of start within SEQ ID NO 321: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 323
- Ceres seq_id 1482051
- Location of start within SEQ ID NO 321: at 27 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 324
- Ceres seq_id 1482052
- Location of start within SEQ ID NO 321: at 45 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 271936

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 325
- Ceres seq_id 1482053

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 326
- Ceres seq_id 1482054
- Location of start within SEQ ID NO 325: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272121

(A) Polynucleotide Sequence

- ```
- Pat. Appln. SEQ ID NO 327
- Ceres seq_id 1482066
```

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 328
- Ceres seq_id 1482067
- Location of start within SEQ ID NO 327: at 2 nt.
```

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 329
- Ceres seq_id 1482068
- Location of start within SEQ ID NO 327: at 113 nt.
```

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

#### (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272124

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 330  
- Ceres seq id 1482069

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 331
- Ceres seq_id 1482070
- Location of start within SEQ ID NO 330: at 3 nt.
```

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 332
- Ceres seq_id 1482071
- Location of start within SEO ID NO 330: at 162 nt.
```

(C) Nomination and Annotation of Domains within Predicted

## Polypeptide(s)

#### (D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 333
- Ceres seq\_id 1482072
- Location of start within SEQ ID NO 330: at 186 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

#### (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272142

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 334  
- Ceres seq id 1482073

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 335
- Ceres seq\_id 1482074
- Location of start within SEQ ID NO 334: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 336
- Ceres seq\_id 1482075
- Location of start within SEQ ID NO 334: at 272 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 337
- Ceres seq\_id 1482076
- Location of start within SEQ ID NO 334: at 344 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272155

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 338
- Ceres seq\_id 1482081

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 339
- Ceres seq\_id 1482082
- Location of start within SEQ ID NO 338: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 340
- Ceres seq\_id 1482083
- Location of start within SEQ ID NO 338: at 8 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 341
- Ceres seq\_id 1482084
- Location of start within SEQ ID NO 338: at 178 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272156



- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 342
  - Ceres seq\_id 1482085
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 343
  - Ceres seq\_id 1482086
  - Location of start within SEQ ID NO 342: at 302 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272162

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 344
  - Ceres seq\_id 1482091
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 345
  - Ceres seq\_id 1482092
  - Location of start within SEQ ID NO 344: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 346
  - Ceres seq\_id 1482093
  - Location of start within SEQ ID NO 344: at 3 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 347
  - Ceres seq\_id 1482094
  - Location of start within SEQ ID NO 344: at 102 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272166

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 348
  - Ceres seq\_id 1482095
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 349
  - Ceres seq\_id 1482096
  - Location of start within SEQ ID NO 348: at 229 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 350
  - Ceres seq\_id 1482097

- Location of start within SEQ ID NO 348: at 322 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272200

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 351

- Ceres seq\_id 1482102

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 352

- Ceres seq\_id 1482103

- Location of start within SEQ ID NO 351: at 282 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 353

- Ceres seq\_id 1482104

- Location of start within SEQ ID NO 351: at 309 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 354

- Ceres seq\_id 1482105

- Location of start within SEQ ID NO 351: at 366 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272214

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 355

- Ceres seq\_id 1482106

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 356

- Ceres seq\_id 1482107

- Location of start within SEQ ID NO 355: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 357

- Ceres seq\_id 1482108

- Location of start within SEQ ID NO 355: at 240 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

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Maximum Length Sequence corresponding to clone ID 272239

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 358
- Ceres seq\_id 1482113

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 359
- Ceres seq\_id 1482114
- Location of start within SEQ ID NO 358: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 360
- Ceres seq\_id 1482115
- Location of start within SEQ ID NO 358: at 97 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 361
- Ceres seq\_id 1482116
- Location of start within SEQ ID NO 358: at 121 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272250

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 362
- Ceres seq\_id 1482117

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 363
- Ceres seq\_id 1482118
- Location of start within SEQ ID NO 362: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 364
- Ceres seq\_id 1482119
- Location of start within SEQ ID NO 362: at 69 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 365
- Ceres seq\_id 1482120
- Location of start within SEQ ID NO 362: at 264 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272258

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 366
- Ceres seq\_id 1482121

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 367
- Ceres seq\_id 1482122
- Location of start within SEQ ID NO 366: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272301

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 368
- Ceres seq\_id 1482127

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 369
- Ceres seq\_id 1482128
- Location of start within SEQ ID NO 368: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 370
- Ceres seq\_id 1482129
- Location of start within SEQ ID NO 368: at 92 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 371
- Ceres seq\_id 1482130
- Location of start within SEQ ID NO 368: at 529 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272312

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 372
- Ceres seq\_id 1482131

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 373
- Ceres seq\_id 1482132
- Location of start within SEQ ID NO 372: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 374
  - Ceres seq\_id 1482133
  - Location of start within SEQ ID NO 372: at 42 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 375
  - Ceres seq\_id 1482134
  - Location of start within SEQ ID NO 372: at 168 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272389

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 376
  - Ceres seq\_id 1482135
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 377
  - Ceres seq\_id 1482136
  - Location of start within SEQ ID NO 376: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 378
  - Ceres seq\_id 1482137
  - Location of start within SEQ ID NO 376: at 7 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272410

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 379
  - Ceres seq\_id 1482142
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 380
  - Ceres seq\_id 1482143
  - Location of start within SEQ ID NO 379: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 381
  - Ceres seq\_id 1482144
  - Location of start within SEQ ID NO 379: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 382
- Ceres seq\_id 1482145
- Location of start within SEQ ID NO 379: at 92 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272459

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 383
- Ceres seq\_id 1482153

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 384
- Ceres seq\_id 1482154
- Location of start within SEQ ID NO 383: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 385
- Ceres seq\_id 1482155
- Location of start within SEQ ID NO 383: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 386
- Ceres seq\_id 1482156
- Location of start within SEQ ID NO 383: at 326 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272486

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 387
- Ceres seq\_id 1482157

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 388
- Ceres seq\_id 1482158
- Location of start within SEQ ID NO 387: at 139 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 389
- Ceres seq\_id 1482159
- Location of start within SEQ ID NO 387: at 301 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272506

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 390
- Ceres seq\_id 1482164

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 391
- Ceres seq\_id 1482165
- Location of start within SEQ ID NO 390: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 392
- Ceres seq\_id 1482166
- Location of start within SEQ ID NO 390: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 275387

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 393
- Ceres seq\_id 1482167

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 394
- Ceres seq\_id 1482168
- Location of start within SEQ ID NO 393: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 275402

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 395
- Ceres seq\_id 1482169

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 396
- Ceres seq\_id 1482170
- Location of start within SEQ ID NO 395: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 397
- Ceres seq\_id 1482171

- Location of start within SEQ ID NO 395: at 79 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 398

- Ceres seq\_id 1482172

- Location of start within SEQ ID NO 395: at 360 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 275778

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 399

- Ceres seq\_id 1482177

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 400

- Ceres seq\_id 1482178

- Location of start within SEQ ID NO 399: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 401

- Ceres seq\_id 1482179

- Location of start within SEQ ID NO 399: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 402

- Ceres seq\_id 1482180

- Location of start within SEQ ID NO 399: at 277 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 275803

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 403

- Ceres seq\_id 1482188

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 404

- Ceres seq\_id 1482189

- Location of start within SEQ ID NO 403: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences



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Maximum Length Sequence corresponding to clone ID 276193

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 405
- Ceres seq\_id 1482193

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 406
- Ceres seq\_id 1482194
- Location of start within SEQ ID NO 405: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 294676

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 407
- Ceres seq\_id 1482205

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 408
- Ceres seq\_id 1482206
- Location of start within SEQ ID NO 407: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296069

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 409
- Ceres seq\_id 1482207

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 410
- Ceres seq\_id 1482208
- Location of start within SEQ ID NO 409: at 124 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 411
- Ceres seq\_id 1482209
- Location of start within SEQ ID NO 409: at 226 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 412
- Ceres seq\_id 1482210
- Location of start within SEQ ID NO 409: at 271 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296091

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 413

- Ceres seq\_id 1482217

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 414

- Ceres seq\_id 1482218

- Location of start within SEQ ID NO 413: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296096

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 415

- Ceres seq\_id 1482219

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 416

- Ceres seq\_id 1482220

- Location of start within SEQ ID NO 415: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 417

- Ceres seq\_id 1482221

- Location of start within SEQ ID NO 415: at 72 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296205

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 418

- Ceres seq\_id 1482230

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 419

- Ceres seq\_id 1482231

- Location of start within SEQ ID NO 418: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 420

- Ceres seq\_id 1482232

- Location of start within SEQ ID NO 418: at 125 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 421

- Ceres seq\_id 1482233

- Location of start within SEQ ID NO 418: at 152 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296209

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 422
- Ceres seq\_id 1482234

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 423
- Ceres seq\_id 1482235
- Location of start within SEQ ID NO 422: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 424
- Ceres seq\_id 1482236
- Location of start within SEQ ID NO 422: at 221 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 425
- Ceres seq\_id 1482237
- Location of start within SEQ ID NO 422: at 287 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296211

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 426
- Ceres seq\_id 1482238

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 427
- Ceres seq\_id 1482239
- Location of start within SEQ ID NO 426: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 428
- Ceres seq\_id 1482240
- Location of start within SEQ ID NO 426: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296215

(A) Polynucleotide Sequence  
- Pat. Appln. SEQ ID NO 429  
- Ceres seq\_id 1482245  
(B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 430  
- Ceres seq\_id 1482246  
- Location of start within SEQ ID NO 429: at 2 nt.  
(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)  
(D) Related Amino Acid Sequences

(B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 431  
- Ceres seq\_id 1482247  
- Location of start within SEQ ID NO 429: at 176 nt.  
(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)  
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296228

(A) Polynucleotide Sequence  
- Pat. Appln. SEQ ID NO 432  
- Ceres seq\_id 1482248  
(B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 433  
- Ceres seq\_id 1482249  
- Location of start within SEQ ID NO 432: at 120 nt.  
(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)  
(D) Related Amino Acid Sequences

(B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 434  
- Ceres seq\_id 1482250  
- Location of start within SEQ ID NO 432: at 249 nt.  
(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)  
(D) Related Amino Acid Sequences

(B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 435  
- Ceres seq\_id 1482251  
- Location of start within SEQ ID NO 432: at 312 nt.  
(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)  
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296237

(A) Polynucleotide Sequence  
- Pat. Appln. SEQ ID NO 436  
- Ceres seq\_id 1482254  
(B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 437  
- Ceres seq\_id 1482255

- Location of start within SEQ ID NO 436: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 438

- Ceres seq\_id 1482256

- Location of start within SEQ ID NO 436: at 58 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296246

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 439

- Ceres seq\_id 1482257

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 440

- Ceres seq\_id 1482258

- Location of start within SEQ ID NO 439: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 441

- Ceres seq\_id 1482259

- Location of start within SEQ ID NO 439: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 442

- Ceres seq\_id 1482260

- Location of start within SEQ ID NO 439: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296620

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 443

- Ceres seq\_id 1482261

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 444

- Ceres seq\_id 1482262

- Location of start within SEQ ID NO 443: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 445
- Ceres seq\_id 1482263
- Location of start within SEQ ID NO 443: at 313 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 296648

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 446
- Ceres seq\_id 1482264

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 447
- Ceres seq\_id 1482265
- Location of start within SEQ ID NO 446: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 297691

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 448
- Ceres seq\_id 1482270

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 449
- Ceres seq\_id 1482271
- Location of start within SEQ ID NO 448: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 450
- Ceres seq\_id 1482272
- Location of start within SEQ ID NO 448: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 451
- Ceres seq\_id 1482273
- Location of start within SEQ ID NO 448: at 199 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 297711

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 452
- Ceres seq\_id 1482274

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 453

- Ceres seq\_id 1482275
- Location of start within SEQ ID NO 452: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 454
- Ceres seq\_id 1482276
- Location of start within SEQ ID NO 452: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 455
- Ceres seq\_id 1482277
- Location of start within SEQ ID NO 452: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 299123

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 456
- Ceres seq\_id 1482282

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 457
- Ceres seq\_id 1482283
- Location of start within SEQ ID NO 456: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 458
- Ceres seq\_id 1482284
- Location of start within SEQ ID NO 456: at 223 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 459
- Ceres seq\_id 1482285
- Location of start within SEQ ID NO 456: at 286 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 299990

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 460

- Ceres seq\_id 1482289

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 461

- Ceres seq\_id 1482290

- Location of start within SEQ ID NO 460: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 462

- Ceres seq\_id 1482291

- Location of start within SEQ ID NO 460: at 21 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 463

- Ceres seq\_id 1482292

- Location of start within SEQ ID NO 460: at 123 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 299991

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 464

- Ceres seq\_id 1482293

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 465

- Ceres seq\_id 1482294

- Location of start within SEQ ID NO 464: at 184 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 466

- Ceres seq\_id 1482295

- Location of start within SEQ ID NO 464: at 226 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 467

- Ceres seq\_id 1482296

- Location of start within SEQ ID NO 464: at 349 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences



Maximum Length Sequence corresponding to clone ID 300985

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 468
- Ceres seq\_id 1482297

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 469
- Ceres seq\_id 1482298
- Location of start within SEQ ID NO 468: at 72 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 300986

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 470
- Ceres seq\_id 1482299

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 471
- Ceres seq\_id 1482300
- Location of start within SEQ ID NO 470: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 472
- Ceres seq\_id 1482301
- Location of start within SEQ ID NO 470: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 300987

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 473
- Ceres seq\_id 1482302

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 474
- Ceres seq\_id 1482303
- Location of start within SEQ ID NO 473: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301009

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 475
- Ceres seq\_id 1482307

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 476
- Ceres seq\_id 1482308
- Location of start within SEQ ID NO 475: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 477
  - Ceres seq\_id 1482309
  - Location of start within SEQ ID NO 475: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301084

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 478
  - Ceres seq\_id 1482322
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 479
  - Ceres seq\_id 1482323
  - Location of start within SEQ ID NO 478: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 480
  - Ceres seq\_id 1482324
  - Location of start within SEQ ID NO 478: at 86 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 481
  - Ceres seq\_id 1482325
  - Location of start within SEQ ID NO 478: at 319 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301128

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 482
  - Ceres seq\_id 1482334
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 483
  - Ceres seq\_id 1482335
  - Location of start within SEQ ID NO 482: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301143

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 484
  - Ceres seq\_id 1482336

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 485
  - Ceres seq\_id 1482337
  - Location of start within SEQ ID NO 484: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)  
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 486
  - Ceres seq\_id 1482338
  - Location of start within SEQ ID NO 484: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)  
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301452

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 487
  - Ceres seq\_id 1482339
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 488
  - Ceres seq\_id 1482340
  - Location of start within SEQ ID NO 487: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)  
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 489
  - Ceres seq\_id 1482341
  - Location of start within SEQ ID NO 487: at 96 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)  
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 490
  - Ceres seq\_id 1482342
  - Location of start within SEQ ID NO 487: at 138 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)  
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301456

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 491
  - Ceres seq\_id 1482346
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 492
  - Ceres seq\_id 1482347
  - Location of start within SEQ ID NO 491: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 493
- Ceres seq\_id 1482348
- Location of start within SEQ ID NO 491: at 120 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301464

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 494
- Ceres seq\_id 1482349

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 495
- Ceres seq\_id 1482350
- Location of start within SEQ ID NO 494: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 496
- Ceres seq\_id 1482351
- Location of start within SEQ ID NO 494: at 135 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 497
- Ceres seq\_id 1482352
- Location of start within SEQ ID NO 494: at 195 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301481

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 498
- Ceres seq\_id 1482353

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 499
- Ceres seq\_id 1482354
- Location of start within SEQ ID NO 498: at 98 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 500

- Ceres seq\_id 1482355

- Location of start within SEQ ID NO 498: at 242 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301483

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 501

- Ceres seq\_id 1482356

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 502

- Ceres seq\_id 1482357

- Location of start within SEQ ID NO 501: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 503

- Ceres seq\_id 1482358

- Location of start within SEQ ID NO 501: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301504

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 504

- Ceres seq\_id 1482359

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 505

- Ceres seq\_id 1482360

- Location of start within SEQ ID NO 504: at 14 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 506

- Ceres seq\_id 1482361

- Location of start within SEQ ID NO 504: at 294 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 507

- Ceres seq\_id 1482362

- Location of start within SEQ ID NO 504: at 297 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(A) Polynucleotide Sequence

- ```

- Pat. Appln. SEQ ID NO 508
- Ceres seq_id 1482363
(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 509
- Ceres seq_id 1482364
- Location of start within SEQ ID NO 508: at 51 nt.

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(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 510
 - Ceres seq_id 1482365
 - Location of start within SEQ ID NO 508: at 86 nt.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 511
 - Ceres seq_id 1482366
 - Location of start within SEQ ID NO 508: at 205 nt.

(D) Related Amino Acid Sequences

(A) Polynucleotide Sequence

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 513
 - Ceres seq_id 1482372
 - Location of start within SEQ ID NO 512: at 2 nt.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 514
 - Ceres seq_id 1482373
 - Location of start within SEQ ID NO 512: at 206 nt.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 515
 - Ceres seq_id 1482374
 - Location of start within SEQ ID NO 512: at 224 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301552

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 516
- Ceres seq_id 1482375

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 517
- Ceres seq_id 1482376
- Location of start within SEQ ID NO 516: at 151 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 518
- Ceres seq_id 1482377
- Location of start within SEQ ID NO 516: at 166 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301559

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 519
- Ceres seq_id 1482378

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 520
- Ceres seq_id 1482379
- Location of start within SEQ ID NO 519: at 83 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 521
- Ceres seq_id 1482380
- Location of start within SEQ ID NO 519: at 113 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 522
- Ceres seq_id 1482381
- Location of start within SEQ ID NO 519: at 143 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301584

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 523
- Ceres seq_id 1482382

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 524
- Ceres seq_id 1482383
- Location of start within SEQ ID NO 523: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 525
- Ceres seq_id 1482384
- Location of start within SEQ ID NO 523: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 526
- Ceres seq_id 1482385
- Location of start within SEQ ID NO 523: at 191 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301586

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 527
- Ceres seq_id 1482386

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 528
- Ceres seq_id 1482387
- Location of start within SEQ ID NO 527: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 529
- Ceres seq_id 1482388
- Location of start within SEQ ID NO 527: at 34 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 530
- Ceres seq_id 1482389
- Location of start within SEQ ID NO 527: at 437 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301930

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 531
- Ceres seq_id 1482398

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 532
- Ceres seq_id 1482399
- Location of start within SEQ ID NO 531: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 533
- Ceres seq_id 1482400
- Location of start within SEQ ID NO 531: at 98 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 534
- Ceres seq_id 1482401
- Location of start within SEQ ID NO 531: at 425 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301956

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 535
- Ceres seq_id 1482402

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 536
- Ceres seq_id 1482403
- Location of start within SEQ ID NO 535: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301961

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 537
- Ceres seq_id 1482404

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 538
- Ceres seq_id 1482405
- Location of start within SEQ ID NO 537: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

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- Pat. Appln. SEQ ID NO 539
- Ceres seq_id 1482406
- Location of start within SEQ ID NO 537: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 540
- Ceres seq_id 1482407
- Location of start within SEQ ID NO 537: at 182 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301981

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 541
- Ceres seq_id 1482408

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 542
- Ceres seq_id 1482409
- Location of start within SEQ ID NO 541: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 543
- Ceres seq_id 1482410
- Location of start within SEQ ID NO 541: at 442 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 301994

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 544
- Ceres seq_id 1482411

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 545
- Ceres seq_id 1482412
- Location of start within SEQ ID NO 544: at 94 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 546
- Ceres seq_id 1482413
- Location of start within SEQ ID NO 544: at 155 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 547
- Ceres seq_id 1482414
- Location of start within SEQ ID NO 544: at 620 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 302016

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 548
- Ceres seq_id 1482415

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 549
- Ceres seq_id 1482416
- Location of start within SEQ ID NO 548: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 550
- Ceres seq_id 1482417
- Location of start within SEQ ID NO 548: at 107 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 302030

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 551
- Ceres seq_id 1482418

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 552
- Ceres seq_id 1482419
- Location of start within SEQ ID NO 551: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 553
- Ceres seq_id 1482420
- Location of start within SEQ ID NO 551: at 105 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 554
- Ceres seq_id 1482421
- Location of start within SEQ ID NO 551: at 135 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 302415

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 555
 - Ceres seq_id 1482422
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 556
 - Ceres seq_id 1482423
 - Location of start within SEQ ID NO 555: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 304700

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 557
 - Ceres seq_id 1482424
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 558
 - Ceres seq_id 1482425
 - Location of start within SEQ ID NO 557: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 559
 - Ceres seq_id 1482426
 - Location of start within SEQ ID NO 557: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 560
 - Ceres seq_id 1482427
 - Location of start within SEQ ID NO 557: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 304743

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 561
 - Ceres seq_id 1482428
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 562
 - Ceres seq_id 1482429
 - Location of start within SEQ ID NO 561: at 206 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 304764

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 563
- Ceres seq_id 1482430

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 564
- Ceres seq_id 1482431
- Location of start within SEQ ID NO 563: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 565
- Ceres seq_id 1482432
- Location of start within SEQ ID NO 563: at 11 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 566
- Ceres seq_id 1482433
- Location of start within SEQ ID NO 563: at 86 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 304769

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 567
- Ceres seq_id 1482434

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 568
- Ceres seq_id 1482435
- Location of start within SEQ ID NO 567: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 569
- Ceres seq_id 1482436
- Location of start within SEQ ID NO 567: at 9 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 570

- Ceres seq_id 1482437
- Location of start within SEQ ID NO 567: at 18 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 305124

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 571
- Ceres seq_id 1482438

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 572
- Ceres seq_id 1482439
- Location of start within SEQ ID NO 571: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 30994

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 573
- Ceres seq_id 1482444

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 574
- Ceres seq_id 1482445
- Location of start within SEQ ID NO 573: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 575
- Ceres seq_id 1482446
- Location of start within SEQ ID NO 573: at 134 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 576
- Ceres seq_id 1482447
- Location of start within SEQ ID NO 573: at 143 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 33213

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 577
- Ceres seq_id 1482457

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 578
- Ceres seq_id 1482458
- Location of start within SEQ ID NO 577: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 579
 - Ceres seq_id 1482459
 - Location of start within SEQ ID NO 577: at 35 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 35310

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 580
 - Ceres seq_id 1482460

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 581
 - Ceres seq_id 1482461
 - Location of start within SEQ ID NO 580: at 119 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 582
 - Ceres seq_id 1482462
 - Location of start within SEQ ID NO 580: at 203 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 583
 - Ceres seq_id 1482463
 - Location of start within SEQ ID NO 580: at 470 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 37200

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 584
 - Ceres seq_id 1482481

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 585
 - Ceres seq_id 1482482
 - Location of start within SEQ ID NO 584: at 110 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence

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- Pat. Appln. SEQ ID NO 586
- Ceres seq_id 1482483
- Location of start within SEQ ID NO 584: at 233 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 587
- Ceres seq_id 1482484
- Location of start within SEQ ID NO 584: at 425 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 38293

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 588
- Ceres seq_id 1482490

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 589
- Ceres seq_id 1482491
- Location of start within SEQ ID NO 588: at 104 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 590
- Ceres seq_id 1482492
- Location of start within SEQ ID NO 588: at 138 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 591
- Ceres seq_id 1482493
- Location of start within SEQ ID NO 588: at 151 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 40190

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 592
- Ceres seq_id 1482504

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 593
- Ceres seq_id 1482505
- Location of start within SEQ ID NO 592: at 113 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 594
- Ceres seq_id 1482506
- Location of start within SEQ ID NO 592: at 149 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 595
- Ceres seq_id 1482507
- Location of start within SEQ ID NO 592: at 642 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 4026

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 596
- Ceres seq_id 1482508

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 597
- Ceres seq_id 1482509
- Location of start within SEQ ID NO 596: at 139 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 598
- Ceres seq_id 1482510
- Location of start within SEQ ID NO 596: at 475 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 40770

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 599
- Ceres seq_id 1482514

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 600
- Ceres seq_id 1482515
- Location of start within SEQ ID NO 599: at 33 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 601
- Ceres seq_id 1482516
- Location of start within SEQ ID NO 599: at 39 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 602
- Ceres seq_id 1482517
- Location of start within SEQ ID NO 599: at 66 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 6091

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 603
- Ceres seq_id 1482525

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 604
- Ceres seq_id 1482526
- Location of start within SEQ ID NO 603: at 79 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 9184

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 605
- Ceres seq_id 1482535

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 606
- Ceres seq_id 1482536
- Location of start within SEQ ID NO 605: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 607
- Ceres seq_id 1482537
- Location of start within SEQ ID NO 605: at 33 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 608
- Ceres seq_id 1482538
- Location of start within SEQ ID NO 605: at 198 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 92491

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 609
- Ceres seq_id 1482542
(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 610
- Ceres seq_id 1482543
- Location of start within SEQ ID NO 609: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 611
- Ceres seq_id 1482544
- Location of start within SEQ ID NO 609: at 227 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 612
- Ceres seq_id 1482545
- Location of start within SEQ ID NO 609: at 275 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 93534

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 613
- Ceres seq_id 1482546
(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 614
- Ceres seq_id 1482547
- Location of start within SEQ ID NO 613: at 218 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 615
- Ceres seq_id 1482548
- Location of start within SEQ ID NO 613: at 227 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 616
- Ceres seq_id 1482549
- Location of start within SEQ ID NO 613: at 260 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

[illegible]

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1458
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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atccggtttcg ccatttttgt ttctcagtg tctctgaaat ggtctcttct ctttttttgg      60
tcgaatccaa tctcaattat gttgttatct ttcttccatc aatgggtaat caaaacatag      120
aattgatgcg gtaagactat aaagggttag tctttaacca ttgtagattc ctctgtctct      180
tgtgtatttg attgatctgt taatggataa ccaaaaagggt gctctctttc ccgatgaggt      240
tattctccag attcttgcta gattacctgt taaatctctc ttcaggttca aatccgtttg      300
caaatcatgg tacagattac cttctgacaa atatttctact tccttgttca atcaactctc      360
tgtaaaagag caattgcttg tggctcaagt atcagattct tctagtttga tctgtgttga      420
taatctgaga ggtgtttctg agttatcatt ggattttgtt agagataggg tgaggattag      480
ggtttcttct aatgggttgg tgtgtgttgc aagcattcct gaaaagggtg tttactatgt      540
ttgtaatccg tcgactagag agtacaggaa attgcctaag agtcgagaaa gaccggttac      600
tcgggttttat cctgacggtg aggctacact tgttggtttg gcttgtgatt tgagtaggaa      660
caagtttaat gtggtgttgg ctggttacca taggtctttt ggtcagagac ctgatgggag      720
tttcatttgc ttggtgttgg attctgagag taacaaatgg aggaagtttg tttcgggtgtt      780
agaagaatgt agtttcacac acatgagtaa gaaccaagtg gtgtttgtta atgggatgct      840
tcattgggtg atgagtgtt tgtgttatat acttgcactt gatgttgaac atgatgtgtg      900
gagaaagatt tctttgcctg atgagattaa aatcgggaat ggtggtggtg atcgggttta      960
tctcttgtaa tccgatgggt ttttgcggtt gattcagtta tcagatgtat ggatgaagat     1020
ttggaagatg agtgagtatg agactgaaac ttggagtgtt gttgatagca taagtttaag     1080
gtgcattaaa ggattggtac ctggaatctt cccgatttgt cagaccggtg agtatgtttt     1140
cttggtact cataaacagg ttttggtgta tcaaagacga agtaagttat ggaaagagat     1200
gttttctgta aaaggaagct cttctctgcc tttgtggttc tctgctcacg cctttcgcag     1260
caccatagta ccctgtaatt agcatgttta tgtttccttc tctactcttt tatttttttg     1320
gtttatgttc agctcttggg tcttttaggg cttatgaaaa tttgttcaag gttttataat     1380
ctttctggga taacatcata taaagtaatg tacagttgat ttcttctgtt gcttttagta     1440
caaataagat tttggttg
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..359
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Asp Asn Gln Lys Gly Ala Leu Phe Pro Asp Glu Val Ile Leu Gln
1           5           10           15
Ile Leu Ala Arg Leu Pro Val Lys Ser Leu Phe Arg Phe Lys Ser Val
20           25           30
Cys Lys Ser Trp Tyr Arg Leu Pro Ser Asp Lys Tyr Phe Thr Ser Leu
35           40           45
Phe Asn Gln Leu Ser Val Lys Glu Gln Leu Leu Val Ala Gln Val Ser
50           55           60
Asp Ser Ser Ser Leu Ile Cys Val Asp Asn Leu Arg Gly Val Ser Glu
65           70           75           80
```

Leu Ser Leu Asp Phe Val Arg Asp Arg Val Arg Ile Arg Val Ser Ser
85 90 95
Asn Gly Leu Leu Cys Cys Ser Ser Ile Pro Glu Lys Gly Val Tyr Tyr
100 105 110
Val Cys Asn Pro Ser Thr Arg Glu Tyr Arg Lys Leu Pro Lys Ser Arg
115 120 125
Glu Arg Pro Val Thr Arg Phe Tyr Pro Asp Gly Glu Ala Thr Leu Val
130 135 140
Gly Leu Ala Cys Asp Leu Ser Arg Asn Lys Phe Asn Val Val Leu Ala
145 150 155 160
Gly Tyr His Arg Ser Phe Gly Gln Arg Pro Asp Gly Ser Phe Ile Cys
165 170 175
Leu Val Phe Asp Ser Glu Ser Asn Lys Trp Arg Lys Phe Val Ser Val
180 185 190
Leu Glu Glu Cys Ser Phe Thr His Met Ser Lys Asn Gln Val Val Phe
195 200 205
Val Asn Gly Met Leu His Trp Leu Met Ser Gly Leu Cys Tyr Ile Leu
210 215 220
Ala Leu Asp Val Glu His Asp Val Trp Arg Lys Ile Ser Leu Pro Asp
225 230 235 240
Glu Ile Lys Ile Gly Asn Gly Gly Gly Asn Arg Val Tyr Leu Leu Glu
245 250 255
Ser Asp Gly Phe Leu Ser Val Ile Gln Leu Ser Asp Val Trp Met Lys
260 265 270
Ile Trp Lys Met Ser Glu Tyr Glu Thr Glu Thr Trp Ser Val Val Asp
275 280 285
Ser Ile Ser Leu Arg Cys Ile Lys Gly Leu Val Pro Gly Ile Phe Pro
290 295 300
Ile Cys Gln Thr Gly Glu Tyr Val Phe Leu Ala Thr His Lys Gln Val
305 310 315 320
Leu Val Tyr Gln Arg Arg Ser Lys Leu Trp Lys Glu Met Phe Ser Val
325 330 335
Lys Gly Ser Ser Ser Leu Pro Leu Trp Phe Ser Ala His Ala Phe Arg
340 345 350
Ser Thr Ile Val Pro Cys Asn
355

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1353
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | |
|--|-----|
| casragamcc atwacywaga amcaycctaa tcgaaaaaac gccacaatca tggctttggt | 60 |
| cttatctcct aaaaccatca ctcttctctt ctctctccctc tccctcgcac tctactgcag | 120 |
| catcgatcct ttccaccact gcgccatttc cgatttcccc aatttcgtct ctcacgaagt | 180 |
| tatctctcca cgtcccgacg aagttccatg ggagagagat tcacaaaatt cacttcagaa | 240 |
| atcaaagatt ctgtttttta accaaatcca aggtccagag agcgtcgcct ttgattctct | 300 |
| cggacgtggt ccgtacacag gcgttgctga tggtaggggt ttgttttggg atggagagaa | 360 |
| atggattgat ttcgcttata cttcgagtaa tcgatcggag atttgtgatc cgaagccttc | 420 |
| tgctttgagt tacttgagga atgaacatat atgtggtcgt cctttaggtc ttcgtttcga | 480 |
| taagagaacc ggagatttgt atatagctga tgcttatatg ggacttttga aagttgggtcc | 540 |
| tgaaggtggt ttagcaacgc cgcttgtaac tgaagctgaa ggtgtgccgt tgggggtttac | 600 |
| taatgatctt gacattgctg atgatggaac tgtttacttt acagatagca gcattagtta | 660 |

```
ccagaggagg aacttcttgc agctcgtttt ctctggagac aatactggga gggttctaaa 720
gtatgatcca gtagctaaga aagctgttgt tttgggtctca aatcttcagt ttccgaatgg 780
tgtctctatc agcagagacg gttctttctt tgtattctgc gaaggagata ttggaagcct 840
acgaagatac tgggtgaaag gcgagaaagc tggaacgaca gatgtgtttg cgtatttacc 900
agggcatcct gataacgtaa gaaccaacca aaagggtgaa ttttgggtag cgcttcattg 960
cagacgcaac tactactcat acttaatggc aagatatcct aagctgagga tgttcatact 1020
gagactgcca atcactgcga gaactcacta ctctgtccag atagggttac ggccgcacgg 1080
gttgggtggtt aagtatagtc ctgaaggga gcttatgcat gttttggaag atagtgaagg 1140
gaaagtgtgt agatcagtaa gtgaagtgga agaaaaagat gggaagcttt ggatgggaag 1200
tgtgttgatg aactttgttg ctgtctatga cctctgatta cttgacctat acgtaaacca 1260
cttcactcag tttctagatt tagcaaattc tcaaaactgt taggtgtgta ctgaaaaaat 1320
caaacactta gcacaaacaa actcaatggtt att
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..411

(D) OTHER INFORMATION: / Ceres Seq. ID 1481343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Xaa Arg Xaa Xaa Xaa Xaa Xaa Pro Asn Arg Lys Asn Ala Thr Ile
1      5      10      15
Met Ala Leu Phe Leu Ser Pro Lys Thr Ile Thr Leu Leu Phe Phe Ser
20      25      30
Leu Ser Leu Ala Leu Tyr Cys Ser Ile Asp Pro Phe His His Cys Ala
35      40      45
Ile Ser Asp Phe Pro Asn Phe Val Ser His Glu Val Ile Ser Pro Arg
50      55      60
Pro Asp Glu Val Pro Trp Glu Arg Asp Ser Gln Asn Ser Leu Gln Lys
65      70      75      80
Ser Lys Ile Leu Phe Phe Asn Gln Ile Gln Gly Pro Glu Ser Val Ala
85      90      95
Phe Asp Ser Leu Gly Arg Gly Pro Tyr Thr Gly Val Ala Asp Gly Arg
100     105     110
Val Leu Phe Trp Asp Gly Glu Lys Trp Ile Asp Phe Ala Tyr Thr Ser
115     120     125
Ser Asn Arg Ser Glu Ile Cys Asp Pro Lys Pro Ser Ala Leu Ser Tyr
130     135     140
Leu Arg Asn Glu His Ile Cys Gly Arg Pro Leu Gly Leu Arg Phe Asp
145     150     155     160
Lys Arg Thr Gly Asp Leu Tyr Ile Ala Asp Ala Tyr Met Gly Leu Leu
165     170     175
Lys Val Gly Pro Glu Gly Gly Leu Ala Thr Pro Leu Val Thr Glu Ala
180     185     190
Glu Gly Val Pro Leu Gly Phe Thr Asn Asp Leu Asp Ile Ala Asp Asp
195     200     205
Gly Thr Val Tyr Phe Thr Asp Ser Ser Ile Ser Tyr Gln Arg Arg Asn
210     215     220
Phe Leu Gln Leu Val Phe Ser Gly Asp Asn Thr Gly Arg Val Leu Lys
225     230     235     240
Tyr Asp Pro Val Ala Lys Lys Ala Val Val Leu Val Ser Asn Leu Gln
245     250     255
Phe Pro Asn Gly Val Ser Ile Ser Arg Asp Gly Ser Phe Phe Val Phe
260     265     270
Cys Glu Gly Asp Ile Gly Ser Leu Arg Arg Tyr Trp Leu Lys Gly Glu
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| | | |
|---|-----|-----|
| 275 | 280 | 285 |
| Lys Ala Gly Thr Thr Asp Val Phe Ala Tyr Leu Pro Gly His Pro Asp | | |
| 290 | 295 | 300 |
| Asn Val Arg Thr Asn Gln Lys Gly Glu Phe Trp Val Ala Leu His Cys | | |
| 305 | 310 | 315 |
| Arg Arg Asn Tyr Tyr Ser Tyr Leu Met Ala Arg Tyr Pro Lys Leu Arg | | |
| | 325 | 330 |
| Met Phe Ile Leu Arg Leu Pro Ile Thr Ala Arg Thr His Tyr Ser Phe | | |
| | 340 | 345 |
| Gln Ile Gly Leu Arg Pro His Gly Leu Val Val Lys Tyr Ser Pro Glu | | |
| | 355 | 360 |
| Gly Lys Leu Met His Val Leu Glu Asp Ser Glu Gly Lys Val Val Arg | | |
| | 370 | 375 |
| Ser Val Ser Glu Val Glu Glu Lys Asp Gly Lys Leu Trp Met Gly Ser | | |
| 385 | 390 | 395 |
| Val Leu Met Asn Phe Val Ala Val Tyr Asp Leu | | 400 |
| | 405 | 410 |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 395 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..395

(D) OTHER INFORMATION: / Ceres Seq. ID 1481344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | | |
|---|-----|-----|
| Met Ala Leu Phe Leu Ser Pro Lys Thr Ile Thr Leu Leu Phe Phe Ser | | |
| 1 | 5 | 10 |
| Leu Ser Leu Ala Leu Tyr Cys Ser Ile Asp Pro Phe His His Cys Ala | | |
| | 20 | 25 |
| Ile Ser Asp Phe Pro Asn Phe Val Ser His Glu Val Ile Ser Pro Arg | | |
| | 35 | 40 |
| Pro Asp Glu Val Pro Trp Glu Arg Asp Ser Gln Asn Ser Leu Gln Lys | | |
| | 50 | 55 |
| Ser Lys Ile Leu Phe Phe Asn Gln Ile Gln Gly Pro Glu Ser Val Ala | | |
| 65 | 70 | 75 |
| Phe Asp Ser Leu Gly Arg Gly Pro Tyr Thr Gly Val Ala Asp Gly Arg | | |
| | 85 | 90 |
| Val Leu Phe Trp Asp Gly Glu Lys Trp Ile Asp Phe Ala Tyr Thr Ser | | |
| | 100 | 105 |
| Ser Asn Arg Ser Glu Ile Cys Asp Pro Lys Pro Ser Ala Leu Ser Tyr | | |
| | 115 | 120 |
| Leu Arg Asn Glu His Ile Cys Gly Arg Pro Leu Gly Leu Arg Phe Asp | | |
| | 130 | 135 |
| Lys Arg Thr Gly Asp Leu Tyr Ile Ala Asp Ala Tyr Met Gly Leu Leu | | |
| 145 | 150 | 155 |
| Lys Val Gly Pro Glu Gly Gly Leu Ala Thr Pro Leu Val Thr Glu Ala | | |
| | 165 | 170 |
| Glu Gly Val Pro Leu Gly Phe Thr Asn Asp Leu Asp Ile Ala Asp Asp | | |
| | 180 | 185 |
| Gly Thr Val Tyr Phe Thr Asp Ser Ser Ile Ser Tyr Gln Arg Arg Asn | | |
| | 195 | 200 |
| Phe Leu Gln Leu Val Phe Ser Gly Asp Asn Thr Gly Arg Val Leu Lys | | |
| | 210 | 215 |
| Tyr Asp Pro Val Ala Lys Lys Ala Val Val Leu Val Ser Asn Leu Gln | | |
| 225 | 230 | 235 |
| | | 240 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Phe | Pro | Asn | Gly | Val | Ser | Ile | Ser | Arg | Asp | Gly | Ser | Phe | Phe | Val | Phe | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Cys | Glu | Gly | Asp | Ile | Gly | Ser | Leu | Arg | Arg | Tyr | Trp | Leu | Lys | Gly | Glu | |
| | | | | 260 | | | | | 265 | | | | | 270 | | |
| Lys | Ala | Gly | Thr | Thr | Asp | Val | Phe | Ala | Tyr | Leu | Pro | Gly | His | Pro | Asp | |
| | | | | 275 | | | | | 280 | | | | | 285 | | |
| Asn | Val | Arg | Thr | Asn | Gln | Lys | Gly | Glu | Phe | Trp | Val | Ala | Leu | His | Cys | |
| | | | | 290 | | | | | 295 | | | | | 300 | | |
| Arg | Arg | Asn | Tyr | Tyr | Ser | Tyr | Leu | Met | Ala | Arg | Tyr | Pro | Lys | Leu | Arg | |
| | | | | 305 | | | | | 310 | | | | | 315 | | |
| Met | Phe | Ile | Leu | Arg | Leu | Pro | Ile | Thr | Ala | Arg | Thr | His | Tyr | Ser | Phe | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| Gln | Ile | Gly | Leu | Arg | Pro | His | Gly | Leu | Val | Val | Lys | Tyr | Ser | Pro | Glu | |
| | | | | 340 | | | | | 345 | | | | | 350 | | |
| Gly | Lys | Leu | Met | His | Val | Leu | Glu | Asp | Ser | Glu | Gly | Lys | Val | Val | Arg | |
| | | | | 355 | | | | | 360 | | | | | 365 | | |
| Ser | Val | Ser | Glu | Val | Glu | Glu | Lys | Asp | Gly | Lys | Leu | Trp | Met | Gly | Ser | |
| | | | | 370 | | | | | 375 | | | | | 380 | | |
| Val | Leu | Met | Asn | Phe | Val | Ala | Val | Tyr | Asp | Leu | | | | | | |
| | | | | 385 | | | | | 390 | | | | | 395 | | |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..239
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1481345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Leu | Leu | Lys | Val | Gly | Pro | Glu | Gly | Gly | Leu | Ala | Thr | Pro | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Thr | Glu | Ala | Glu | Gly | Val | Pro | Leu | Gly | Phe | Thr | Asn | Asp | Leu | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ala | Asp | Asp | Gly | Thr | Val | Tyr | Phe | Thr | Asp | Ser | Ser | Ile | Ser | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Arg | Arg | Asn | Phe | Leu | Gln | Leu | Val | Phe | Ser | Gly | Asp | Asn | Thr | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Val | Leu | Lys | Tyr | Asp | Pro | Val | Ala | Lys | Lys | Ala | Val | Val | Leu | Val |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Asn | Leu | Gln | Phe | Pro | Asn | Gly | Val | Ser | Ile | Ser | Arg | Asp | Gly | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Phe | Val | Phe | Cys | Glu | Gly | Asp | Ile | Gly | Ser | Leu | Arg | Arg | Tyr | Trp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Lys | Gly | Glu | Lys | Ala | Gly | Thr | Thr | Asp | Val | Phe | Ala | Tyr | Leu | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | His | Pro | Asp | Asn | Val | Arg | Thr | Asn | Gln | Lys | Gly | Glu | Phe | Trp | Val |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Leu | His | Cys | Arg | Arg | Asn | Tyr | Tyr | Ser | Tyr | Leu | Met | Ala | Arg | Tyr |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Pro | Lys | Leu | Arg | Met | Phe | Ile | Leu | Arg | Leu | Pro | Ile | Thr | Ala | Arg | Thr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Tyr | Ser | Phe | Gln | Ile | Gly | Leu | Arg | Pro | His | Gly | Leu | Val | Val | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |     |     |
| Tyr | Ser | Pro | Glu | Gly | Lys | Leu | Met | His | Val | Leu | Glu | Asp | Ser | Glu | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Val | Val | Arg | Ser | Val | Ser | Glu | Val | Glu | Glu | Lys | Asp | Gly | Lys | Leu |

210 215 220  
Trp Met Gly Ser Val Leu Met Asn Phe Val Ala Val Tyr Asp Leu  
225 230 235

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1279
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
atcaccattg ctttgttttg ttcgtcaaat ataatacaatt tttaaatttct tctcttctct 60
tcaaacgaat cgcctttttc gataatctct ttgcatcgat ttcacatggg ctactcaaac 120
ggatctcgct cagcccaagc ttgatatgac caaggaggag aaagagaggt tgaagtattt 180
gcaattcgct caagctgctg ctgtggaagc tctgcttcgc tttgctctta tttacgctaa 240
ggcaaaggac aagtctggct ctttgaaacc tgggtgtgaa tctgttgaag gagctgtcaa 300
gactgtcggt ggtcctgtct acgagaaata ccacgacgtc cctgttgagg tccttaaata 360
catggaccag aagggtacaat ttgactcctt tccctatctt tggatccttg tgaaagtgcc 420
tttgttgatg aacaatgaat gaatctgtgt tgttgattgt atatccactt catcgaacat 480
atgtgattaa aaaagtacag ttaaagttgt gatgatttca tatcatctct ttggtagaag 540
gttcaggtta acgggtcaat gtcattatgt tctgtagagt cctctttttt gaagctgaca 600
agtttgtttt gcgttggttg aggttgatat gtctgtgact gagcttgacc gtcgtgtccc 660
accagtcgtc aagcaagtgt ctgcccaagc catctccgct gctcagatag caccattgt 720
ggcagctgct ttggcctctg aggttcgacg tgctggtgtt gttgaaaccg cttctggaat 780
ggctaaatcc gtctactcca agtacgagcc tgctgctaag gagttgtatg caaactatga 840
gccaaaagca aagcagtgtg ccgtttcagc ttggaagaag cttaccagc ttcctctatt 900
cccaaggctg gctcaagtgt ctgtaccaac agctgctttc tgctctgaga agtacaatga 960
tactgtggtt aaggctgcag agaaagggtg cagagtcaca tcgtacatgc cattggttcc 1020
aacagagagg atctcaaaaa tcttcgctga ggagaaagct gagaccgagc ctttgagatt 1080
ccatccactt gattgatatg ggtgttttgt tagtgtgatt tttgttttg ttgggattaa 1140
ggtgaaccgg atcttggtta gcgattgatc tctggttctc gttctttttt ttctttgtca 1200
tgaacttttg ttgtttcggt taataatcaa aagttgtata atctaagttt gggattacca 1260
ccctattgag tattgagtg
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Met Ser Val Thr Glu Leu Asp Arg Arg Pro Pro Val Val Lys Gln
1 5 10 15
Val Ser Ala Gln Ala Ile Ser Ala Ala Gln Ile Ala Pro Ile Val Ala
20 25 30
Arg Ala Leu Ala Ser Glu Val Arg Arg Ala Gly Val Val Glu Thr Ala
35 40 45
Ser Gly Met Ala Lys Ser Val Tyr Ser Lys Tyr Glu Pro Ala Ala Lys
50 55 60
Glu Leu Tyr Ala Asn Tyr Glu Pro Lys Ala Lys Gln Cys Ala Val Ser
65 70 75 80
```

Ala Trp Lys Lys Leu Asn Gln Leu Pro Leu Phe Pro Arg Leu Ala Gln  
85 90 95  
Val Ala Val Pro Thr Ala Ala Phe Cys Ser Glu Lys Tyr Asn Asp Thr  
100 105 110  
Val Val Lys Ala Ala Glu Lys Gly Tyr Arg Val Thr Ser Tyr Met Pro  
115 120 125  
Leu Val Pro Thr Glu Arg Ile Ser Lys Ile Phe Ala Glu Glu Lys Ala  
130 135 140  
Glu Thr Glu Pro Leu Glu Phe His Pro Leu Asp  
145 150 155

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Lys Ser Val Tyr Ser Lys Tyr Glu Pro Ala Ala Lys Glu Leu  
1 5 10 15  
Tyr Ala Asn Tyr Glu Pro Lys Ala Lys Gln Cys Ala Val Ser Ala Trp  
20 25 30  
Lys Lys Leu Asn Gln Leu Pro Leu Phe Pro Arg Leu Ala Gln Val Ala  
35 40 45  
Val Pro Thr Ala Ala Phe Cys Ser Glu Lys Tyr Asn Asp Thr Val Val  
50 55 60  
Lys Ala Ala Glu Lys Gly Tyr Arg Val Thr Ser Tyr Met Pro Leu Val  
65 70 75 80  
Pro Thr Glu Arg Ile Ser Lys Ile Phe Ala Glu Glu Lys Ala Glu Thr  
85 90 95  
Glu Pro Leu Glu Phe His Pro Leu Asp  
100 105

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Gln Thr Met Ser Gln Lys Gln Ser Ser Val Pro Phe Gln Leu Gly  
1 5 10 15  
Arg Ser Leu Thr Ser Phe Leu Tyr Ser Gln Gly Trp Leu Lys Leu Leu  
20 25 30  
Tyr Gln Gln Leu Leu Ser Ala Leu Arg Ser Thr Met Ile Leu Trp Leu  
35 40 45  
Arg Leu Gln Arg Lys Gly Thr Glu Ser His Arg Thr Cys His Trp Phe  
50 55 60  
Gln Gln Arg Gly Ser Gln Lys Ser Ser Leu Arg Arg Lys Leu Arg Pro  
65 70 75 80  
Ser Leu Trp Ser Ser Ile His Leu Ile Asp Met Gly Val Leu Leu Val

85

90

95

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1211
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

|            |            |             |            |            |            |      |
|------------|------------|-------------|------------|------------|------------|------|
| aacatcctaa | tcgaaaaaaa | aaaacataaa  | acacataggg | gtgggtctct | ctcctccgga | 60   |
| attcgatcac | gacggcaagg | acgacgcatac | tccttctccc | acagggctgg | agatggatct | 120  |
| ggtccggtga | tttctgagat | ttaagtcgat  | cgagtttcca | gatatatctc | tcaagtagag | 180  |
| atggcttgg  | tcagtggcaa | agtttctctg  | ggaggattcc | cagatctcac | tggcgctgtc | 240  |
| aataaattcc | agagagcggt | aaaaacattg  | aaaagaattt | cgacaacgcc | cttggcttcg | 300  |
| acgacaagtc | cgattctgcc | gctgaagatg  | cagcttcaag | tatgtggcca | cctgcagttg | 360  |
| ataccaaaag | cctctttgat | cccgttatgt  | ccttcatggg | taacacctct | gatgagaaac | 420  |
| ctgatacatt | ggaagactct | gtgcgtacag  | aaaatccgtc | tcaaattgaa | caaaaagaag | 480  |
| aagaagctgg | atcggttaag | ctagctactg  | aacaagcagt | atctgttgaa | gcaaataaag | 540  |
| aaacaaacat | gagaagagaa | gctgatcaag  | cagataatcc | tgaggtaaca | gaaactgttg | 600  |
| ttttggatcc | caacgatgat | gaaccgcaat  | cgcagatact | tctcgaagag | tcctctgaat | 660  |
| attctcttca | gactcctgaa | tcctcagggt  | acaagactag | tcttcaacct | aatgaaaagc | 720  |
| tggaaatgac | agcttctcaa | gattcacagc  | ccgagcaacc | caagtcagag | gctgaggaat | 780  |
| cacagcctga | ggattctgaa | gcaaaagagg  | ttactgtaga | aaacaaagac | actgttcact | 840  |
| cccctgtgtt | agatggacag | cataagatta  | cttatatgga | tgagacaaca | aatgaacaag | 900  |
| aaattctggg | tgaaaatctg | gaagggagaa  | cctcgtctaa | aatttttgaa | gtttcaccag | 960  |
| atatcaatca | tgtaaatagg | atagagtccc  | ttgttgctca | tccgtcttta | atttttgagt | 1020 |
| ctgatggttc | tccttacgag | tcttctatac  | caaagagatc | gtcgtcagat | gaaatttcgg | 1080 |
| agagaattgt | ggattttgtt | tctcgtgaaa  | tagattcaag | actggatact | agtgaattaa | 1140 |
| atgaaagcca | gcgttcaagc | tctgcgacaa  | atgtttccga | ctctgctgat | gttattctgg | 1200 |
| aattagagaa | g          |             |            |            |            |      |

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..290
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Trp | Pro | Pro | Ala | Val | Asp | Thr | Lys | Ser | Leu | Phe | Asp | Pro | Val | Met |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Phe | Met | Gly | Asn | Thr | Ser | Asp | Glu | Lys | Pro | Asp | Thr | Leu | Glu | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Val | Arg | Thr | Glu | Asn | Pro | Ser | Gln | Ile | Glu | Gln | Lys | Glu | Glu | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Gly | Ser | Val | Lys | Leu | Ala | Thr | Glu | Gln | Ala | Val | Ser | Val | Glu | Ala |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asn | Lys | Glu | Thr | Asn | Met | Arg | Arg | Glu | Ala | Asp | Gln | Ala | Asp | Asn | Pro |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Val | Thr | Glu | Thr | Val | Val | Leu | Asp | Pro | Asn | Asp | Asp | Glu | Pro | Gln |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Phe | Met | Gly | Asn | Thr | Ser | Asp | Glu | Lys | Pro | Asp | Thr | Leu | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Ser | Val | Arg | Thr | Glu | Asn | Pro | Ser | Gln | Ile | Glu | Gln | Lys | Glu | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Ala | Gly | Ser | Val | Lys | Leu | Ala | Thr | Glu | Gln | Ala | Val | Ser | Val | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Asn | Lys | Glu | Thr | Asn | Met | Arg | Arg | Glu | Ala | Asp | Gln | Ala | Asp | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Glu | Val | Thr | Glu | Thr | Val | Val | Leu | Asp | Pro | Asn | Asp | Asp | Glu | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gln | Ser | Gln | Ile | Leu | Leu | Glu | Glu | Ser | Ser | Glu | Tyr | Ser | Leu | Gln | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Glu | Ser | Ser | Gly | Tyr | Lys | Thr | Ser | Leu | Gln | Pro | Asn | Glu | Lys | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Met | Thr | Ala | Ser | Gln | Asp | Ser | Gln | Pro | Glu | Gln | Pro | Lys | Ser | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Glu | Glu | Ser | Gln | Pro | Glu | Asp | Ser | Glu | Ala | Lys | Glu | Val | Thr | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Asn | Lys | Asp | Thr | Val | His | Ser | Pro | Val | Leu | Asp | Gly | Gln | His | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Thr | Tyr | Met | Asp | Glu | Thr | Thr | Asn | Glu | Gln | Glu | Ile | Leu | Gly | Glu |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Asn | Leu | Glu | Gly | Arg | Thr | Ser | Ser | Lys | Ile | Phe | Glu | Val | Ser | Pro | Asp |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Ile | Asn | His | Val | Asn | Arg | Ile | Glu | Ser | Leu | Val | Ala | His | Pro | Ser | Leu |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Ile | Phe | Glu | Ser | Asp | Gly | Ser | Pro | Tyr | Glu | Ser | Ser | Ile | Pro | Lys | Arg |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Ser | Ser | Ser | Asp | Glu | Ile | Ser | Glu | Arg | Ile | Val | Asp | Phe | Val | Ser | Arg |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Glu | Ile | Asp | Ser | Arg | Leu | Asp | Thr | Ser | Glu | Leu | Asn | Glu | Ser | Gln | Arg |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Ser | Ser | Ser | Ala | Thr | Asn | Val | Ser | Asp | Ser | Ala | Asp | Val | Ile | Leu | Glu |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Leu | Glu | Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     | 275 |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..272
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Asn | Thr | Ser | Asp | Glu | Lys | Pro | Asp | Thr | Leu | Glu | Asp | Ser | Val |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Arg | Thr | Glu | Asn | Pro | Ser | Gln | Ile | Glu | Gln | Lys | Glu | Glu | Glu | Ala | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | Val | Lys | Leu | Ala | Thr | Glu | Gln | Ala | Val | Ser | Val | Glu | Ala | Asn | Lys |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Glu | Thr | Asn | Met | Arg | Arg | Glu | Ala | Asp | Gln | Ala | Asp | Asn | Pro | Glu | Val |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Thr | Glu | Thr | Val | Val | Leu | Asp | Pro | Asn | Asp | Asp | Glu | Pro | Gln | Ser | Gln |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Ile | Leu | Leu | Glu | Glu | Ser | Ser | Glu | Tyr | Ser | Leu | Gln | Thr | Pro | Glu | Ser |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Ser | Gly | Tyr | Lys | Thr | Ser | Leu | Gln | Pro | Asn | Glu | Lys | Leu | Glu | Met | Thr |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ala | Ser | Gln | Asp | Ser | Gln | Pro | Glu | Gln | Pro | Lys | Ser | Glu | Ala | Glu | Glu |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ser | Gln | Pro | Glu | Asp | Ser | Glu | Ala | Lys | Glu | Val | Thr | Val | Glu | Asn | Lys |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Asp | Thr | Val | His | Ser | Pro | Val | Leu | Asp | Gly | Gln | His | Lys | Ile | Thr | Tyr |  |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Met | Asp | Glu | Thr | Thr | Asn | Glu | Gln | Glu | Ile | Leu | Gly | Glu | Asn | Leu | Glu |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |  |
| Gly | Arg | Thr | Ser | Ser | Lys | Ile | Phe | Glu | Val | Ser | Pro | Asp | Ile | Asn | His |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Val | Asn | Arg | Ile | Glu | Ser | Leu | Val | Ala | His | Pro | Ser | Leu | Ile | Phe | Glu |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Ser | Asp | Gly | Ser | Pro | Tyr | Glu | Ser | Ser | Ile | Pro | Lys | Arg | Ser | Ser | Ser |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Asp | Glu | Ile | Ser | Glu | Arg | Ile | Val | Asp | Phe | Val | Ser | Arg | Glu | Ile | Asp |  |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |  |
| Ser | Arg | Leu | Asp | Thr | Ser | Glu | Leu | Asn | Glu | Ser | Gln | Arg | Ser | Ser | Ser |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 245 |     | 250 |     | 255 |     |     |     |     |     |     |     |     |     |     |
| Ala | Thr | Asn | Val | Ser | Asp | Ser | Ala | Asp | Val | Ile | Leu | Glu | Leu | Glu | Lys |
|     | 260 |     |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..592
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

|       |        |        |         |        |        |       |        |       |        |        |        |       |     |
|-------|--------|--------|---------|--------|--------|-------|--------|-------|--------|--------|--------|-------|-----|
| cta   | atc    | gaaa   | aaaa    | agcgag | aaaga  | aagac | gaact  | gatca | gcaat  | gggaa  | gctta  | agggt | 60  |
| gag   | cac    | agtt   | gttat   | tgcag  | tagtg  | gcttg | tctct  | ccatc | ctcct  | catat  | ctcct  | acaga | 120 |
| agta  | gat    | ggg    | cgttt   | agtgt  | gtgac  | actcc | agcgg  | gtaca | tgtac  | cctcg  | gctct  | acttg | 180 |
| caat  | gacca  | tgca   | atacat  | ggggc  | ggcaa  | ttat  | agtgg  | ggcga | aatgtg | cagatt | caag   |       | 240 |
| cttt  | cctgg  | tta    | agtatat | gttat  | tgtctg | ccatt | atgta  | gggag | cagtg  | ctgaa  | atgga  |       | 300 |
| aagc  | atgtg  | ttgc   | agatga  | tagaa  | aacga  | cgtc  | gctttg | tgtgc | gtatg  | tgtgt  | gtttt  |       | 360 |
| ttgc  | taatcg | catgt  | tttatg  | ctttc  | atttc  | acatc | ctatg  | ttttg | agtgt  | ttgc   | ctttgt |       | 420 |
| acttt | gtttgt | tgtgc  | ttctg   | tttgt  | ttttgc | gttgt | caagt  | atcaa | ataaaa | gttgg  | agtg   | gt    | 480 |
| gtttt | taaca  | aatga  | ttttt   | ttatt  | tattct | tggtg | tattt  | agcta | atttta | ttttat | tttaa  |       | 540 |
| gagt  | gtttta | ttttat | caaa    | taata  | aataat | cataa | ttg    | cg    | gtttg  | ttgtg  | cg     |       |     |

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Glu | Lys | Lys | Ala | Arg | Lys | Lys | Asp | Glu | Leu | Ile | Ser | Asn | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Lys | Leu | Lys | Gly | Glu | His | Ser | Cys | Tyr | Cys | Ser | Ser | Gly | Leu | Ser | Leu |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| His | Pro | Pro | His | Ile | Ser | Tyr | Arg | Ser | Arg | Trp | Ala | Phe | Ser | Val |     |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ser | Leu | Arg | Val | Ser | Thr | Val | Val | Ile | Ala | Val | Val | Ala | Cys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |

(2) INFORMATION FOR SEQ ID NO:18:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..46

(D) OTHER INFORMATION: / Ceres Seq. ID 1481375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Val | Phe | Phe | Ala | Asn | Arg | Met | Phe | Met | Leu | Ser | Phe | His | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Cys | Phe | Glu | Cys | Leu | Pro | Leu | Tyr | Phe | Val | Val | Val | Leu | Leu | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Leu | Arg | Cys | Gln | Val | Ser | Asn | Lys | Val | Gly | Val | Cys | Phe |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1135 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1135

(D) OTHER INFORMATION: / Ceres Seq. ID 1481388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

|            |            |             |             |             |             |      |
|------------|------------|-------------|-------------|-------------|-------------|------|
| taaatgagat | gaatagaggt | ccacgagcta  | agggtttcaa  | cagccaagat  | ggttccaagg  | 60   |
| tgatggctgt | gtctttgaag | gagcagagag  | tgactgagac  | tgagaaactc  | agtgaagatg  | 120  |
| tgtctctttt | agatcccaag | gactacaata  | agatagattt  | ccctgagacc  | tacacagaag  | 180  |
| caaagtttta | tgtaatcaaa | tcgtacagtg  | aagatgatat  | tcataaaagt  | atcaaataca  | 240  |
| gtgtttggtc | cagcactcct | aatggtaaca  | agaagctgga  | tgccctcatat | aacgaggcaa  | 300  |
| aacagaagtc | agatggctgt | cccggtgtttc | tactttttctc | tgtaaacact  | agtggacaat  | 360  |
| ttgttggttt | agccgagatg | gtaggccctg  | ttgatttcaa  | taagactgtt  | gaatactggc  | 420  |
| aacaggcaaa | atggatttgg | tgcctccctg  | ttaagtggca  | tttcggttaa  | gatactcccta | 480  |
| atagctcctt | gaggcatata | actctggaga  | acaatgagaa  | caagccgggt  | actaatagca  | 540  |
| gagacacaca | ggaagtaaag | ctcgagcaag  | gcattaaagt  | catcaagatt  | ttcaaggacc  | 600  |
| acgcaagcaa | gacatgcata | ctcgatgatt  | ttgagttcta  | tgagaatcgt  | caaaagatta  | 660  |
| tccaagaaa  | gaaaagcaaa | cacctgcaga  | tcaaaaaaca  | gacattgggtg | gccaatgcag  | 720  |
| acaaaggtgt | aatgtcaaaa | attaatcttg  | tgaaacctca  | agagtctact  | acagcctcag  | 780  |
| aagatgcagc | agcactagga | gttgccggctg | aagtgactaa  | agaatcgaaa  | gtggtgaaa   | 840  |
| agaccgagtt | acctgtggag | aaaaatgctg  | ttgctactgc  | ctgctgaacc  | aacctttggt  | 900  |
| tttaagtggg | aactgagtgg | gctgttttag  | gctattttaga | gcgctttctct | agttttgttt  | 960  |
| ccattcctga | atttgcagac | tttttttttt  | tttttttttg  | aaccgagttg  | agagggtagt  | 1020 |
| ggcttagtag | atgaagtttt | ggcatgagca  | ttcatcatct  | tgcagttatt  | ctctatccct  | 1080 |
| ttagtaatgg | tccaacatat | gaggatatgg  | gtaaaagatt  | ggtattqaat  | caqct       |      |



(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..294
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Asn Glu Met Asn Arg Gly Pro Arg Ala Lys Gly Phe Asn Ser Gln Asp  
1 5 10 15  
Gly Ser Lys Val Met Ala Val Ser Leu Lys Glu Gln Arg Val Thr Glu  
20 25 30  
Thr Glu Lys Leu Ser Glu Asp Val Ser Leu Leu Asp Pro Lys Asp Tyr  
35 40 45  
Asn Lys Ile Asp Phe Pro Glu Thr Tyr Thr Glu Ala Lys Phe Tyr Val  
50 55 60  
Ile Lys Ser Tyr Ser Glu Asp Asp Ile His Lys Ser Ile Lys Tyr Ser  
65 70 75 80  
Val Trp Ser Ser Thr Pro Asn Gly Asn Lys Lys Leu Asp Ala Ser Tyr  
85 90 95  
Asn Glu Ala Lys Gln Lys Ser Asp Gly Cys Pro Val Phe Leu Leu Phe  
100 105 110  
Ser Val Asn Thr Ser Gly Gln Phe Val Gly Leu Ala Glu Met Val Gly  
115 120 125  
Pro Val Asp Phe Asn Lys Thr Val Glu Tyr Trp Gln Gln Asp Lys Trp  
130 135 140  
Ile Gly Cys Phe Pro Val Lys Trp His Phe Val Lys Asp Ile Pro Asn  
145 150 155 160  
Ser Ser Leu Arg His Ile Thr Leu Glu Asn Asn Glu Asn Lys Pro Val  
165 170 175  
Thr Asn Ser Arg Asp Thr Gln Glu Val Lys Leu Glu Gln Gly Ile Lys  
180 185 190  
Val Ile Lys Ile Phe Lys Asp His Ala Ser Lys Thr Cys Ile Leu Asp  
195 200 205  
Asp Phe Glu Phe Tyr Glu Asn Arg Gln Lys Ile Ile Gln Glu Arg Lys  
210 215 220  
Ser Lys His Leu Gln Ile Lys Lys Gln Thr Leu Val Ala Asn Ala Asp  
225 230 235 240  
Lys Gly Val Met Ser Lys Ile Asn Leu Val Lys Pro Gln Glu Ser Thr  
245 250 255  
Thr Ala Ser Glu Asp Ala Ala Ala Leu Gly Val Ala Ala Glu Val Thr  
260 265 270  
Lys Glu Ser Lys Val Val Lys Glu Thr Glu Leu Pro Val Glu Lys Asn  
275 280 285  
Ala Val Ala Thr Ala Cys  
290

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..292

(D) OTHER INFORMATION: / Ceres Seq. ID 1481390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Asn Arg Gly Pro Arg Ala Lys Gly Phe Asn Ser Gln Asp Gly Ser  
1 5 10 15  
Lys Val Met Ala Val Ser Leu Lys Glu Gln Arg Val Thr Glu Thr Glu  
20 25 30  
Lys Leu Ser Glu Asp Val Ser Leu Asp Pro Lys Asp Tyr Asn Lys  
35 40 45  
Ile Asp Phe Pro Glu Thr Tyr Thr Glu Ala Lys Phe Tyr Val Ile Lys  
50 55 60  
Ser Tyr Ser Glu Asp Asp Ile His Lys Ser Ile Lys Tyr Ser Val Trp  
65 70 75 80  
Ser Ser Thr Pro Asn Gly Asn Lys Lys Leu Asp Ala Ser Tyr Asn Glu  
85 90 95  
Ala Lys Gln Lys Ser Asp Gly Cys Pro Val Phe Leu Leu Phe Ser Val  
100 105 110  
Asn Thr Ser Gly Gln Phe Val Gly Leu Ala Glu Met Val Gly Pro Val  
115 120 125  
Asp Phe Asn Lys Thr Val Glu Tyr Trp Gln Gln Asp Lys Trp Ile Gly  
130 135 140  
Cys Phe Pro Val Lys Trp His Phe Val Lys Asp Ile Pro Asn Ser Ser  
145 150 155 160  
Leu Arg His Ile Thr Leu Glu Asn Asn Glu Asn Lys Pro Val Thr Asn  
165 170 175  
Ser Arg Asp Thr Gln Glu Val Lys Leu Glu Gln Gly Ile Lys Val Ile  
180 185 190  
Lys Ile Phe Lys Asp His Ala Ser Lys Thr Cys Ile Leu Asp Asp Phe  
195 200 205  
Glu Phe Tyr Glu Asn Arg Gln Lys Ile Ile Gln Glu Arg Lys Ser Lys  
210 215 220  
His Leu Gln Ile Lys Lys Gln Thr Leu Val Ala Asn Ala Asp Lys Gly  
225 230 235 240  
Val Met Ser Lys Ile Asn Leu Val Lys Pro Gln Glu Ser Thr Thr Ala  
245 250 255  
Ser Glu Asp Ala Ala Ala Leu Gly Val Ala Ala Glu Val Thr Lys Glu  
260 265 270  
Ser Lys Val Val Lys Glu Thr Glu Leu Pro Val Glu Lys Asn Ala Val  
275 280 285  
Ala Thr Ala Cys  
290

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..274

(D) OTHER INFORMATION: / Ceres Seq. ID 1481391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Ala Val Ser Leu Lys Glu Gln Arg Val Thr Glu Thr Glu Lys Leu  
1 5 10 15  
Ser Glu Asp Val Ser Leu Leu Asp Pro Lys Asp Tyr Asn Lys Ile Asp  
20 25 30  
Phe Pro Glu Thr Tyr Thr Glu Ala Lys Phe Tyr Val Ile Lys Ser Tyr  
35 40 45

Ser Glu Asp Asp Ile His Lys Ser Ile Lys Tyr Ser Val Trp Ser Ser  
50 55 60  
Thr Pro Asn Gly Asn Lys Lys Leu Asp Ala Ser Tyr Asn Glu Ala Lys  
65 70 75 80  
Gln Lys Ser Asp Gly Cys Pro Val Phe Leu Leu Phe Ser Val Asn Thr  
85 90 95  
Ser Gly Gln Phe Val Gly Leu Ala Glu Met Val Gly Pro Val Asp Phe  
100 105 110  
Asn Lys Thr Val Glu Tyr Trp Gln Gln Asp Lys Trp Ile Gly Cys Phe  
115 120 125  
Pro Val Lys Trp His Phe Val Lys Asp Ile Pro Asn Ser Ser Leu Arg  
130 135 140  
His Ile Thr Leu Glu Asn Asn Glu Asn Lys Pro Val Thr Asn Ser Arg  
145 150 155 160  
Asp Thr Gln Glu Val Lys Leu Glu Gln Gly Ile Lys Val Ile Lys Ile  
165 170 175  
Phe Lys Asp His Ala Ser Lys Thr Cys Ile Leu Asp Asp Phe Glu Phe  
180 185 190  
Tyr Glu Asn Arg Gln Lys Ile Ile Gln Glu Arg Lys Ser Lys His Leu  
195 200 205  
Gln Ile Lys Lys Gln Thr Leu Val Ala Asn Ala Asp Lys Gly Val Met  
210 215 220  
Ser Lys Ile Asn Leu Val Lys Pro Gln Glu Ser Thr Thr Ala Ser Glu  
225 230 235 240  
Asp Ala Ala Ala Leu Gly Val Ala Ala Glu Val Thr Lys Glu Ser Lys  
245 250 255  
Val Val Lys Glu Thr Glu Leu Pro Val Glu Lys Asn Ala Val Ala Thr  
260 265 270  
Ala Cys

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..796
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| catcctaatac gaaaaaaagc aaccaaacac ataaaagaga gatttaatac aaaagaaaga | 60  |
| gaaaaaagaa agatatggca ggactcatca acaagatcgg agacgcactc cacaggctcga | 120 |
| aggcgaatat ctcaaagata tcagaaacgc caaggatttt acaatacaca gcgttgcgaa  | 180 |
| gtggctcgat gcacagcttc cattgcatcc gcggttgaaa gctttcttta ggacaatttc  | 240 |
| tccgaggcat tttaaaaacg gagattggaa tacagggtgga aactgtaaca acacggttcc | 300 |
| tttgtctaga ggcagcgaaa tcacagggga tgatggatcg atcgatgcaa cagttgagag  | 360 |
| tgctgtgaac gggacaagga tcaagattct tgacataact gcactttctg agctaagaga  | 420 |
| cgaagctcat atctcagggt ctaaactcaa accccgaaaa ccgaagaagg caagtaacgt  | 480 |
| gacctcaact ccaacgatca acgattgctt gcattgggtgc ttaccaggga tcccagatac | 540 |
| ttggaatgaa cttttcattg ctcagatttg aagtattcaa catcatcaca cacacaaagc  | 600 |
| tagctcaatg gattggctct gttgattctt tgttatagaa aggttttttt ttcagattct  | 660 |
| ttcttgggag aataacaaag tttcagttct taaaaatagg ttttagatgg tttgtcagta  | 720 |
| aatgattcat ctgtaacaat cacaatctgg tttttaatta tacacgagaa cattgaaatt  | 780 |
| gaaacaatct ttttcc                                                  |     |

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..76
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1481424
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

His Pro Asn Arg Lys Lys Ala Thr Lys His Ile Lys Glu Arg Phe Asn  
1 5 10 15  
Thr Lys Glu Arg Glu Lys Arg Lys Ile Trp Gln Asp Ser Ser Thr Arg  
20 25 30  
Ser Glu Thr His Ser Thr Gly Arg Arg Arg Ile Ser Gln Arg Tyr Gln  
35 40 45  
Lys Arg Gln Gly Phe Tyr Asn Thr Gln Arg Cys Glu Val Ala Arg Cys  
50 55 60  
Thr Ala Ser Ile Ala Ser Ala Val Glu Ser Phe Leu  
65 70 75

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 47 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..47
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1481425
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Ala Gly Leu Ile Asn Lys Ile Gly Asp Ala Leu His Arg Ser Lys  
1 5 10 15  
Ala Asn Ile Ser Lys Ile Ser Glu Thr Pro Arg Ile Leu Gln Tyr Thr  
20 25 30  
Ala Leu Arg Ser Gly Ser Met His Ser Phe His Cys Ile Arg Gly  
35 40 45

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 492 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..492
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1481471
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

acttcgcctt gaatcgagtc ttcgacgagt ctccggctgc gagtttctct tgctccggca 60  
aacagacctg tcattgcttc tctctccggc taactacaca gaagcatggt gtttgacaa 120  
gtagtaatag gtcctccagg atcgggaaag accacttatt gcaatggaat gtctcagttc 180  
ctctctctaa tgggcaggaa gggtgctatt gttaatctgg atcctgcaaa tgatgcatta 240  
ccttatgagt gtgctgtgaa tatagaagaa ttgatcaagt tagaagatgt tatgtcggaa 300  
cactcgcttg gtcctaattg aggtcttgta tattgtatgg agtacttgga gaaaaacatt 360  
gactggctgg aatctaaact aaagcctctt ctgaaggatc attacattct ctttgatttt 420  
cctggccaag tggaattggt cttcattcat gacagtacca agaattgttct sncgaagctg 480  
attaaatcat tg

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
Met Val Phe Gly Gln Val Val Ile Gly Pro Pro Gly Ser Gly Lys Thr
1 5 10 15
Thr Tyr Cys Asn Gly Met Ser Gln Phe Leu Ser Leu Met Gly Arg Lys
20 25 30
Val Ala Ile Val Asn Leu Asp Pro Ala Asn Asp Ala Leu Pro Tyr Glu
35 40 45
Cys Ala Val Asn Ile Glu Glu Leu Ile Lys Leu Glu Asp Val Met Ser
50 55 60
Glu His Ser Leu Gly Pro Asn Gly Gly Leu Val Tyr Cys Met Glu Tyr
65 70 75 80
Leu Glu Lys Asn Ile Asp Trp Leu Glu Ser Lys Leu Lys Pro Leu Leu
85 90 95
Lys Asp His Tyr Ile Leu Phe Asp Phe Pro Gly Gln Val Glu Leu Phe
100 105 110
Phe Ile His Asp Ser Thr Lys Asn Val Xaa Xaa Lys Leu Ile Lys Ser
115 120 125
Leu
```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
Met Ser Gln Phe Leu Ser Leu Met Gly Arg Lys Val Ala Ile Val Asn
1 5 10 15
Leu Asp Pro Ala Asn Asp Ala Leu Pro Tyr Glu Cys Ala Val Asn Ile
20 25 30
Glu Glu Leu Ile Lys Leu Glu Asp Val Met Ser Glu His Ser Leu Gly
35 40 45
Pro Asn Gly Gly Leu Val Tyr Cys Met Glu Tyr Leu Glu Lys Asn Ile
50 55 60
Asp Trp Leu Glu Ser Lys Leu Lys Pro Leu Leu Lys Asp His Tyr Ile
65 70 75 80
Leu Phe Asp Phe Pro Gly Gln Val Glu Leu Phe Phe Ile His Asp Ser
85 90 95
Thr Lys Asn Val Xaa Xaa Lys Leu Ile Lys Ser Leu
100 105
```

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..101  
(D) OTHER INFORMATION: / Ceres Seq. ID 1481474  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Gly Arg Lys Val Ala Ile Val Asn Leu Asp Pro Ala Asn Asp Ala  
1 5 10 15  
Leu Pro Tyr Glu Cys Ala Val Asn Ile Glu Glu Leu Ile Lys Leu Glu  
20 25 30  
Asp Val Met Ser Glu His Ser Leu Gly Pro Asn Gly Gly Leu Val Tyr  
35 40 45  
Cys Met Glu Tyr Leu Glu Lys Asn Ile Asp Trp Leu Glu Ser Lys Leu  
50 55 60  
Lys Pro Leu Leu Lys Asp His Tyr Ile Leu Phe Asp Phe Pro Gly Gln  
65 70 75 80  
Val Glu Leu Phe Phe Ile His Asp Ser Thr Lys Asn Val Xaa Xaa Lys  
85 90 95  
Leu Ile Lys Ser Leu  
100

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1189 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1189  
(D) OTHER INFORMATION: / Ceres Seq. ID 1481479  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

cagctcacgg aggaaccagt gttgctcctc aaactccaaa cagaaaaggg agtgtacaca 60  
tagctcgctc tcgctctgtg ccccttaacg acaaggaatt aagcctgaag ggaatggatt 120  
catttttccag agtaattcct tcgactcctc gtgttaagga aggagacgtt ttctcaaagt 180  
catcagagggc tggtaatact gaaacaggtg atgctgatgg agaagacata cctgaggatg 240  
aagcagtttg taggatttgt ttggtagagc tctgtgaagg aggagaaacc ttaaaaaatgg 300  
agtgtagttg caaaggcgaa cttgctcttg cccacaaaga ttgtgctctt aaatggttca 360  
ccataaaggg taacaagact tgtgaggtgt gtaaacaaga agttaagaac ttacctgtaa 420  
cactcttacg catccaaagc cttcgaaatt ctggtgttcc tcagctagat gtctctggct 480  
ataggggtgtg gcaggaggta ccggttctag taatcatcag catgctcgct tacttctgct 540  
tcctcgagca gtccttggtt gagaatatgg gtacaggtgc catcgctata tcaactgccg 600  
tttcttggtat tcttggtctt cttgcatcca tgaccgcata aaccatggta atgagaagat 660  
ttgtctggat ttacgcactc gtccagtttg cgttggtcgt tctcttcgcc catatatttt 720  
actctgtggt gaagttgcaa ccagttctgt cagttcttct gtcaacattt gctggatttg 780  
gtgtatgcat atgcggaagt tcagtgatgg ttgagtttgt gagatggaga cgaagatggc 840  
gagccagaag gctagagcaa cagctgaacc atgctttgac tctgtcacia ccgccgcaac 900  
cactggatcc aacaacctct ctgcatcatt caaatacctc atagagagcc aagaagtgga 960  
cagatgattt tacatttata cagtgtagtt tggtaaatg ttatgtaagt atttgtataa 1020  
aagaaaaaga gaaagtgatc caaggaatgc ttaaagatyg ytccttttgt ttgttttaca 1080  
tacacatttg tattgttgta agtttgtaac tttggtttgc tcaatctctg caaatgaaat 1140  
gtttgtagca gtattggttt ctctgtataa taaaagatt taaaattgt

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 313 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..313  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1481480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | His | Gly | Gly | Thr | Ser | Val | Ala | Pro | Gln | Thr | Pro | Asn | Arg | Lys | Gly |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Val | His | Ile | Ala | Arg | Ser | Arg | Ser | Val | Pro | Leu | Asn | Asp | Lys | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ser | Leu | Lys | Gly | Met | Asp | Ser | Phe | Phe | Arg | Val | Ile | Pro | Ser | Thr |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Pro | Arg | Val | Lys | Glu | Gly | Asp | Val | Phe | Ser | Asn | Ala | Ser | Glu | Ala | Gly |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Thr | Glu | Thr | Gly | Asp | Ala | Asp | Gly | Glu | Asp | Ile | Pro | Glu | Asp | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Val | Cys | Arg | Ile | Cys | Leu | Val | Glu | Leu | Cys | Glu | Gly | Gly | Glu | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Lys | Met | Glu | Cys | Ser | Cys | Lys | Gly | Glu | Leu | Ala | Leu | Ala | His | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Asp | Cys | Ala | Leu | Lys | Trp | Phe | Thr | Ile | Lys | Gly | Asn | Lys | Thr | Cys | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Val | Cys | Lys | Gln | Glu | Val | Lys | Asn | Leu | Pro | Val | Thr | Leu | Leu | Arg | Ile |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Ser | Leu | Arg | Asn | Ser | Gly | Val | Pro | Gln | Leu | Asp | Val | Ser | Gly | Tyr |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Arg | Val | Trp | Gln | Glu | Val | Pro | Val | Leu | Val | Ile | Ile | Ser | Met | Leu | Ala |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Tyr | Phe | Cys | Phe | Leu | Glu | Gln | Leu | Leu | Val | Glu | Asn | Met | Gly | Thr | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Ile | Ala | Ile | Ser | Leu | Pro | Phe | Ser | Cys | Ile | Leu | Gly | Leu | Leu | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Met | Thr | Ala | Ser | Thr | Met | Val | Met | Arg | Arg | Phe | Val | Trp | Ile | Tyr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Ser | Val | Gln | Phe | Ala | Leu | Val | Val | Leu | Phe | Ala | His | Ile | Phe | Tyr |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Ser | Val | Val | Lys | Leu | Gln | Pro | Val | Leu | Ser | Val | Leu | Leu | Ser | Thr | Phe |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Ala | Gly | Phe | Gly | Val | Cys | Ile | Cys | Gly | Ser | Ser | Val | Met | Val | Glu | Phe |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Arg | Trp | Arg | Arg | Arg | Trp | Arg | Ala | Arg | Arg | Leu | Glu | Gln | Gln | Leu |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     |     | 285 |     |     |
| Asn | His | Ala | Leu | Thr | Leu | Ser | Gln | Pro | Pro | Gln | Pro | Leu | Asp | Pro | Thr |
|     | 290 |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |
| Thr | Ser | Leu | His | His | Ser | Asn | Thr | Ser |     |     |     |     |     |     |     |
| 305 |     |     |     |     | 310 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 276 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..276  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1481481  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Asp Ser Phe Phe Arg Val Ile Pro Ser Thr Pro Arg Val Lys Glu  
1 5 10 15  
Gly Asp Val Phe Ser Asn Ala Ser Glu Ala Gly Asn Thr Glu Thr Gly  
20 25 30  
Asp Ala Asp Gly Glu Asp Ile Pro Glu Asp Glu Ala Val Cys Arg Ile  
35 40 45  
Cys Leu Val Glu Leu Cys Glu Gly Gly Glu Thr Leu Lys Met Glu Cys  
50 55 60  
Ser Cys Lys Gly Glu Leu Ala Leu Ala His Lys Asp Cys Ala Leu Lys  
65 70 75 80  
Trp Phe Thr Ile Lys Gly Asn Lys Thr Cys Glu Val Cys Lys Gln Glu  
85 90 95  
Val Lys Asn Leu Pro Val Thr Leu Leu Arg Ile Gln Ser Leu Arg Asn  
100 105 110  
Ser Gly Val Pro Gln Leu Asp Val Ser Gly Tyr Arg Val Trp Gln Glu  
115 120 125  
Val Pro Val Leu Val Ile Ile Ser Met Leu Ala Tyr Phe Cys Phe Leu  
130 135 140  
Glu Gln Leu Leu Val Glu Asn Met Gly Thr Gly Ala Ile Ala Ile Ser  
145 150 155 160  
Leu Pro Phe Ser Cys Ile Leu Gly Leu Leu Ala Ser Met Thr Ala Ser  
165 170 175  
Thr Met Val Met Arg Arg Phe Val Trp Ile Tyr Ala Ser Val Gln Phe  
180 185 190  
Ala Leu Val Val Leu Phe Ala His Ile Phe Tyr Ser Val Val Lys Leu  
195 200 205  
Gln Pro Val Leu Ser Val Leu Leu Ser Thr Phe Ala Gly Phe Gly Val  
210 215 220  
Cys Ile Cys Gly Ser Ser Val Met Val Glu Phe Val Arg Trp Arg Arg  
225 230 235 240  
Arg Trp Arg Ala Arg Arg Leu Glu Gln Gln Leu Asn His Ala Leu Thr  
245 250 255  
Leu Ser Gln Pro Pro Gln Pro Leu Asp Pro Thr Thr Ser Leu His His  
260 265 270  
Ser Asn Thr Ser  
275

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..215
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Glu Cys Ser Cys Lys Gly Glu Leu Ala Leu Ala His Lys Asp Cys  
1 5 10 15  
Ala Leu Lys Trp Phe Thr Ile Lys Gly Asn Lys Thr Cys Glu Val Cys  
20 25 30  
Lys Gln Glu Val Lys Asn Leu Pro Val Thr Leu Leu Arg Ile Gln Ser  
35 40 45  
Leu Arg Asn Ser Gly Val Pro Gln Leu Asp Val Ser Gly Tyr Arg Val  
50 55 60  
Trp Gln Glu Val Pro Val Leu Val Ile Ile Ser Met Leu Ala Tyr Phe  
65 70 75 80  
Cys Phe Leu Glu Gln Leu Leu Val Glu Asn Met Gly Thr Gly Ala Ile



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Asp | Asp | Arg | Lys | Glu | Lys | Asn | Thr | Pro | Trp | Leu | Ser | Val | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Phe | Gly | Asp | Trp | Asp | Gln | Lys | Gly | Gly | Gly | Thr | Met | Pro | Asp | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Met | Asp | Phe | Thr | Lys | Ile | Arg | Glu | Met | Arg | Lys | Gln | Asn | Lys | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Pro | Ser | Arg | Ala | Ser | Leu | Gly | Asn | Glu | Glu | Glu | Leu | Ile | Lys | Pro |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
| 50  |     |     |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |  |  |  |
| Pro | Glu | Ser | Ala | Thr | Ser | Thr | Ala | Glu | Leu | Thr | Thr | Val | Gln | Ser | Glu |  |  |  |
| 65  |     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |  |  |  |
| Asn | Arg | Arg | Glu | Phe | Ser | Pro | Ser | His | His | His | Gln | Pro | His | Ser | Pro |  |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |  |  |  |
| Ser | Thr | Arg | Arg | Ser | Met | Phe | Ser | Cys | Phe | Asn | Cys | Cys | Val | Lys | Ala |  |  |  |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |  |  |  |

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1481485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
| Met | Pro | Asp | Tyr | Ser | Met | Asp | Phe | Thr | Lys | Ile | Arg | Glu | Met | Arg | Lys |  |  |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |  |  |
| Gln | Asn | Lys | Arg | Asp | Pro | Ser | Arg | Ala | Ser | Leu | Gly | Asn | Glu | Glu | Glu |  |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |  |
| Leu | Ile | Lys | Pro | Pro | Glu | Ser | Ala | Thr | Ser | Thr | Ala | Glu | Leu | Thr | Thr |  |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |  |
| Val | Gln | Ser | Glu | Asn | Arg | Arg | Glu | Phe | Ser | Pro | Ser | His | His | His | Gln |  |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |  |  |
| Pro | His | Ser | Pro | Ser | Thr | Arg | Arg | Ser | Met | Phe | Ser | Cys | Phe | Asn | Cys |  |  |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |  |  |
| Cys | Val | Lys | Ala |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1481486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
| Met | Asp | Phe | Thr | Lys | Ile | Arg | Glu | Met | Arg | Lys | Gln | Asn | Lys | Arg | Asp |  |  |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |  |  |
| Pro | Ser | Arg | Ala | Ser | Leu | Gly | Asn | Glu | Glu | Glu | Leu | Ile | Lys | Pro | Pro |  |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |  |
| Glu | Ser | Ala | Thr | Ser | Thr | Ala | Glu | Leu | Thr | Thr | Val | Gln | Ser | Glu | Asn |  |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |  |
| Arg | Arg | Glu | Phe | Ser | Pro | Ser | His | His | His | Gln | Pro | His | Ser | Pro | Ser |  |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |  |  |
| Thr | Arg | Arg | Ser | Met | Phe | Ser | Cys | Phe | Asn | Cys | Cys | Val | Lys | Ala |     |  |  |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |     |  |  |  |

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 760 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..760  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1481487  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```
gcmccmbtyy cattayytag aacatcctaw hraaaaaaca aaagtgatca gttttgtttt 60
ctcggggaaa ttttctgaaa gtgaagaaaag ggaaagcaag ttttttttga agtggggaga 120
gagatgggag aaatggggaa ggcgatggga ttgctgatta gcgggacgct tgtgtattac 180
cattgtgcat atcgtaacgc gactcttctc tctctcttct ccgatgtttt cattgttctc 240
ttatgctctc tcgccattct cgggtctcctt tttcgccaac tcaatgtctc ggtaccagtg 300
gatccactag agtggcaaat atcacaggac acagcaagta acatcgttgc acgcttagct 360
aataccgttg gagcagcaga ggggtgttctg aggggttgac caactggaca tgacaagaga 420
ctttttgtca aggtcgtaat ttgcctttac ttcttatcag cgcttgggag actcatatca 480
ggygtaaccg ttgcttatgc aggactatgc ttgttctgtc tctccatgct ctgtcagact 540
tctcaatctc ttggaaactg tgtactaaag cgaggaaatg gccagatttt agaacaagaa 600
gcacattctg atacataata tgtctagctt ttgtttatac ttttcgtctt ttctcatgct 660
tacatgctca tagcttcagt cttcagagta gtttccctt atgtacattg gatttgttgc 720
atactacctt gtgaaaaatg taatgatatt gtttaacctc
```

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 164 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..164  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1481488  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```
Met Gly Glu Met Gly Lys Ala Met Gly Leu Leu Ile Ser Gly Thr Leu
1 5 10 15
Val Tyr Tyr His Cys Ala Tyr Arg Asn Ala Thr Leu Leu Ser Leu Phe
20 25 30
Ser Asp Val Phe Ile Val Leu Leu Cys Ser Leu Ala Ile Leu Gly Leu
35 40 45
Leu Phe Arg Gln Leu Asn Val Ser Val Pro Val Asp Pro Leu Glu Trp
50 55 60
Gln Ile Ser Gln Asp Thr Ala Ser Asn Ile Val Ala Arg Leu Ala Asn
65 70 75 80
Thr Val Gly Ala Ala Glu Gly Val Leu Arg Val Ala Ala Thr Gly His
85 90 95
Asp Lys Arg Leu Phe Val Lys Val Val Ile Cys Leu Tyr Phe Leu Ser
100 105 110
Ala Leu Gly Arg Leu Ile Ser Xaa Val Thr Val Ala Tyr Ala Gly Leu
115 120 125
Cys Leu Phe Cys Leu Ser Met Leu Cys Gln Thr Ser Gln Ser Leu Gly
130 135 140
Asn Cys Val Leu Lys Arg Gly Asn Gly Gln Ile Leu Glu Gln Glu Ala
145 150 155 160
His Ser Asp Thr
```

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 161 amino acids  
    (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..161  
(D) OTHER INFORMATION: / Ceres Seq. ID 1481489  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Gly Lys Ala Met Gly Leu Leu Ile Ser Gly Thr Leu Val Tyr Tyr  
1 5 10 15  
His Cys Ala Tyr Arg Asn Ala Thr Leu Leu Ser Leu Phe Ser Asp Val  
20 25 30  
Phe Ile Val Leu Leu Cys Ser Leu Ala Ile Leu Gly Leu Leu Phe Arg  
35 40 45  
Gln Leu Asn Val Ser Val Pro Val Asp Pro Leu Glu Trp Gln Ile Ser  
50 55 60  
Gln Asp Thr Ala Ser Asn Ile Val Ala Arg Leu Ala Asn Thr Val Gly  
65 70 75 80  
Ala Ala Glu Gly Val Leu Arg Val Ala Ala Thr Gly His Asp Lys Arg  
85 90 95  
Leu Phe Val Lys Val Val Ile Cys Leu Tyr Phe Leu Ser Ala Leu Gly  
100 105 110  
Arg Leu Ile Ser Xaa Val Thr Val Ala Tyr Ala Gly Leu Cys Leu Phe  
115 120 125  
Cys Leu Ser Met Leu Cys Gln Thr Ser Gln Ser Leu Gly Asn Cys Val  
130 135 140  
Leu Lys Arg Gly Asn Gly Gln Ile Leu Glu Gln Glu Ala His Ser Asp  
145 150 155 160  
Thr

- (2) INFORMATION FOR SEQ ID NO:41:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 157 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..157  
(D) OTHER INFORMATION: / Ceres Seq. ID 1481490  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met Gly Leu Leu Ile Ser Gly Thr Leu Val Tyr Tyr His Cys Ala Tyr  
1 5 10 15  
Arg Asn Ala Thr Leu Leu Ser Leu Phe Ser Asp Val Phe Ile Val Leu  
20 25 30  
Leu Cys Ser Leu Ala Ile Leu Gly Leu Leu Phe Arg Gln Leu Asn Val  
35 40 45  
Ser Val Pro Val Asp Pro Leu Glu Trp Gln Ile Ser Gln Asp Thr Ala  
50 55 60  
Ser Asn Ile Val Ala Arg Leu Ala Asn Thr Val Gly Ala Ala Glu Gly  
65 70 75 80  
Val Leu Arg Val Ala Ala Thr Gly His Asp Lys Arg Leu Phe Val Lys  
85 90 95  
Val Val Ile Cys Leu Tyr Phe Leu Ser Ala Leu Gly Arg Leu Ile Ser  
100 105 110  
Xaa Val Thr Val Ala Tyr Ala Gly Leu Cys Leu Phe Cys Leu Ser Met  
115 120 125  
Leu Cys Gln Thr Ser Gln Ser Leu Gly Asn Cys Val Leu Lys Arg Gly

130 135 140  
Asn Gly Gln Ile Leu Glu Gln Glu Ala His Ser Asp Thr  
145 150 155

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..661
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| mcacaaaaya | actaaaaaac | aatcagatct | gagatcgaac  | aaaacaacat | gaacacgtta | 60  |
| atcccatcgg | agaaaagatg | gatcatcacc | ggcgttttac  | tagccgggtt | agttggcggg | 120 |
| gctttgcttt | tcacaagctt | catacgagcc | gctgacgaaa  | cgctcttcct | ctgttccaca | 180 |
| gcaagcgcca | aaagcagagc | ggtggctgcg | gcagctgatt  | acgaagcgac | tccgattcag | 240 |
| cttcaagcga | tcgtccacta | cgcgacatct | aacgttggtc  | cacaacagaa | tcttgctgag | 300 |
| atctcgatct | ctttcaacat | cttgaaaaag | ctagctccgg  | ctaactttct | cgtgttcggg | 360 |
| ctcggtcgtg | actcgctcat | gtgggcttct | ttaaattccac | gtggcaaaac | cttgttcttg | 420 |
| gaagaagatc | ttgaatggtt | tcagaaagtg | accaaagact  | ctcctttctt | acgtgcgcat | 480 |
| cacgtgcgtt | acaggacgca | gcttcaacaa | gccgattcgc  | ttctacgttc | gtacaaaacg | 540 |
| gagcctaact | gttttccggc | gaaatcttat | ctccggggaa  | acgagaagtg | taagctagct | 600 |
| ctcacgggac | tgcccgatga | gttctacgat | acagagtggg  | atctgctgat | ggtcgatgct | 660 |

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..204
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Thr | Leu | Ile | Pro | Ser | Glu | Lys | Arg | Trp | Ile | Ile | Thr | Gly | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Leu | Ala | Gly | Leu | Val | Gly | Gly | Ala | Leu | Leu | Phe | Thr | Ser | Phe | Ile |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Ala | Ala | Asp | Glu | Thr | Leu | Phe | Leu | Cys | Ser | Thr | Ala | Ser | Ala | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Arg | Ala | Val | Ala | Ala | Ala | Ala | Asp | Tyr | Glu | Ala | Thr | Pro | Ile | Gln |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Gln | Ala | Ile | Val | His | Tyr | Ala | Thr | Ser | Asn | Val | Val | Pro | Gln | Gln |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Asn | Leu | Ala | Glu | Ile | Ser | Ile | Ser | Phe | Asn | Ile | Leu | Lys | Lys | Leu | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Pro | Ala | Asn | Phe | Leu | Val | Phe | Gly | Leu | Gly | Arg | Asp | Ser | Leu | Met | Trp |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ala | Ser | Leu | Asn | Pro | Arg | Gly | Lys | Thr | Leu | Phe | Leu | Glu | Glu | Asp | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Trp | Phe | Gln | Lys | Val | Thr | Lys | Asp | Ser | Pro | Phe | Leu | Arg | Ala | His |
|     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| His | Val | Arg | Tyr | Arg | Thr | Gln | Leu | Gln | Gln | Ala | Asp | Ser | Leu | Leu | Arg |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

Ser Tyr Lys Thr Glu Pro Asn Cys Phe Pro Ala Lys Ser Tyr Leu Arg  
165 170 175  
Gly Asn Glu Lys Cys Lys Leu Ala Leu Thr Gly Leu Pro Asp Glu Phe  
180 185 190  
Tyr Asp Thr Glu Trp Asp Leu Leu Met Val Asp Ala  
195 200

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1163 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

aatgctcgta agttcaagca aaatcacaag agcgagagag atggtgacga aaacagagga 60  
gaagcaattg aaccagctag agattcaagt cgataatggc ggaggtggaa catgggagta 120  
tctttgtctc gttcgtaatc tcaaaacttcg tcggtcggag aaagtattaa aacacggttc 180  
ctcgattttg aatgatccga ggaaacgacg tgctctcggg ccatatgaat ggacactaaa 240  
tgagcagggtg gcaattgcag ctatggactg tcaatgtctc ggtgtcgcac agagttgcat 300  
taaggctttg cagaagaaat ttcttgggag caaaagggtt gggaggcttg aggcattgct 360  
tcttgaagca aagggattat ggggagaggc tgaggaagca tatgcgagtc ttttgaaga 420  
taatccactc gaccaagcga tacacaaacg aagagtggct atatccaagg cactaggaaa 480  
accttcata gccattgagc ttcttaacaa atatcttgaa ctattcatgg ctgatcatga 540  
tgcatggaga gaacttgcag agctttatct ttcttgcaa atgtataagc aagcagcttt 600  
ctgctatgaa gagctcatac tatctcagcc tactgttcca ttgtaccacc tcgcatatgc 660  
tgaggttctc tatacaatcg gtggagtaga aaacattatc tcagcaagaa aatactatgc 720  
agcgaccgta gatttaacag gcggcaaaaa cactagagct cttctcggaa tctgcttggtg 780  
tgcatcggcc attgcacagc tctcaaaagg caggaacaaa gaggacaaa acgctacggc 840  
agccccagag cttcattccc tggtcgcagc tgcagtagag aaagaatata agcaaaaagc 900  
cccggacaaa cttcagctca tctcttcgcg gttaagaatc ttgaagactt gatcgcaagt 960  
aaacgatggt ctggcccaca agacgcaaac gacttagcag tagtagatag tcggaaaata 1020  
tcgaactcta aattcaaata actttcttta aagtttaaac caaagagaat tttgattact 1080  
gttagatacc aaaaccaa atactgtatca ctccctagcc tttacgggtt ccatgcttgc 1140  
gacgtgcagc ttcttttcta tcg

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..316
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Leu Val Ser Ser Ser Lys Ile Thr Arg Ala Arg Glu Met Val Thr  
1 5 10 15  
Lys Thr Glu Glu Lys Gln Leu Asn Gln Leu Glu Ile Gln Val Asp Asn  
20 25 30  
Gly Gly Gly Gly Thr Trp Glu Tyr Leu Cys Leu Val Arg Asn Leu Lys  
35 40 45  
Leu Arg Arg Ser Glu Lys Val Leu Lys His Gly Ser Ser Ile Leu Asn  
50 55 60  
Asp Pro Arg Lys Arg Ser Ala Leu Gly Pro Tyr Glu Trp Thr Leu Asn

65 70 75 80  
Glu Gln Val Ala Ile Ala Ala Met Asp Cys Gln Cys Leu Gly Val Ala  
85 90 95  
Gln Ser Cys Ile Lys Ala Leu Gln Lys Lys Phe Pro Gly Ser Lys Arg  
100 105 110  
Val Gly Arg Leu Glu Ala Leu Leu Glu Ala Lys Gly Leu Trp Gly  
115 120 125  
Glu Ala Glu Glu Ala Tyr Ala Ser Leu Leu Glu Asp Asn Pro Leu Asp  
130 135 140  
Gln Ala Ile His Lys Arg Arg Val Ala Ile Ser Lys Ala Leu Gly Lys  
145 150 155 160  
Pro Ser Ile Ala Ile Glu Leu Leu Asn Lys Tyr Leu Glu Leu Phe Met  
165 170 175  
Ala Asp His Asp Ala Trp Arg Glu Leu Ala Glu Leu Tyr Leu Ser Leu  
180 185 190  
Gln Met Tyr Lys Gln Ala Ala Phe Cys Tyr Glu Glu Leu Ile Leu Ser  
195 200 205  
Gln Pro Thr Val Pro Leu Tyr His Leu Ala Tyr Ala Glu Val Leu Tyr  
210 215 220  
Thr Ile Gly Gly Val Glu Asn Ile Ile Ser Ala Arg Lys Tyr Tyr Ala  
225 230 235 240  
Ala Thr Val Asp Leu Thr Gly Gly Lys Asn Thr Arg Ala Leu Leu Gly  
245 250 255  
Ile Cys Leu Cys Ala Ser Ala Ile Ala Gln Leu Ser Lys Gly Arg Asn  
260 265 270  
Lys Glu Asp Lys Asp Ala Thr Ala Pro Glu Leu His Ser Leu Ala  
275 280 285  
Ala Ala Ala Val Glu Lys Glu Tyr Lys Gln Lys Ala Pro Asp Lys Leu  
290 295 300  
Gln Leu Ile Ser Ser Ala Leu Arg Ile Leu Lys Thr  
305 310 315

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..316
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Leu Val Ser Ser Lys Ile Thr Arg Ala Arg Glu Met Val Thr  
1 5 10 15  
Lys Thr Glu Glu Lys Gln Leu Asn Gln Leu Glu Ile Gln Val Asp Asn  
20 25 30  
Gly Gly Gly Gly Thr Trp Glu Tyr Leu Cys Leu Val Arg Asn Leu Lys  
35 40 45  
Leu Arg Arg Ser Glu Lys Val Leu Lys His Gly Ser Ser Ile Leu Asn  
50 55 60  
Asp Pro Arg Lys Arg Ser Ala Leu Gly Pro Tyr Glu Trp Thr Leu Asn  
65 70 75 80  
Glu Gln Val Ala Ile Ala Ala Met Asp Cys Gln Cys Leu Gly Val Ala  
85 90 95  
Gln Ser Cys Ile Lys Ala Leu Gln Lys Lys Phe Pro Gly Ser Lys Arg  
100 105 110  
Val Gly Arg Leu Glu Ala Leu Leu Glu Ala Lys Gly Leu Trp Gly  
115 120 125

Glu Ala Glu Glu Ala Tyr Ala Ser Leu Leu Glu Asp Asn Pro Leu Asp  
130 135 140  
Gln Ala Ile His Lys Arg Arg Val Ala Ile Ser Lys Ala Leu Gly Lys  
145 150 155 160  
Pro Ser Ile Ala Ile Glu Leu Leu Asn Lys Tyr Leu Glu Leu Phe Met  
165 170 175  
Ala Asp His Asp Ala Trp Arg Glu Leu Ala Glu Leu Tyr Leu Ser Leu  
180 185 190  
Gln Met Tyr Lys Gln Ala Ala Phe Cys Tyr Glu Glu Leu Ile Leu Ser  
195 200 205  
Gln Pro Thr Val Pro Leu Tyr His Leu Ala Tyr Ala Glu Val Leu Tyr  
210 215 220  
Thr Ile Gly Gly Val Glu Asn Ile Ile Ser Ala Arg Lys Tyr Tyr Ala  
225 230 235 240  
Ala Thr Val Asp Leu Thr Gly Gly Lys Asn Thr Arg Ala Leu Leu Gly  
245 250 255  
Ile Cys Leu Cys Ala Ser Ala Ile Ala Gln Leu Ser Lys Gly Arg Asn  
260 265 270  
Lys Glu Asp Lys Asp Ala Thr Ala Ala Pro Glu Leu His Ser Leu Ala  
275 280 285  
Ala Ala Ala Val Glu Lys Glu Tyr Lys Gln Lys Ala Pro Asp Lys Leu  
290 295 300  
Gln Leu Ile Ser Ser Ala Leu Arg Ile Leu Lys Thr  
305 310 315

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..303

(D) OTHER INFORMATION: / Ceres Seq. ID 1481507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Val Thr Lys Thr Glu Glu Lys Gln Leu Asn Gln Leu Glu Ile Gln  
1 5 10 15  
Val Asp Asn Gly Gly Gly Gly Thr Trp Glu Tyr Leu Cys Leu Val Arg  
20 25 30  
Asn Leu Lys Leu Arg Arg Ser Glu Lys Val Leu Lys His Gly Ser Ser  
35 40 45  
Ile Leu Asn Asp Pro Arg Lys Arg Ser Ala Leu Gly Pro Tyr Glu Trp  
50 55 60  
Thr Leu Asn Glu Gln Val Ala Ile Ala Ala Met Asp Cys Gln Cys Leu  
65 70 75 80  
Gly Val Ala Gln Ser Cys Ile Lys Ala Leu Gln Lys Lys Phe Pro Gly  
85 90 95  
Ser Lys Arg Val Gly Arg Leu Glu Ala Leu Leu Leu Glu Ala Lys Gly  
100 105 110  
Leu Trp Gly Glu Ala Glu Glu Ala Tyr Ala Ser Leu Leu Glu Asp Asn  
115 120 125  
Pro Leu Asp Gln Ala Ile His Lys Arg Arg Val Ala Ile Ser Lys Ala  
130 135 140  
Leu Gly Lys Pro Ser Ile Ala Ile Glu Leu Leu Asn Lys Tyr Leu Glu  
145 150 155 160  
Leu Phe Met Ala Asp His Asp Ala Trp Arg Glu Leu Ala Glu Leu Tyr  
165 170 175  
Leu Ser Leu Gln Met Tyr Lys Gln Ala Ala Phe Cys Tyr Glu Glu Leu



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Leu | Ser | Gln | Pro | Thr | Val | Pro | Leu | Tyr | His | Leu | Ala | Tyr | Ala | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Leu | Tyr | Thr | Ile | Gly | Gly | Val | Glu | Asn | Ile | Ile | Ser | Ala | Arg | Lys |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Tyr | Tyr | Ala | Ala | Thr | Val | Asp | Leu | Thr | Gly | Gly | Lys | Asn | Thr | Arg | Ala |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Leu | Leu | Gly | Ile | Cys | Leu | Cys | Ala | Ser | Ala | Ile | Ala | Gln | Leu | Ser | Lys |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |
| Gly | Arg | Asn | Lys | Glu | Asp | Lys | Asp | Ala | Thr | Ala | Ala | Pro | Glu | Leu | His |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Ser | Leu | Ala | Ala | Ala | Ala | Val | Glu | Lys | Glu | Tyr | Lys | Gln | Lys | Ala | Pro |
|     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Asp | Lys | Leu | Gln | Leu | Ile | Ser | Ser | Ala | Leu | Arg | Ile | Leu | Lys | Thr |     |
| 290 |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1259
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| atttcacttt  | ccgattttat  | aaaattgatt | cttctcttct  | tcttaaacc   | atgaagagtt  | 60   |
| catgatttct  | taagctcgca  | gcataatcga | tggcgaattt  | gagtttgagc  | ttgtatctaa  | 120  |
| tcctccggat  | ttacgctctt  | ttgttgctgt | tcaatgtctc  | cttcgctaaa  | acacttaaac  | 180  |
| gagacatgaa  | agctttgaat  | gagataaaga | aattgggtggg | atggagattg  | gtataactctt | 240  |
| gggttgagga  | tgatccttgt  | ggcgaaggag | ttttgcctcc  | gtggctctgga | gttacttgct  | 300  |
| ctaaagttgg  | cgattatcgt  | gtcgtcgtca | agctagaagt  | gtattcaatg  | tcgatagttg  | 360  |
| ggaatttccc  | aaaggctata  | acgaagctct | tagatctcac  | tgttttggat  | atgcataata  | 420  |
| acaaattaac  | aggctctatt  | cctccagaaa | ttgggcggct  | taagcggctt  | atcacactga  | 480  |
| atttgagggtg | gaacaaactt  | caacaggcac | tgctccttga  | aattgggtgga | ttgaagagtc  | 540  |
| taacttatct  | gtacctgagt  | tttaacaatt | tcaaaggaga  | aatcccaaaa  | gaacttgcaa  | 600  |
| atctccatga  | gctccagtac  | ttacatatct | aggagaatca  | ttttactggg  | cgaattccag  | 660  |
| cagagctggg  | aacattacaa  | aaacttcgcc | acttggtatg  | tggaacaat   | aacttagtgg  | 720  |
| ggagtataag  | cgatcttttt  | cgcattgaag | gatgctttcc  | agctcttaga  | aacctgtttt  | 780  |
| taaacaataa  | ttacttgact  | ggaggactcc | caaacaagct  | tgcaaatact  | acaaacctgg  | 840  |
| agatcttgta  | cttatctttc  | aacaaaatga | ctggagcaat  | acccgctgca  | cttgccagta  | 900  |
| taccaagact  | aactaacttg  | cacttggaac | acaatctatt  | caatggaagt  | atacctgaag  | 960  |
| ccttctacaa  | gcataccaaac | ctaaaagata | tgtacataga  | agggaaatgct | ttcaaatcag  | 1020 |
| acgtgaaggc  | gattgggtgca | cataaggctc | tcgaactttc  | tgacacagac  | ttccttggtt  | 1080 |
| agttatgtat  | agcacaactt  | tgtttcattt | acagatagga  | atttggcagt  | gttatctggt  | 1140 |
| tatttaagat  | tcattttctc  | tgttaaagcg | agattgtagt  | tgatgtgttt  | tctgaatgta  | 1200 |
| aaagattcct  | tatccatgta  | tgaaaattga | atataaaggg  | aatctggttt  | gttctttcc   |      |

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..330
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asn | Leu | Ser | Leu | Ser | Leu | Tyr | Leu | Ile | Leu | Arg | Ile | Tyr | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Leu | Leu | Leu | Phe | Asn | Val | Ser | Phe | Ala | Lys | Thr | Leu | Lys | Arg | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Lys | Ala | Leu | Asn | Glu | Ile | Lys | Lys | Leu | Val | Gly | Trp | Arg | Leu | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Ser | Trp | Val | Gly | Asp | Asp | Pro | Cys | Gly | Asp | Gly | Val | Leu | Pro | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Trp | Ser | Gly | Val | Thr | Cys | Ser | Lys | Val | Gly | Asp | Tyr | Arg | Val | Val | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Leu | Glu | Val | Tyr | Ser | Met | Ser | Ile | Val | Gly | Asn | Phe | Pro | Lys | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Thr | Lys | Leu | Leu | Asp | Leu | Thr | Val | Leu | Asp | Met | His | Asn | Asn | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Thr | Gly | Pro | Ile | Pro | Pro | Glu | Ile | Gly | Arg | Leu | Lys | Arg | Leu | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Thr | Leu | Asn | Leu | Arg | Trp | Asn | Lys | Leu | Gln | Gln | Ala | Leu | Pro | Pro | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Gly | Gly | Leu | Lys | Ser | Leu | Thr | Tyr | Leu | Tyr | Leu | Ser | Phe | Asn | Asn |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Phe | Lys | Gly | Glu | Ile | Pro | Lys | Glu | Leu | Ala | Asn | Leu | His | Glu | Leu | Gln |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Tyr | Leu | His | Ile | Gln | Glu | Asn | His | Phe | Thr | Gly | Arg | Ile | Pro | Ala | Glu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Gly | Thr | Leu | Gln | Lys | Leu | Arg | His | Leu | Asp | Ala | Gly | Asn | Asn | Asn |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Leu | Val | Gly | Ser | Ile | Ser | Asp | Leu | Phe | Arg | Ile | Glu | Gly | Cys | Phe | Pro |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Leu | Arg | Asn | Leu | Phe | Leu | Asn | Asn | Asn | Tyr | Leu | Thr | Gly | Gly | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Pro | Asn | Lys | Leu | Ala | Asn | Leu | Thr | Asn | Leu | Glu | Ile | Leu | Tyr | Leu | Ser |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Phe | Asn | Lys | Met | Thr | Gly | Ala | Ile | Pro | Ala | Ala | Leu | Ala | Ser | Ile | Pro |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Arg | Leu | Thr | Asn | Leu | His | Leu | Asp | His | Asn | Leu | Phe | Asn | Gly | Ser | Ile |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Pro | Glu | Ala | Phe | Tyr | Lys | His | Pro | Asn | Leu | Lys | Asp | Met | Tyr | Ile | Glu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gly | Asn | Ala | Phe | Lys | Ser | Asp | Val | Lys | Ala | Ile | Gly | Ala | His | Lys | Val |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Leu | Glu | Leu | Ser | Asp | Thr | Asp | Phe | Leu | Val |     |     |     |     |     |     |
|     |     |     |     | 325 |     |     |     | 330 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..298
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ala | Leu | Asn | Glu | Ile | Lys | Lys | Leu | Val | Gly | Trp | Arg | Leu | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Ser | Trp | Val | Gly | Asp | Asp | Pro | Cys | Gly | Asp | Gly | Val | Leu | Pro | Pro |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ser | Gly | Val | Thr | Cys | Ser | Lys | Val | Gly | Asp | Tyr | Arg | Val | Val | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Leu | Glu | Val | Tyr | Ser | Met | Ser | Ile | Val | Gly | Asn | Phe | Pro | Lys | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Thr | Lys | Leu | Leu | Asp | Leu | Thr | Val | Leu | Asp | Met | His | Asn | Asn | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Thr | Gly | Pro | Ile | Pro | Pro | Glu | Ile | Gly | Arg | Leu | Lys | Arg | Leu | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Leu | Asn | Leu | Arg | Trp | Asn | Lys | Leu | Gln | Gln | Ala | Leu | Pro | Pro | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Gly | Gly | Leu | Lys | Ser | Leu | Thr | Tyr | Leu | Tyr | Leu | Ser | Phe | Asn | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Lys | Gly | Glu | Ile | Pro | Lys | Glu | Leu | Ala | Asn | Leu | His | Glu | Leu | Gln |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Tyr | Leu | His | Ile | Gln | Glu | Asn | His | Phe | Thr | Gly | Arg | Ile | Pro | Ala | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Gly | Thr | Leu | Gln | Lys | Leu | Arg | His | Leu | Asp | Ala | Gly | Asn | Asn | Asn |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Val | Gly | Ser | Ile | Ser | Asp | Leu | Phe | Arg | Ile | Glu | Gly | Cys | Phe | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Leu | Arg | Asn | Leu | Phe | Leu | Asn | Asn | Asn | Tyr | Leu | Thr | Gly | Gly | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Asn | Lys | Leu | Ala | Asn | Leu | Thr | Asn | Leu | Glu | Ile | Leu | Tyr | Leu | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Asn | Lys | Met | Thr | Gly | Ala | Ile | Pro | Ala | Ala | Leu | Ala | Ser | Ile | Pro |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Arg | Leu | Thr | Asn | Leu | His | Leu | Asp | His | Asn | Leu | Phe | Asn | Gly | Ser | Ile |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Pro | Glu | Ala | Phe | Tyr | Lys | His | Pro | Asn | Leu | Lys | Asp | Met | Tyr | Ile | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Asn | Ala | Phe | Lys | Ser | Asp | Val | Lys | Ala | Ile | Gly | Ala | His | Lys | Val |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Leu | Glu | Leu | Ser | Asp | Thr | Asp | Phe | Leu | Val |     |     |     |     |     |     |
|     | 290 |     |     |     |     | 295 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..244
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ile | Val | Gly | Asn | Phe | Pro | Lys | Ala | Ile | Thr | Lys | Leu | Leu | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Thr | Val | Leu | Asp | Met | His | Asn | Asn | Lys | Leu | Thr | Gly | Pro | Ile | Pro |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Glu | Ile | Gly | Arg | Leu | Lys | Arg | Leu | Ile | Thr | Leu | Asn | Leu | Arg | Trp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Lys | Leu | Gln | Gln | Ala | Leu | Pro | Pro | Glu | Ile | Gly | Gly | Leu | Lys | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Thr | Tyr | Leu | Tyr | Leu | Ser | Phe | Asn | Asn | Phe | Lys | Gly | Glu | Ile | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Glu | Leu | Ala | Asn | Leu | His | Glu | Leu | Gln | Tyr | Leu | His | Ile | Gln | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Asn | His | Phe | Thr | Gly | Arg | Ile | Pro | Ala | Glu | Leu | Gly | Thr | Leu | Gln | Lys |

|                                                                 |                                                     |  |     |  |     |
|-----------------------------------------------------------------|-----------------------------------------------------|--|-----|--|-----|
|                                                                 | 100                                                 |  | 105 |  | 110 |
| Leu Arg His                                                     | Leu Asp Ala Gly Asn Asn Asn Leu Val Gly Ser Ile Ser |  |     |  |     |
|                                                                 | 115                                                 |  | 120 |  | 125 |
| Asp Leu Phe Arg Ile Glu Gly Cys Phe Pro Ala Leu Arg Asn Leu Phe |                                                     |  |     |  |     |
|                                                                 | 130                                                 |  | 135 |  | 140 |
| Leu Asn Asn Asn Tyr Leu Thr Gly Gly Leu Pro Asn Lys Leu Ala Asn |                                                     |  |     |  |     |
|                                                                 | 145                                                 |  | 150 |  | 155 |
| Leu Thr Asn Leu Glu Ile Leu Tyr Leu Ser Phe Asn Lys Met Thr Gly |                                                     |  |     |  |     |
|                                                                 | 165                                                 |  | 170 |  | 175 |
| Ala Ile Pro Ala Ala Leu Ala Ser Ile Pro Arg Leu Thr Asn Leu His |                                                     |  |     |  |     |
|                                                                 | 180                                                 |  | 185 |  | 190 |
| Leu Asp His Asn Leu Phe Asn Gly Ser Ile Pro Glu Ala Phe Tyr Lys |                                                     |  |     |  |     |
|                                                                 | 195                                                 |  | 200 |  | 205 |
| His Pro Asn Leu Lys Asp Met Tyr Ile Glu Gly Asn Ala Phe Lys Ser |                                                     |  |     |  |     |
|                                                                 | 210                                                 |  | 215 |  | 220 |
| Asp Val Lys Ala Ile Gly Ala His Lys Val Leu Glu Leu Ser Asp Thr |                                                     |  |     |  |     |
|                                                                 | 225                                                 |  | 230 |  | 235 |
| Asp Phe Leu Val                                                 |                                                     |  |     |  | 240 |

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 860 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..860
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481520

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| cattaagctg actaagttcg agaacgagga agctgtctgc aacccccaaa gaactcgtgc  | 60  |
| taatgatatg aagaatttag cactgctgc tgtaaaagca agcagatttt atagggagtt   | 120 |
| gaattcccaa actgtcaaac acttgacac actccatgag taccttgga tgatgatggc    | 180 |
| tgtccaaggc gcatttgcag atagatctag tgctttactg acagttcaga cgcttctatc  | 240 |
| agagcttctt tctctgcaaa ctagagttga gaagctagag gctgcatcat cgaagggtatt | 300 |
| tggtggtgac aaatcaagga tccgaaaaat agaagagtta aaagaaacaa tcaagggtcac | 360 |
| tgaggatgca aaaaatggtt ccatcaaagg gtatgagcga atcaaggaaa acaaccgatc  | 420 |
| tgaggttgag aggttggaca gagaaaggcg tgcagacttc atgaacatga tgaagggttt  | 480 |
| tgttgttaac caggttggat acgcagagaa aatgggaaac gtctgggcaa aggttgcaga  | 540 |
| agagaccagc caatacgata gagagaagca gagcagctaa caaacacaga aaaaaagaga  | 600 |
| gtgaacgatg ttcatttttg cataaccata ccaaattccat gtatggcaca gaatcacatt | 660 |
| gcgtaataat ggtttgtcaa aaagtgtagt ttcctttttc atatggttga tctatcttga  | 720 |
| tagagattgg taaacgttct tgtttgtttt ctttagttgc tgtaaattag ttttctagaa  | 780 |
| gcattctctg ctacagctgc attgactcat acccattgtt ttctggtata tgccgcaaaa  | 840 |
| gatatatctg atagtttggc                                              |     |

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..192
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Ile Lys Leu Thr Lys Phe Glu Asn Glu Glu Ala Val Cys Asn Pro Gln

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   |     | 5   |     | 10  |     | 15  |     |     |     |     |     |     |     |     |     |
| Arg | Thr | Arg | Ala | Asn | Asp | Met | Lys | Asn | Leu | Ala | Thr | Ala | Ala | Val | Lys |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ser | Arg | Phe | Tyr | Arg | Glu | Leu | Asn | Ser | Gln | Thr | Val | Lys | His | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Thr | Leu | His | Glu | Tyr | Leu | Gly | Met | Met | Met | Ala | Val | Gln | Gly | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Ala | Asp | Arg | Ser | Ser | Ala | Leu | Leu | Thr | Val | Gln | Thr | Leu | Leu | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Leu | Pro | Ser | Leu | Gln | Thr | Arg | Val | Glu | Lys | Leu | Glu | Ala | Ala | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ser | Lys | Val | Phe | Gly | Gly | Asp | Lys | Ser | Arg | Ile | Arg | Lys | Ile | Glu | Glu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Lys | Glu | Thr | Ile | Lys | Val | Thr | Glu | Asp | Ala | Lys | Asn | Val | Ala | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Gly | Tyr | Glu | Arg | Ile | Lys | Glu | Asn | Asn | Arg | Ser | Glu | Val | Glu | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Asp | Arg | Glu | Arg | Arg | Ala | Asp | Phe | Met | Asn | Met | Met | Lys | Gly | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Val | Asn | Gln | Val | Gly | Tyr | Ala | Glu | Lys | Met | Gly | Asn | Val | Trp | Ala |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Lys | Val | Ala | Glu | Thr | Ser | Gln | Tyr | Asp | Arg | Glu | Lys | Gln | Ser | Ser |     |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1481522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Asn | Leu | Ala | Thr | Ala | Ala | Val | Lys | Ala | Ser | Arg | Phe | Tyr | Arg |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Glu | Leu | Asn | Ser | Gln | Thr | Val | Lys | His | Leu | Asp | Thr | Leu | His | Glu | Tyr |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Leu | Gly | Met | Met | Met | Ala | Val | Gln | Gly | Ala | Phe | Ala | Asp | Arg | Ser | Ser |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ala | Leu | Leu | Thr | Val | Gln | Thr | Leu | Leu | Ser | Glu | Leu | Pro | Ser | Leu | Gln |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Thr | Arg | Val | Glu | Lys | Leu | Glu | Ala | Ala | Ser | Ser | Lys | Val | Phe | Gly | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Asp | Lys | Ser | Arg | Ile | Arg | Lys | Ile | Glu | Glu | Leu | Lys | Glu | Thr | Ile | Lys |
|     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Val | Thr | Glu | Asp | Ala | Lys | Asn | Val | Ala | Ile | Lys | Gly | Tyr | Glu | Arg | Ile |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Lys | Glu | Asn | Asn | Arg | Ser | Glu | Val | Glu | Arg | Leu | Asp | Arg | Glu | Arg | Arg |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Ala | Asp | Phe | Met | Asn | Met | Met | Lys | Gly | Phe | Val | Val | Asn | Gln | Val | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Tyr | Ala | Glu | Lys | Met | Gly | Asn | Val | Trp | Ala | Lys | Val | Ala | Glu | Glu | Thr |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Ser | Gln | Tyr | Asp | Arg | Glu | Lys | Gln | Ser | Ser |     |     |     |     |     |     |
|     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```
Met Met Met Ala Val Gln Gly Ala Phe Ala Asp Arg Ser Ser Ala Leu
1 5 10 15
Leu Thr Val Gln Thr Leu Leu Ser Glu Leu Pro Ser Leu Gln Thr Arg
20 25 30
Val Glu Lys Leu Glu Ala Ala Ser Lys Val Phe Gly Gly Asp Lys
35 40 45
Ser Arg Ile Arg Lys Ile Glu Glu Leu Lys Glu Thr Ile Lys Val Thr
50 55 60
Glu Asp Ala Lys Asn Val Ala Ile Lys Gly Tyr Glu Arg Ile Lys Glu
65 70 75 80
Asn Asn Arg Ser Glu Val Glu Arg Leu Asp Arg Glu Arg Arg Ala Asp
85 90 95
Phe Met Asn Met Met Lys Gly Phe Val Val Asn Gln Val Gly Tyr Ala
100 105 110
Glu Lys Met Gly Asn Val Trp Ala Lys Val Ala Glu Glu Thr Ser Gln
115 120 125
Tyr Asp Arg Glu Lys Gln Ser Ser
130 135
```

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2180
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```
attactcaat tagtacaagt tggtatacaa ctaaattcttc atttggttaa tcattctttac 60
tcaaattgaa tagtagtggt cgtgtgaaaa caagaaaagt ggaaaaggac aaaagagaga 120
gtaaaggacg cctcctaata aagcactctt cttccttttc actttcctca ttgaagagag 180
agccaaattc agcttaaagc cccataagcg taagcgtaag cgtaagcgta agcgtaagcg 240
taagcgtaag cgtaagcgta agcgtaagcg taagcgtaag cgcggggata aatctctctc 300
ttcctcacct gcgttttcgt ggagcatctt cttcaacaat ggctgcttct ccgatctgat 360
catatcctga tttgaatttt gctatctctc atgcctcgaa ctgcgtttgt cgacgtagca 420
tcctagtgcg tgaggaagaa gaagaagatg agcttcttta tcctctccgt cgtcgttttc 480
gtttctctcg ctttcttctc tcttcgcgat tccgttgatt catctgtttc cgcttcacag 540
gatcctctca gactcatatt aggttcaccg aattttggaa catggaaagg tggaatctca 600
ttagcaccag gacctgaatc tgatgatgtt gtctctgatt acctcctctt agcagctcat 660
agaaccaaga gacctgacat tcttagagct ttttaagcctt accatggtgg ctggaacatc 720
accaataatc actattgggc ttctgttgga tttacaggtg ctcttggttt catactagct 780
gttatctggc tcttgctctt tggtctctct cttgttggtt atcattgctt caaatggaga 840
atatgtgata aagctaaagg atcatcattc gatacacgaa gaatctgttt cattttgttg 900
attgtgttta catgtgttgc agcgggtgga tgcattcttt tatctgttgg acaagataag 960
tttcataccg aagctatgca tactcttaag tatgttgtaa accagtcaga ctacactgtg 1020
```

(2) INFORMATION FOR SEO ID NO:57:

(A) LENGTH: 245 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..245

(D) OTHER INFORMATION: / Ceres Seq. ID 1481525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Phe | Phe | Ile | Leu | Ser | Val | Val | Val | Phe | Val | Ser | Leu | Ala | Phe |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Phe | Ser | Leu | Pro | His | Ser | Val | Asp | Ser | Ser | Val | Ser | Ala | Ser | Gln | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Leu | Arg | Leu | Ile | Leu | Gly | Ser | Pro | Asn | Phe | Gly | Thr | Trp | Lys | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Ile | Ser | Leu | Ala | Pro | Gly | Pro | Glu | Ser | Asp | Asp | Val | Val | Ser | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Leu | Leu | Leu | Ala | Ala | His | Arg | Thr | Lys | Arg | Pro | Asp | Ile | Leu | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Phe | Lys | Pro | Tyr | His | Gly | Gly | Trp | Asn | Ile | Thr | Asn | Asn | His | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Trp | Ala | Ser | Val | Gly | Phe | Thr | Gly | Ala | Pro | Gly | Phe | Ile | Leu | Ala | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Trp | Leu | Leu | Ser | Phe | Gly | Ser | Leu | Leu | Val | Val | Tyr | His | Cys | Phe |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Trp | Arg | Ile | Cys | Asp | Lys | Ala | Lys | Gly | Ser | Ser | Phe | Asp | Thr | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Ile | Cys | Phe | Ile | Leu | Leu | Ile | Val | Phe | Thr | Cys | Val | Ala | Ala | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Cys | Ile | Leu | Leu | Ser | Val | Gly | Gln | Asp | Lys | Phe | His | Thr | Glu | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Met | His | Thr | Leu | Lys | Tyr | Val | Val | Asn | Gln | Ser | Asp | Tyr | Thr | Val | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Leu | Gln | Asn | Val | Thr | Gln | Tyr | Leu | Ser | Leu | Ala | Lys | Thr | Ile | Asn |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Thr | Gln | Ile | Val | Ile | Pro | Ser | Asp | Val | Met | Gly | Glu | Ile | Asp | Lys |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 210                                                             | 215 | 220 |
| Leu Asn Val Asn Leu Asn Thr Ala Ala Val Thr Leu Gly Glu Thr Thr |     |     |
| 225                                                             | 230 | 235 |
| Thr Asp Lys Arg Cys                                             |     | 240 |
|                                                                 | 245 |     |

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..289
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ile | Leu | Ser | Phe | Val | Gly | Leu | Leu | Ser | Val | Leu | Arg | His |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | His | Val | Val | His | Ile | Phe | Val | Val | Ser | Gly | Trp | Ile | Leu | Val |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Val | Thr | Phe | Val | Leu | Cys | Gly | Val | Phe | Leu | Ile | Leu | Asn | Asn | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ser | Asp | Thr | Cys | Val | Ala | Met | Lys | Glu | Trp | Val | Asp | Asn | Pro | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Glu | Thr | Ala | Leu | Ser | Ser | Ile | Leu | Pro | Cys | Val | Asp | Gln | Gln | Thr |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Asn | Gln | Thr | Leu | Ser | Gln | Ser | Lys | Val | Val | Ile | Asn | Ser | Ile | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |
| Val | Val | Asn | Thr | Phe | Val | Tyr | Ala | Val | Ala | Asn | Thr | Asn | Pro | Ala |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Gly | Gln | Asp | Arg | Tyr | Tyr | Asn | Gln | Ser | Gly | Pro | Pro | Met | Pro | Pro |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Cys | Ile | Pro | Phe | Asp | Ala | Asn | Met | Glu | Asp | Arg | Gln | Cys | Ser | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Glu | Leu | Ser | Ile | Glu | Asn | Ala | Ser | Ser | Val | Trp | Glu | Asn | Tyr | Lys |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| Glu | Val | Thr | Pro | Ser | Gly | Ile | Cys | Thr | Thr | Val | Gly | Arg | Val | Thr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |
| Asp | Thr | Phe | Gly | Gln | Leu | Val | Ala | Ala | Val | Asn | Glu | Ser | Tyr | Ala |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |
| Glu | His | Tyr | Thr | Pro | Pro | Leu | Leu | Ser | Phe | Arg | Asp | Cys | Asn | Phe |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |
| Arg | Glu | Thr | Phe | Met | Ser | Ile | Thr | Ser | Asp | Tyr | Cys | Pro | Pro | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Arg | Asn | Leu | Arg | Ile | Val | Asn | Ala | Gly | Leu | Gly | Leu | Ile | Ser | Val |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Val | Leu | Leu | Cys | Leu | Val | Leu | Trp | Ile | Phe | Tyr | Ala | Asn | Pro | Pro |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |
| Gly | Arg | Lys | Cys | Leu | Arg | Ile | His | Thr | Leu | Lys | Glu | Lys | Met | Ile |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Leu | Val | Thr | Ala | Trp | Ile | Leu | Ile | Thr | Gln | Met | Thr | Asn | Leu | Ser |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |

Leu

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid



(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..235  
(D) OTHER INFORMATION: / Ceres Seq. ID 1481527  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:  
Met Lys Glu Trp Val Asp Asn Pro His Ala Glu Thr Ala Leu Ser Ser  
1 5 10 15  
Ile Leu Pro Cys Val Asp Gln Gln Thr Thr Asn Gln Thr Leu Ser Gln  
20 25 30  
Ser Lys Val Val Ile Asn Ser Ile Val Thr Val Val Asn Thr Phe Val  
35 40 45  
Tyr Ala Val Ala Asn Thr Asn Pro Ala Pro Gly Gln Asp Arg Tyr Tyr  
50 55 60  
Asn Gln Ser Gly Pro Pro Met Pro Pro Leu Cys Ile Pro Phe Asp Ala  
65 70 75 80  
Asn Met Glu Asp Arg Gln Cys Ser Pro Trp Glu Leu Ser Ile Glu Asn  
85 90 95  
Ala Ser Ser Val Trp Glu Asn Tyr Lys Cys Glu Val Thr Pro Ser Gly  
100 105 110  
Ile Cys Thr Thr Val Gly Arg Val Thr Pro Asp Thr Phe Gly Gln Leu  
115 120 125  
Val Ala Ala Val Asn Glu Ser Tyr Ala Leu Glu His Tyr Thr Pro Pro  
130 135 140  
Leu Leu Ser Phe Arg Asp Cys Asn Phe Val Arg Glu Thr Phe Met Ser  
145 150 155 160  
Ile Thr Ser Asp Tyr Cys Pro Pro Leu Val Arg Asn Leu Arg Ile Val  
165 170 175  
Asn Ala Gly Leu Gly Leu Ile Ser Val Gly Val Leu Leu Cys Leu Val  
180 185 190  
Leu Trp Ile Phe Tyr Ala Asn Pro Lys Gly Arg Lys Cys Leu Arg  
195 200 205  
Ile His Thr Leu Lys Glu Lys Met Ile Ala Leu Val Thr Ala Trp Ile  
210 215 220  
Leu Ile Thr Gln Met Thr Asn Leu Ser Phe Leu  
225 230 235

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..634  
(D) OTHER INFORMATION: / Ceres Seq. ID 1481532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| aaaacatctc | tcgccgtcag | gttacatcta | tcgccaccgc | aaagagacca  | ccgtctcctc  | 60  |
| cgcaatcttc | ataacctaaa | caaccctcat | cccctggtac | ttaaacaatg  | ggaaagagga  | 120 |
| aatcaagagc | aaagcctgct | cctacgaagc | gaatggataa | gcttgacaca  | atcttttagtt | 180 |
| gtcctttctg | caatcacggg | tctagtgtcg | aatgcatcat | tgatatgaag  | catctgattg  | 240 |
| gtaaagcagc | ttgtagaatc | tgtgaagaaa | gctttaggta | ctactatcac  | agctttgact  | 300 |
| gaagctatag | acatttatag | cgaatggatc | gatgagtgcg | agaggggttaa | taccgcggaa  | 360 |
| gatgatgttg | tgcaagaaga | ggaggatgat | gaagatgacc | atgtctctgt  | caaaaggaag  | 420 |
| tataacttct | gagacgagtg | ttttatcgaa | aatcatgtaa | gtcgtcgtct  | tagagttatc  | 480 |
| tgctttatgt | tgtaatatct | atctgatgaa | atcacaagaa | caatcttttag | tgtttttctca | 540 |

gtgtctgata gagaaacata catttaagtg aacaatcttt aatcacaata acagtgtatg 600  
attatgattt gtaagtggat ttaaggcttt gctt

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Lys Thr Ser Leu Ala Val Arg Leu His Leu Ser Pro Pro Gln Arg Asp  
1 5 10 15  
His Arg Leu Leu Arg Asn Leu His Asn Leu Asn Asn Pro His Pro Leu  
20 25 30  
Val Leu Lys Gln Trp Glu Arg Gly Asn Gln Glu Gln Ser Leu Leu Leu  
35 40 45  
Arg Ser Glu Trp Ile Ser Leu Thr Gln Ser Leu Val Val Leu Ser Ala  
50 55 60  
Ile Thr Gly Leu Val Ser Asn Ala Ser Leu Ile  
65 70 75

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met Gly Lys Arg Lys Ser Arg Ala Lys Pro Ala Pro Thr Lys Arg Met  
1 5 10 15  
Asp Lys Leu Asp Thr Ile Phe Ser Cys Pro Phe Cys Asn His Gly Ser  
20 25 30  
Ser Val Glu Cys Ile Ile Asp Met Lys His Leu Ile Gly Lys Ala Ala  
35 40 45  
Cys Arg Ile Cys Glu Glu Ser Phe Arg Tyr Tyr Tyr His Ser Phe Asp  
50 55 60

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Asp Lys Leu Asp Thr Ile Phe Ser Cys Pro Phe Cys Asn His Gly

|                                                                 |    |    |    |
|-----------------------------------------------------------------|----|----|----|
| 1                                                               | 5  | 10 | 15 |
| Ser Ser Val Glu Cys Ile Ile Asp Met Lys His Leu Ile Gly Lys Ala |    |    |    |
|                                                                 | 20 | 25 | 30 |
| Ala Cys Arg Ile Cys Glu Glu Ser Phe Arg Tyr Tyr Tyr His Ser Phe |    |    |    |
|                                                                 | 35 | 40 | 45 |

Asp

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1668 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1668
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| atctgcattg ttctccgcct ctctctctca aactcttcag tttgcaaaac ccttaagaag  | 60   |
| gtgtgaatta gtaagtaatg gggaagaaga agttttattga taagaaaaag gcggcgactt | 120  |
| tcgagttgtg tcctcgtgat acgtcagacc caagatacag tgatgcacca ggtggtgata  | 180  |
| agatcttctt acgagttgat caaaaccctg ttaacatcaa tggtttcatt gaagaagatg  | 240  |
| aagaagattt tagagttagg gtatcctgat gatggttata attacttgga gcatttgaga  | 300  |
| gagattaaga atactgggtg tggttctaata ttctatgtga atcctaagta tgaggttgct | 360  |
| cagttacctc gtgatgttaa ggcttatgat gcgtctcgtg ttaagatctc tggtatggtg  | 420  |
| aatgaagaag gtaatgataa taagttgatg tatagtgttg cgtccaagac tgttaacgtc  | 480  |
| aagggtgcaga aagctattga tcctgaagtt gctgcgttgc ttgaaaacag tgatgggtct | 540  |
| gagtttggtt ctgatgttga ggatttgga gaagattttg ttgttcaagc taatcttact   | 600  |
| caaaaggggtg aatcttctgg tgtgagcaat ggagagctcg agttttctgt aagacgtgag | 660  |
| gtagagagaaa gagaaagtga tgaacctgtg gctgaaaacc cgagagttcc tcgtcaaatt | 720  |
| gatgagctat ttgatcagct cgaactcaat gaatatggaa gtgatagtga cggtgatggt  | 780  |
| tacatagctg aagatggaga agaagaagaa gaagaagact tcatggctca agaagttcag  | 840  |
| aatcttattc atgggaaggc aaaagattat gagcttgaag aaaaatatat gaaccctgcg  | 900  |
| gatatactga agaacagtga ctctgtcaga gataaagagg aagtggacac tgctgctcat  | 960  |
| gttatccgcc gaactgtaga atatggtgaa aattttgata acgggaatga agatgaattt  | 1020 |
| gtagagctga ctgaagaaag cagcgatgaa agcgagaagc atgattgtga aaccatagtc  | 1080 |
| tcaacatact cgaatctcga taacctccct ggtaaaatcc ttgctgcaga gtcagctagg  | 1140 |
| cagaagaagc tgagtgaaac attagctaac gcattgagtt caaatggaag aatcattaat  | 1200 |
| ctccaaggga gagagaggat tcctgtcagag tttttacctg gtaggagagc tgaacaaacc | 1260 |
| gatgtcaaag cggaaatccc aaaagctgaa ccgatcaaga ggaagactca tggtaagag   | 1320 |
| tcgaaagaag agaagaaga gcggaataat gctgtaaaag ccgaaaagcg agaagcaagg   | 1380 |
| ataattaaga aacagacaaa gatgctgtat tgcggtgaaa cgcagcgtgc tcaaagagct  | 1440 |
| gttgctacct ctggtccatc gtcgagacct ctaaaataat atgttactaa ggtaaaacaa  | 1500 |
| aacaattctc agactgttta aaaccagttt ttccagccat ttcgtgtaat atttgctgtt  | 1560 |
| tgtttttttc tttttcatca agatttgaaa atcttgaatc ttgttttgga tgtggacgtt  | 1620 |
| ttgaatatta tttattactt ttactagtct aatttcgaga aagtgatg               |      |

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..438
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met His Gln Val Val Ile Arg Ser Ser Tyr Glu Leu Ile Lys Thr Leu  
1 5 10 15  
Leu Thr Ser Met Val Ser Leu Lys Lys Met Lys Lys Ile Leu Glu Leu  
20 25 30  
Gly Tyr Pro Asp Asp Gly Tyr Asn Tyr Leu Glu His Leu Arg Glu Ile  
35 40 45  
Lys Asn Thr Gly Gly Gly Ser Asn Phe Tyr Val Asn Pro Lys Tyr Glu  
50 55 60  
Val Ala Gln Leu Pro Arg Asp Val Lys Ala Tyr Asp Ala Ser Arg Val  
65 70 75 80  
Lys Ile Ser Gly Met Val Asn Glu Glu Gly Asn Asp Asn Lys Leu Met  
85 90 95  
Tyr Ser Val Ala Ser Lys Thr Val Asn Val Lys Val Gln Lys Ala Ile  
100 105 110  
Asp Pro Glu Val Ala Ala Leu Leu Glu Asn Ser Asp Gly Ser Glu Phe  
115 120 125  
Gly Ser Asp Val Glu Asp Leu Glu Glu Asp Phe Val Val Gln Ala Asn  
130 135 140  
Leu Thr Gln Lys Gly Glu Ser Ser Gly Val Ser Asn Gly Glu Leu Glu  
145 150 155 160  
Phe Ser Val Arg Arg Glu Val Arg Glu Arg Glu Ser Asp Glu Pro Val  
165 170 175  
Ala Glu Asn Pro Arg Val Pro Arg Gln Ile Asp Glu Leu Phe Asp Gln  
180 185 190  
Leu Glu Leu Asn Glu Tyr Gly Ser Asp Ser Asp Gly Asp Gly Tyr Ile  
195 200 205  
Ala Glu Asp Gly Glu Glu Glu Glu Glu Asp Phe Met Ala Gln Glu  
210 215 220  
Val Gln Asn Leu Ile His Gly Lys Ala Lys Asp Tyr Glu Leu Glu Glu  
225 230 235 240  
Lys Tyr Met Asn Pro Ala Asp Ile Leu Lys Asn Ser Asp Ser Val Arg  
245 250 255  
Asp Lys Glu Glu Val Asp Thr Ala Ala His Val Ile Arg Arg Thr Val  
260 265 270  
Glu Tyr Gly Glu Asn Phe Asp Asn Gly Asn Glu Asp Glu Phe Val Glu  
275 280 285  
Leu Thr Glu Glu Ser Ser Asp Glu Ser Glu Lys His Asp Cys Glu Thr  
290 295 300  
Ile Val Ser Thr Tyr Ser Asn Leu Asp Asn Leu Pro Gly Lys Ile Leu  
305 310 315 320  
Ala Ala Glu Ser Ala Arg Gln Lys Lys Leu Ser Glu Thr Leu Ala Asn  
325 330 335  
Ala Leu Ser Ser Asn Gly Arg Ile Ile Asn Leu Gln Gly Arg Glu Arg  
340 345 350  
Ile Pro Val Glu Phe Leu Pro Gly Arg Arg Ala Glu Gln Thr Asp Val  
355 360 365  
Lys Ala Glu Ile Pro Lys Ala Glu Pro Ile Lys Arg Lys Thr His Gly  
370 375 380  
Gln Glu Ser Lys Glu Glu Lys Lys Glu Arg Lys Asn Ala Val Lys Ala  
385 390 395 400  
Glu Lys Arg Glu Ala Arg Ile Ile Lys Lys Gln Thr Lys Met Leu Tyr  
405 410 415  
Cys Gly Glu Thr Gln Arg Ala Gln Arg Ala Val Ala Thr Ser Gly Pro  
420 425 430  
Ser Ser Arg Pro Leu Lys  
435

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 419 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..419  
(D) OTHER INFORMATION: / Ceres Seq. ID 1481542

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ser | Leu | Lys | Lys | Met | Lys | Lys | Ile | Leu | Glu | Leu | Gly | Tyr | Pro |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Asp | Gly | Tyr | Asn | Tyr | Leu | Glu | His | Leu | Arg | Glu | Ile | Lys | Asn | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Gly | Gly | Ser | Asn | Phe | Tyr | Val | Asn | Pro | Lys | Tyr | Glu | Val | Ala | Gln |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Pro | Arg | Asp | Val | Lys | Ala | Tyr | Asp | Ala | Ser | Arg | Val | Lys | Ile | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Met | Val | Asn | Glu | Glu | Gly | Asn | Asp | Asn | Lys | Leu | Met | Tyr | Ser | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Ser | Lys | Thr | Val | Asn | Val | Lys | Val | Gln | Lys | Ala | Ile | Asp | Pro | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Ala | Ala | Leu | Leu | Glu | Asn | Ser | Asp | Gly | Ser | Glu | Phe | Gly | Ser | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Glu | Asp | Leu | Glu | Glu | Asp | Phe | Val | Val | Gln | Ala | Asn | Leu | Thr | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Lys | Gly | Glu | Ser | Ser | Gly | Val | Ser | Asn | Gly | Glu | Leu | Glu | Phe | Ser | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Arg | Glu | Val | Arg | Glu | Arg | Glu | Ser | Asp | Glu | Pro | Val | Ala | Glu | Asn |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Arg | Val | Pro | Arg | Gln | Ile | Asp | Glu | Leu | Phe | Asp | Gln | Leu | Glu | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asn | Glu | Tyr | Gly | Ser | Asp | Ser | Asp | Gly | Asp | Gly | Tyr | Ile | Ala | Glu | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Glu | Glu | Glu | Glu | Glu | Glu | Asp | Phe | Met | Ala | Gln | Glu | Val | Gln | Asn |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Ile | His | Gly | Lys | Ala | Lys | Asp | Tyr | Glu | Leu | Glu | Glu | Lys | Tyr | Met |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asn | Pro | Ala | Asp | Ile | Leu | Lys | Asn | Ser | Asp | Ser | Val | Arg | Asp | Lys | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Val | Asp | Thr | Ala | Ala | His | Val | Ile | Arg | Arg | Thr | Val | Glu | Tyr | Gly |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Asn | Phe | Asp | Asn | Gly | Asn | Glu | Asp | Glu | Phe | Val | Glu | Leu | Thr | Glu |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Glu | Ser | Ser | Asp | Glu | Ser | Glu | Lys | His | Asp | Cys | Glu | Thr | Ile | Val | Ser |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Thr | Tyr | Ser | Asn | Leu | Asp | Asn | Leu | Pro | Gly | Lys | Ile | Leu | Ala | Ala | Glu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ser | Ala | Arg | Gln | Lys | Lys | Leu | Ser | Glu | Thr | Leu | Ala | Asn | Ala | Leu | Ser |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ser | Asn | Gly | Arg | Ile | Asn | Leu | Gln | Gly | Arg | Glu | Arg | Ile | Pro | Val |     |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Glu | Phe | Leu | Pro | Gly | Arg | Arg | Ala | Glu | Gln | Thr | Asp | Val | Lys | Ala | Glu |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     |     | 350 |     |     |
| Ile | Pro | Lys | Ala | Glu | Pro | Ile | Lys | Arg | Lys | Thr | His | Gly | Gln | Glu | Ser |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Lys | Glu | Glu | Lys | Lys | Glu | Arg | Lys | Asn | Ala | Val | Lys | Ala | Glu | Lys | Arg |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Glu | Ala | Arg | Ile | Ile | Lys | Lys | Gln | Thr | Lys | Met | Leu | Tyr | Cys | Gly | Glu |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |

Thr Gln Arg Ala Gln Arg Ala Val Ala Thr Ser Gly Pro Ser Ser Arg  
405 410 415  
Pro Leu Lys

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 413 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..413

(D) OTHER INFORMATION: / Ceres Seq. ID 1481543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Lys | Ile | Leu | Glu | Leu | Gly | Tyr | Pro | Asp | Asp | Gly | Tyr | Asn | Tyr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Glu | His | Leu | Arg | Glu | Ile | Lys | Asn | Thr | Gly | Gly | Gly | Ser | Asn | Phe |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Tyr | Val | Asn | Pro | Lys | Tyr | Glu | Val | Ala | Gln | Leu | Pro | Arg | Asp | Val | Lys |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ala | Tyr | Asp | Ala | Ser | Arg | Val | Lys | Ile | Ser | Gly | Met | Val | Asn | Glu | Glu |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Gly | Asn | Asp | Asn | Lys | Leu | Met | Tyr | Ser | Val | Ala | Ser | Lys | Thr | Val | Asn |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Val | Lys | Val | Gln | Lys | Ala | Ile | Asp | Pro | Glu | Val | Ala | Ala | Leu | Leu | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Ser | Asp | Gly | Ser | Glu | Phe | Gly | Ser | Asp | Val | Glu | Asp | Leu | Glu | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Phe | Val | Val | Gln | Ala | Asn | Leu | Thr | Gln | Lys | Gly | Glu | Ser | Ser | Gly |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Ser | Asn | Gly | Glu | Leu | Glu | Phe | Ser | Val | Arg | Arg | Glu | Val | Arg | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Arg | Glu | Ser | Asp | Glu | Pro | Val | Ala | Glu | Asn | Pro | Arg | Val | Pro | Arg | Gln |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Asp | Glu | Leu | Phe | Asp | Gln | Leu | Glu | Leu | Asn | Glu | Tyr | Gly | Ser | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Asp | Gly | Asp | Gly | Tyr | Ile | Ala | Glu | Asp | Gly | Glu | Glu | Glu | Glu | Glu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Asp | Phe | Met | Ala | Gln | Glu | Val | Gln | Asn | Leu | Ile | His | Gly | Lys | Ala |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Lys | Asp | Tyr | Glu | Leu | Glu | Glu | Lys | Tyr | Met | Asn | Pro | Ala | Asp | Ile | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Asn | Ser | Asp | Ser | Val | Arg | Asp | Lys | Glu | Glu | Val | Asp | Thr | Ala | Ala |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| His | Val | Ile | Arg | Arg | Thr | Val | Glu | Tyr | Gly | Glu | Asn | Phe | Asp | Asn | Gly |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asn | Glu | Asp | Glu | Phe | Val | Glu | Leu | Thr | Glu | Glu | Ser | Ser | Asp | Glu | Ser |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Glu | Lys | His | Asp | Cys | Glu | Thr | Ile | Val | Ser | Thr | Tyr | Ser | Asn | Leu | Asp |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asn | Leu | Pro | Gly | Lys | Ile | Leu | Ala | Ala | Glu | Ser | Ala | Arg | Gln | Lys | Lys |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu | Ser | Glu | Thr | Leu | Ala | Asn | Ala | Leu | Ser | Ser | Asn | Gly | Arg | Ile | Ile |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Asn | Leu | Gln | Gly | Arg | Glu | Arg | Ile | Pro | Val | Glu | Phe | Leu | Pro | Gly | Arg |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Arg | Ala | Glu | Gln | Thr | Asp | Val | Lys | Ala | Glu | Ile | Pro | Lys | Ala | Glu | Pro |

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 340 345 350
Ile Lys Arg Lys Thr His Gly Gln Glu Ser Lys Glu Glu Lys Lys Glu
 355 360 365
Arg Lys Asn Ala Val Lys Ala Glu Lys Arg Glu Ala Arg Ile Ile Lys
 370 375 380
Lys Gln Thr Lys Met Leu Tyr Cys Gly Glu Thr Gln Arg Ala Gln Arg
 385 390 395 400
Ala Val Ala Thr Ser Gly Pro Ser Ser Arg Pro Leu Lys
 405 410
```

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1601
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

aatcttcctc attcgaaggt tactcgcaact tcctctgcac acttcttcct ctccatctaa 60
cctcagttact cctacaatcc tctaagaatc catagatcta ctgctgggaa aagcttcgcg 120
acaatgtctt ggcctacgga ttctgagtta aattccataa aggaggcagt ggctcagatg 180
agtggaagag ataaaggaga agttcgagtg gtggtcgctc cttatcgtat atgtccttta 240
ggagctcaca ttgatcacca ggggtggaact gtatcagcta tgacgattaa agggatcctt 300
cttggttttg ttccatcggg tgatactcag gtccagttgc gctctgcaca atttgaagga 360
gaagtatgtt tcagagtaga tgaaatccag cacccaatag gcctagcaaa caagaatggt 420
gcaagcacgc catctccatc gaaggaaaaa agtatctggg gtacttatgc cagaggagca 480
gtttatgcgt tacagagcag caaaaagaat ctcaaacagg gcattattgg ttacctcagt 540
ggctcaaattg gactagatag ctccgggctt agctcatcag ctgctgttgg tgtggcatat 600
ctgctagctc tagagaatgc aaacgaattg actgtatccc caacagaaaa tatcgaatat 660
gacaggctta ttgagaatgt gtatctgggt ctgcggaatg gaattttgga tcaatcagct 720
atthttgcttt cgaattatgg gtgtctaaca tacatggact gcaagacttt ggaccacgag 780
cttgtagagg ctccctgaact ggagaaaccg ttcaggatat tgtagcatt ctcaggcttg 840
aggcaggcgt tgaccaccaa cccaggatat aatctgcgag tttctgagtg tcaagaggca 900
gcaaaagtgc ttttgactgc atctgggaac agtgagctgg aacctacgtt gtgcaatgtt 960
gagcatgcgg tctatgaagc tcacaagcat gagctgaaac cggtttttagc taaaagagca 1020
gagcattatt tctcggagaa catgcgagtt atcaaaggac gggaagcctg ggcttcaggg 1080
aatcttgaag aatttggaag gctaatttca gcatccggct tgagttccat tgagaattac 1140
gaatgcggtg cggagccact gatccagcta tacaagattc ttctgaaggc tcctggtgta 1200
tatggagcta gattcagcgg tgcaggtttc aggggatgtt gtctagcctt tgtagatgca 1260
gtaaaagctg aggcagctgc ttcatatgtg aaggatgaat atgaaaaggc ccaaccgag 1320
tttgctaaca atctaaatgg aggaaaacct gttctcatct gtgaagcagg tgacgctgct 1380
cgtgttcttc tctgatcaat cctggagttt ttggtttctt cccacttaa actcgatttt 1440
tttgctccct atatatctca cgcttattga ttctttgctt gtttatctct ttttgatcct 1500
gtctgagaaa ttctctggtc tctttggtcg gagtttcatc attgcttgat acattttttt 1560
tgctacaaat acataatgta aatcattctc taccgttttc c
```

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..423
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Trp | Pro | Thr | Asp | Ser | Glu | Leu | Asn | Ser | Ile | Lys | Glu | Ala | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Gln | Met | Ser | Gly | Arg | Asp | Lys | Gly | Glu | Val | Arg | Val | Val | Val | Ala |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Pro | Tyr | Arg | Ile | Cys | Pro | Leu | Gly | Ala | His | Ile | Asp | His | Gln | Gly | Gly |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Thr | Val | Ser | Ala | Met | Thr | Ile | Lys | Gly | Ile | Leu | Leu | Gly | Phe | Val | Pro |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ser | Gly | Asp | Thr | Gln | Val | Gln | Leu | Arg | Ser | Ala | Gln | Phe | Glu | Gly | Glu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Val | Cys | Phe | Arg | Val | Asp | Glu | Ile | Gln | His | Pro | Ile | Gly | Leu | Ala | Asn |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Asn | Gly | Ala | Ser | Thr | Pro | Ser | Pro | Ser | Lys | Glu | Lys | Ser | Ile | Trp |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Gly | Thr | Tyr | Ala | Arg | Gly | Ala | Val | Tyr | Ala | Leu | Gln | Ser | Ser | Lys | Lys |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Leu | Lys | Gln | Gly | Ile | Ile | Gly | Tyr | Leu | Ser | Gly | Ser | Asn | Gly | Leu |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Asp | Ser | Ser | Gly | Leu | Ser | Ser | Ser | Ala | Ala | Val | Gly | Val | Ala | Tyr | Leu |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Ala | Leu | Glu | Asn | Ala | Asn | Glu | Leu | Thr | Val | Ser | Pro | Thr | Glu | Asn |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ile | Glu | Tyr | Asp | Arg | Leu | Ile | Glu | Asn | Val | Tyr | Leu | Gly | Leu | Arg | Asn |
|     | 180 |     |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Gly | Ile | Leu | Asp | Gln | Ser | Ala | Ile | Leu | Leu | Ser | Asn | Tyr | Gly | Cys | Leu |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Tyr | Met | Asp | Cys | Lys | Thr | Leu | Asp | His | Glu | Leu | Val | Gln | Ala | Pro |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | Leu | Glu | Lys | Pro | Phe | Arg | Ile | Leu | Leu | Ala | Phe | Ser | Gly | Leu | Arg |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Gln | Ala | Leu | Thr | Thr | Asn | Pro | Gly | Tyr | Asn | Leu | Arg | Val | Ser | Glu | Cys |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gln | Glu | Ala | Ala | Lys | Val | Leu | Leu | Thr | Ala | Ser | Gly | Asn | Ser | Glu | Leu |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Glu | Pro | Thr | Leu | Cys | Asn | Val | Glu | His | Ala | Val | Tyr | Glu | Ala | His | Lys |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| His | Glu | Leu | Lys | Pro | Val | Leu | Ala | Lys | Arg | Ala | Glu | His | Tyr | Phe | Ser |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Glu | Asn | Met | Arg | Val | Ile | Lys | Gly | Arg | Glu | Ala | Trp | Ala | Ser | Gly | Asn |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Leu | Glu | Glu | Phe | Gly | Lys | Leu | Ile | Ser | Ala | Ser | Gly | Leu | Ser | Ser | Ile |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Glu | Asn | Tyr | Glu | Cys | Gly | Ala | Glu | Pro | Leu | Ile | Gln | Leu | Tyr | Lys | Ile |
|     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| Leu | Leu | Lys | Ala | Pro | Gly | Val | Tyr | Gly | Ala | Arg | Phe | Ser | Gly | Ala | Gly |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Phe | Arg | Gly | Cys | Cys | Leu | Ala | Phe | Val | Asp | Ala | Val | Lys | Ala | Glu | Ala |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ala | Ala | Ser | Tyr | Val | Lys | Asp | Glu | Tyr | Glu | Lys | Ala | Gln | Pro | Glu | Phe |
| 385 |     |     |     | 390 |     |     |     |     |     | 395 |     |     |     |     | 400 |
| Ala | Asn | Asn | Leu | Asn | Gly | Gly | Lys | Pro | Val | Leu | Ile | Cys | Glu | Ala | Gly |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Asp | Ala | Ala | Arg | Val | Leu | Leu |     |     |     |     |     |     |     |     |     |
|     |     |     | 420 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 amino acids

(B) TYPE: amino acid



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 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..405
 (D) OTHER INFORMATION: / Ceres Seq. ID 1481546
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

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[illegible]

405

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 371 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..371

(D) OTHER INFORMATION: / Ceres Seq. ID 1481547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Ile | Lys | Gly | Ile | Leu | Leu | Gly | Phe | Val | Pro | Ser | Gly | Asp | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Val | Gln | Leu | Arg | Ser | Ala | Gln | Phe | Glu | Gly | Glu | Val | Cys | Phe | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Asp | Glu | Ile | Gln | His | Pro | Ile | Gly | Leu | Ala | Asn | Lys | Asn | Gly | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Thr | Pro | Ser | Pro | Ser | Lys | Glu | Lys | Ser | Ile | Trp | Gly | Thr | Tyr | Ala |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Gly | Ala | Val | Tyr | Ala | Leu | Gln | Ser | Ser | Lys | Lys | Asn | Leu | Lys | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Ile | Ile | Gly | Tyr | Leu | Ser | Gly | Ser | Asn | Gly | Leu | Asp | Ser | Ser | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Ser | Ser | Ser | Ala | Ala | Val | Gly | Val | Ala | Tyr | Leu | Leu | Ala | Leu | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Ala | Asn | Glu | Leu | Thr | Val | Ser | Pro | Thr | Glu | Asn | Ile | Glu | Tyr | Asp |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Arg | Leu | Ile | Glu | Asn | Val | Tyr | Leu | Gly | Leu | Arg | Asn | Gly | Ile | Leu | Asp |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Gln | Ser | Ala | Ile | Leu | Leu | Ser | Asn | Tyr | Gly | Cys | Leu | Thr | Tyr | Met | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Cys | Lys | Thr | Leu | Asp | His | Glu | Leu | Val | Gln | Ala | Pro | Glu | Leu | Glu | Lys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Phe | Arg | Ile | Leu | Leu | Ala | Phe | Ser | Gly | Leu | Arg | Gln | Ala | Leu | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Asn | Pro | Gly | Tyr | Asn | Leu | Arg | Val | Ser | Glu | Cys | Gln | Glu | Ala | Ala |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Val | Leu | Leu | Thr | Ala | Ser | Gly | Asn | Ser | Glu | Leu | Glu | Pro | Thr | Leu |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Cys | Asn | Val | Glu | His | Ala | Val | Tyr | Glu | Ala | His | Lys | His | Glu | Leu | Lys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Pro | Val | Leu | Ala | Lys | Arg | Ala | Glu | His | Tyr | Phe | Ser | Glu | Asn | Met | Arg |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Ile | Lys | Gly | Arg | Glu | Ala | Trp | Ala | Ser | Gly | Asn | Leu | Glu | Glu | Phe |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Lys | Leu | Ile | Ser | Ala | Ser | Gly | Leu | Ser | Ser | Ile | Glu | Asn | Tyr | Glu |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Cys | Gly | Ala | Glu | Pro | Leu | Ile | Gln | Leu | Tyr | Lys | Ile | Leu | Leu | Lys | Ala |
|     |     |     | 290 |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Pro | Gly | Val | Tyr | Gly | Ala | Arg | Phe | Ser | Gly | Ala | Gly | Phe | Arg | Gly | Cys |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Cys | Leu | Ala | Phe | Val | Asp | Ala | Val | Lys | Ala | Glu | Ala | Ala | Ala | Ser | Tyr |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Val | Lys | Asp | Glu | Tyr | Glu | Lys | Ala | Gln | Pro | Glu | Phe | Ala | Asn | Asn | Leu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Asn | Gly | Gly | Lys | Pro | Val | Leu | Ile | Cys | Glu | Ala | Gly | Asp | Ala | Ala | Arg |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |

Val Leu Leu  
370

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..915
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| caaaagagag | aaaaggatgg  | tcaataacgg | tccatgatct | ctccggttca | cccgtggcta  | 60  |
| tggcctctat | ggtaacacct  | ttcgtacct  | ctcctggttc | gaaccgggtg | actcgggtcaa | 120 |
| gtcccggagc | gtggcttatt  | cttcgacctg | acggttgac  | atggaagcca | tggggaagac  | 180 |
| tagaagcatg | gcgtgaggct  | ggttactctg | acactctagg | ttatcgtttc | gagcttttcc  | 240 |
| aagacggtat | agccaccgca  | gtttctgcat | cgctcgat   | cagtttgaaa | aatggcggga  | 300 |
| gttttggtat | tgatgttacc  | ggcgggtaca | gcacaacggc | gtctacgccg | acaacgagtc  | 360 |
| ctcaaggaag | ctgggatctc  | ggatccgggt | caagcgccgg | ttcaagaccc | gcgtcgagac  | 420 |
| caggatcagg | atccgggtcg  | gatttcggat | atctactacc | gcaacatccg | tctgcggccg  | 480 |
| cgcaaaacag | agggttcgtt  | atgtcggcta | cgggtgaagg | agttgggaaa | cgaagcaaac  | 540 |
| cagaagtaga | agtcgggtgtg | acgcacgtga | catgtacgga | ggatgcagca | gcgcacgtgg  | 600 |
| cattagctgc | ggcgggtgat  | ctgagtttgg | atgcttgacg | gcttttctca | cacaagctaa  | 660 |
| ggaaagagct | gagacagcaa  | agccagcttg | gtgtcggttg | acttggttcg | ctttgtcgtt  | 720 |
| ttaccaattc | atgagttgtc  | ttccactcac | atttttttgg | tttgaatttt | ctattttttt  | 780 |
| ctttttaaga | tagcgttagg  | aattagccag | ccattttttt | gagaggtgga | tgtcatcatt  | 840 |
| attaaaaatt | gttaatatct  | ttctcagtac | agctaagaaa | tgacagtaac | aactaacaaa  | 900 |
| caactcatta | tctcc       |            |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..232
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Glu | Arg | Lys | Gly | Trp | Ser | Ile | Thr | Val | His | Asp | Leu | Ser | Gly | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Pro | Val | Ala | Met | Ala | Ser | Met | Val | Thr | Pro | Phe | Val | Pro | Ser | Pro | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Ser | Asn | Arg | Val | Thr | Arg | Ser | Ser | Pro | Gly | Ala | Trp | Leu | Ile | Leu | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Pro | Asp | Gly | Cys | Thr | Trp | Lys | Pro | Trp | Gly | Arg | Leu | Glu | Ala | Trp | Arg |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Ala | Gly | Tyr | Ser | Asp | Thr | Leu | Gly | Tyr | Arg | Phe | Glu | Leu | Phe | Gln |
|     |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Gly | Ile | Ala | Thr | Ala | Val | Ser | Ala | Ser | Ser | Ser | Ile | Ser | Leu | Lys |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asn | Gly | Gly | Ser | Phe | Val | Ile | Asp | Val | Thr | Gly | Gly | Thr | Ser | Thr | Thr |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Ala | Ser | Thr | Pro | Thr | Thr | Ser | Pro | Gln | Gly | Ser | Trp | Asp | Leu | Gly | Ser |
|     |     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Ser | Ser | Ala | Gly | Ser | Arg | Pro | Ala | Ser | Arg | Pro | Gly | Ser | Gly | Ser |

(2) INFORMATION FOR SEQ ID NO:74:

(A) LENGTH: 213 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..213

(D) OTHER INFORMATION: / Ceres Seq. ID 1481566

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..210

(D) OTHER INFORMATION: / Ceres Seq. ID 1481567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Thr | Pro | Phe | Val | Pro | Ser | Pro | Gly | Ser | Asn | Arg | Val | Thr | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ser | Pro | Gly | Ala | Trp | Leu | Ile | Leu | Arg | Pro | Asp | Gly | Cys | Thr | Trp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Pro | Trp | Gly | Arg | Leu | Glu | Ala | Trp | Arg | Glu | Ala | Gly | Tyr | Ser | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Leu | Gly | Tyr | Arg | Phe | Glu | Leu | Phe | Gln | Asp | Gly | Ile | Ala | Thr | Ala |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Val | Ser | Ala | Ser | Ser | Ser | Ile | Ser | Leu | Lys | Asn | Gly | Gly | Ser | Phe | Val |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Asp | Val | Thr | Gly | Gly | Thr | Ser | Thr | Thr | Ala | Ser | Thr | Pro | Thr | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Pro | Gln | Gly | Ser | Trp | Asp | Leu | Gly | Ser | Gly | Ser | Ser | Ala | Gly | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Pro | Ala | Ser | Arg | Pro | Gly | Ser | Gly | Ser | Gly | Ser | Asp | Phe | Gly | Tyr |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Leu | Pro | Gln | His | Pro | Ser | Ala | Ala | Ala | Gln | Asn | Arg | Gly | Phe | Val |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Met | Ser | Ala | Thr | Val | Glu | Gly | Val | Gly | Lys | Arg | Ser | Lys | Pro | Glu | Val |
|     |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Glu | Val | Gly | Val | Thr | His | Val | Thr | Cys | Thr | Glu | Asp | Ala | Ala | Ala | His |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Ala | Leu | Ala | Ala | Ala | Val | Asp | Leu | Ser | Leu | Asp | Ala | Cys | Arg | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Phe | Ser | His | Lys | Leu | Arg | Lys | Glu | Leu | Arg | Gln | Gln | Ser | Gln | Leu | Gly |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |
| Val | Val |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 210 |

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1330 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1330

(D) OTHER INFORMATION: / Ceres Seq. ID 1481580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

|            |            |            |             |            |             |     |
|------------|------------|------------|-------------|------------|-------------|-----|
| atcccaaagt | ctcctaaggc | gagaagggat | ccggctgctcg | cactaggttt | ccttttcttt  | 60  |
| tttttttttg | gtttcaaatt | ttttcatcat | atctcctgaa  | aatcttcttc | attcgctcc   | 120 |
| aattttgctc | atgttcgtcc | gatccaacat | tcttcgtgct  | ctgattttta | ctgtgctgga  | 180 |
| aacagttacc | tcctcttgat | tcagttttga | ttcttcaaag  | cctcagagat | aatttggttt  | 240 |
| tctctaattc | cttgtaagga | gaaaacttgc | ttggagatca  | aatgatgca  | ttcaagctgc  | 300 |
| aaaggacttg | tgtctgttct | attcttattt | gtcgttgat   | tcattggaaa | caccgatgcg  | 360 |
| aatgctcagt | gggaggtttc | acataaagta | agagcttctc  | cccatgaaaa | catgggacgt  | 420 |
| aatgttattg | acggaagtgg | tgtagagaaa | acgttacatg  | acattggaat | gggtgaaaag  | 480 |
| agaggcactc | acaacaaagt | ttcagttctc | acagttgcgt  | tgttcacctt | ggctatggct  | 540 |
| gctgccactg | ggttaggtgc | tgtgcccttc | ttctttgttg  | agcttgatcc | tcaatgggct  | 600 |
| ggaatttgca | atggcatggc | tgtctggttg | tggtggccgc  | tagctttgat | cttggttaagg | 660 |
| aagggcagga | acatggctct | ggaaactggg | ttgttactgg  | gacccatagc | gggtgctttgt | 720 |
| tcatttggct | ctgtaagcag | attcttgaac | aatatggtga  | agttagtatg | ctggatatta  | 780 |

|             |            |             |            |             |             |      |
|-------------|------------|-------------|------------|-------------|-------------|------|
| aaggcgcaga  | tgcaactaaa | gttggttctcg | tcataggaat | tatgacactt  | cattcttttcg | 840  |
| gggaaggatc  | aggggttggt | gtatcattcg  | ctggctcaaa | agggttttagc | caagggcttc  | 900  |
| tggtcacttt  | ggccatagct | gttcataaca  | ttccagaagg | gttggtctgtt | agcatgggtg  | 960  |
| tggtcatcaag | gggtgtctct | ccacaaaatg  | ccatgctctg | gagtataata  | acatccttac  | 1020 |
| ctcagcctct  | cgtcgccgtg | ccagcttttt  | tatgcgctga | tgcgttcagc  | aagtttttgc  | 1080 |
| ctttttgcac  | tggatttgct | gccggatgca  | tgatttggat | ggttattgct  | gaagtgcttc  | 1140 |
| ctgatgcttt  | taaggaagcg | tctccttcgc  | aagtggcatc | tcagaccacc  | atatcagtag  | 1200 |
| catccatgga  | agctcttagc | actcttttgc  | agagtttcac | acatgattac  | aactcagagg  | 1260 |
| atgcttctgg  | cttcttcggt | tcactcctct  | ttggtctggg | tccattgctt  | gggggagtat  | 1320 |
| ttctggttgc  |            |             |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..245

(D) OTHER INFORMATION: / Ceres Seq. ID 1481581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Trp | Asn | Leu | Gln | Trp | His | Gly | Cys | Trp | Leu | Met | Leu | Ala | Ala |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ser | Phe | Asp | Leu | Val | Lys | Glu | Gly | Gln | Glu | His | Gly | Ser | Gly | Asn | Trp |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Val | Thr | Gly | Ile | Leu | Ala | Gly | Ala | Leu | Phe | Ile | Trp | Leu | Cys | Lys |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |  |
| Gln | Ile | Leu | Glu | Gln | Tyr | Gly | Glu | Val | Ser | Met | Leu | Asp | Ile | Lys | Gly |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Ala | Asp | Ala | Thr | Lys | Val | Val | Leu | Val | Ile | Gly | Ile | Met | Thr | Leu | His |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Ser | Phe | Gly | Glu | Gly | Ser | Gly | Val | Gly | Val | Ser | Phe | Ala | Gly | Ser | Lys |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Gly | Phe | Ser | Gln | Gly | Leu | Leu | Val | Thr | Leu | Ala | Ile | Ala | Val | His | Asn |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ile | Pro | Glu | Gly | Leu | Ala | Val | Ser | Met | Val | Leu | Ala | Ser | Arg | Gly | Val |  |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |  |
| Ser | Pro | Gln | Asn | Ala | Met | Leu | Trp | Ser | Ile | Ile | Thr | Ser | Leu | Pro | Gln |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Pro | Leu | Val | Ala | Val | Pro | Ala | Phe | Leu | Cys | Ala | Asp | Ala | Phe | Ser | Lys |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |
| Phe | Leu | Pro | Phe | Cys | Thr | Gly | Phe | Ala | Ala | Gly | Cys | Met | Ile | Trp | Met |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Val | Ile | Ala | Glu | Val | Leu | Pro | Asp | Ala | Phe | Lys | Glu | Ala | Ser | Pro | Ser |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Gln | Val | Ala | Ser | Ala | Ala | Thr | Ile | Ser | Val | Ala | Ser | Met | Glu | Ala | Leu |  |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Ser | Thr | Leu | Phe | Glu | Ser | Phe | Thr | His | Asp | Tyr | Asn | Ser | Glu | Asp | Ala |  |
|     |     |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |  |
| Ser | Gly | Phe | Phe | Val | Ser | Leu | Leu | Phe | Gly | Leu | Gly | Pro | Leu | Leu | Gly |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Gly | Val | Phe | Leu | Val |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..233  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1481582  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met Leu Ala Ala Ser Phe Asp Leu Val Lys Glu Gly Gln Glu His Gly  
1                  5                  10                  15  
Ser Gly Asn Trp Val Val Thr Gly Ile Leu Ala Gly Ala Leu Phe Ile  
                  20                  25                  30  
Trp Leu Cys Lys Gln Ile Leu Glu Gln Tyr Gly Glu Val Ser Met Leu  
                  35                  40                  45  
Asp Ile Lys Gly Ala Asp Ala Thr Lys Val Val Leu Val Ile Gly Ile  
50                  55                  60  
Met Thr Leu His Ser Phe Gly Glu Gly Ser Gly Val Gly Val Ser Phe  
65                  70                  75                  80  
Ala Gly Ser Lys Gly Phe Ser Gln Gly Leu Leu Val Thr Leu Ala Ile  
                  85                  90                  95  
Ala Val His Asn Ile Pro Glu Gly Leu Ala Val Ser Met Val Leu Ala  
                  100                 105                 110  
Ser Arg Gly Val Ser Pro Gln Asn Ala Met Leu Trp Ser Ile Ile Thr  
115                 120                 125  
Ser Leu Pro Gln Pro Leu Val Ala Val Pro Ala Phe Leu Cys Ala Asp  
130                 135                 140  
Ala Phe Ser Lys Phe Leu Pro Phe Cys Thr Gly Phe Ala Ala Gly Cys  
145                 150                 155                 160  
Met Ile Trp Met Val Ile Ala Glu Val Leu Pro Asp Ala Phe Lys Glu  
                  165                 170                 175  
Ala Ser Pro Ser Gln Val Ala Ser Ala Ala Thr Ile Ser Val Ala Ser  
180                 185                 190  
Met Glu Ala Leu Ser Thr Leu Phe Glu Ser Phe Thr His Asp Tyr Asn  
195                 200                 205  
Ser Glu Asp Ala Ser Gly Phe Phe Val Ser Leu Leu Phe Gly Leu Gly  
210                 215                 220  
Pro Leu Leu Gly Gly Val Phe Leu Val  
225                 230

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 187 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..187  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1481583  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Leu Asp Ile Lys Gly Ala Asp Ala Thr Lys Val Val Leu Val Ile  
1                  5                  10                  15  
Gly Ile Met Thr Leu His Ser Phe Gly Glu Gly Ser Gly Val Gly Val  
                  20                  25                  30  
Ser Phe Ala Gly Ser Lys Gly Phe Ser Gln Gly Leu Leu Val Thr Leu  
35                  40                  45  
Ala Ile Ala Val His Asn Ile Pro Glu Gly Leu Ala Val Ser Met Val  
50                  55                  60  
Leu Ala Ser Arg Gly Val Ser Pro Gln Asn Ala Met Leu Trp Ser Ile  
65                  70                  75                  80

Ile Thr Ser Leu Pro Gln Pro Leu Val Ala Val Pro Ala Phe Leu Cys  
85 90 95  
Ala Asp Ala Phe Ser Lys Phe Leu Pro Phe Cys Thr Gly Phe Ala Ala  
100 105 110  
Gly Cys Met Ile Trp Met Val Ile Ala Glu Val Leu Pro Asp Ala Phe  
115 120 125  
Lys Glu Ala Ser Pro Ser Gln Val Ala Ser Ala Ala Thr Ile Ser Val  
130 135 140  
Ala Ser Met Glu Ala Leu Ser Thr Leu Phe Glu Ser Phe Thr His Asp  
145 150 155 160  
Tyr Asn Ser Glu Asp Ala Ser Gly Phe Phe Val Ser Leu Leu Phe Gly  
165 170 175  
Leu Gly Pro Leu Leu Gly Gly Val Phe Leu Val  
180 185

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1180
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

|                                                                      |      |
|----------------------------------------------------------------------|------|
| acaatttctaa aaccctaattc tcacaaaaaa ccctaattctc acaaaaaccc tcctctcttc | 60   |
| atcgacatct ctcttttcaact gcttcaatgg cgtcttttga gcgttttgac gacatgtgtg  | 120  |
| acctgagatt gaaacctaac atttctccgaa accttctctc cgaatatgtt cccaacgaga   | 180  |
| agcagcctct caccaacttt ctatcactct ccaaggttgt atcaaccatc tccacacaca    | 240  |
| agctcttattc tgagtctcct ccagcttcaa ttgaccagaa gcttcatgct aaatcgaaat   | 300  |
| cagccgttga tgattgggtt gctagattat cagctttgat ttcttctgat atgccggata    | 360  |
| aaagctgggt gggatattgt ttgattggag taacatgtca agaatgtagc tcagatcggt    | 420  |
| tctttaagtc atactctgtt tggtttaaca gtttattatc acatcttaag aatccagcaa    | 480  |
| gttctagaat tgtccgagtg gcttcatgta cctcaatctc tgatctactt acaaggctgt    | 540  |
| ctagattttc gaatacgaag aaagatgcag ttccacacgc ttcgaaacta atcctgccta    | 600  |
| tcattaaatt attggatgaa gattcttcag aagcactatt ggaaggcatt gtccatctgc    | 660  |
| taagtacaat tgtactcttg tttcctgctg ccttccacag taattatgac aagattgaag    | 720  |
| ccgctattgc ctccaaaata ttttcggcga aaaccagttc taatatgtta aagaaatttg    | 780  |
| cccactttct agcattgctc cccaaagcta aagggtgacga gggcacctgg tccttgatga   | 840  |
| tgcaaaagct gctgatattc ataaacgtac atttaaataa ttttttccaa ggtctagaag    | 900  |
| aagaaacaaa aggaacaaaa gcaatccaac gattgactcc tcctggaaaa gactctcctt    | 960  |
| tgccccctcg aggtcaaaat gggggattgg atgatgcac atggaactct gaacaattga     | 1020 |
| ttgtatccag agtttctgca cttatgttct gcacctcaac gatgttaact acctcgta      | 1080 |
| aatccaagat taatattcca gttggctcat tgttatccct tgttgagcga gtgctgttgg    | 1140 |
| tgaacggctc tctacctga gccatgtcac ccttcatgac                           |      |

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..392
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Asn Ser Lys Thr Leu Ile Ser Gln Lys Thr Leu Ile Ser Gln Lys Pro



|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| 1   |     | 5   |     | 10  |     | 15  |
| Ser | Ser | Leu | His | Arg | His | Leu |
|     |     | 20  |     |     |     | 25  |
| Glu | Arg | Phe | Asp | Asp | Met | Cys |
|     |     | 35  |     |     |     | 40  |
| Arg | Asn | Leu | Leu | Ser | Glu | Tyr |
|     |     | 50  |     |     |     | 55  |
| Asn | Phe | Leu | Ser | Leu | Ser | Lys |
|     |     | 65  |     |     |     | 70  |
| Leu | Leu | Ser | Glu | Ser | Pro | Pro |
|     |     |     |     |     |     | 85  |
| Lys | Ser | Lys | Ser | Ala | Val | Asp |
|     |     |     |     |     |     | 100 |
| Ile | Ser | Ser | Asp | Met | Pro | Asp |
|     |     |     |     |     |     | 115 |
| Gly | Val | Thr | Cys | Gln | Glu | Cys |
|     |     |     |     |     |     | 130 |
| Ser | Val | Trp | Phe | Asn | Ser | Leu |
|     |     |     |     |     |     | 145 |
| Ser | Arg | Ile | Val | Arg | Val | Ala |
|     |     |     |     |     |     | 165 |
| Thr | Arg | Leu | Ser | Arg | Phe | Ser |
|     |     |     |     |     |     | 180 |
| Ala | Ser | Lys | Leu | Ile | Leu | Pro |
|     |     |     |     |     |     | 195 |
| Ser | Glu | Ala | Leu | Leu | Glu | Gly |
|     |     |     |     |     |     | 210 |
| Leu | Leu | Phe | Pro | Ala | Ala | Phe |
|     |     |     |     |     |     | 225 |
| Ala | Ile | Ala | Ser | Lys | Ile | Phe |
|     |     |     |     |     |     | 245 |
| Lys | Lys | Phe | Ala | His | Phe | Leu |
|     |     |     |     |     |     | 260 |
| Glu | Gly | Thr | Trp | Ser | Leu | Met |
|     |     |     |     |     |     | 275 |
| Val | His | Leu | Asn | Asn | Phe | Phe |
|     |     |     |     |     |     | 290 |
| Thr | Lys | Ala | Ile | Gln | Arg | Leu |
|     |     |     |     |     |     | 305 |
| Pro | Leu | Gly | Gly | Gln | Asn | Gly |
|     |     |     |     |     |     | 325 |
| Glu | Gln | Leu | Ile | Val | Ser | Arg |
|     |     |     |     |     |     | 340 |
| Thr | Met | Leu | Thr | Thr | Ser | Tyr |
|     |     |     |     |     |     | 355 |
| Ser | Leu | Leu | Ser | Leu | Val | Glu |
|     |     |     |     |     |     | 370 |
| Pro | Arg | Ala | Met | Ser | Pro | Phe |
|     |     |     |     |     |     | 385 |

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..364

(D) OTHER INFORMATION: / Ceres Seq. ID 1481598

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met Ala Ser Phe Glu Arg Phe Asp Asp Met Cys Asp Leu Arg Leu Lys  
1 5 10 15  
Pro Asn Ile Leu Arg Asn Leu Leu Ser Glu Tyr Val Pro Asn Glu Lys  
20 25 30  
Gln Pro Leu Thr Asn Phe Leu Ser Leu Ser Lys Val Val Ser Thr Ile  
35 40 45  
Ser Thr His Lys Leu Leu Ser Glu Ser Pro Pro Ala Ser Ile Asp Gln  
50 55 60  
Lys Leu His Ala Lys Ser Lys Ser Ala Val Asp Asp Trp Val Ala Arg  
65 70 75 80  
Leu Ser Ala Leu Ile Ser Ser Asp Met Pro Asp Lys Ser Trp Val Gly  
85 90 95  
Ile Cys Leu Ile Gly Val Thr Cys Gln Glu Cys Ser Ser Asp Arg Phe  
100 105 110  
Phe Lys Ser Tyr Ser Val Trp Phe Asn Ser Leu Leu Ser His Leu Lys  
115 120 125  
Asn Pro Ala Ser Ser Arg Ile Val Arg Val Ala Ser Cys Thr Ser Ile  
130 135 140  
Ser Asp Leu Leu Thr Arg Leu Ser Arg Phe Ser Asn Thr Lys Lys Asp  
145 150 155 160  
Ala Val Ser His Ala Ser Lys Leu Ile Leu Pro Ile Ile Lys Leu Leu  
165 170 175  
Asp Glu Asp Ser Ser Glu Ala Leu Leu Glu Gly Ile Val His Leu Leu  
180 185 190  
Ser Thr Ile Val Leu Leu Phe Pro Ala Ala Phe His Ser Asn Tyr Asp  
195 200 205  
Lys Ile Glu Ala Ala Ile Ala Ser Lys Ile Phe Ser Ala Lys Thr Ser  
210 215 220  
Ser Asn Met Leu Lys Lys Phe Ala His Phe Leu Ala Leu Leu Pro Lys  
225 230 235 240  
Ala Lys Gly Asp Glu Gly Thr Trp Ser Leu Met Met Gln Lys Leu Leu  
245 250 255  
Ile Ser Ile Asn Val His Leu Asn Asn Phe Phe Gln Gly Leu Glu Glu  
260 265 270  
Glu Thr Lys Gly Thr Lys Ala Ile Gln Arg Leu Thr Pro Pro Gly Lys  
275 280 285  
Asp Ser Pro Leu Pro Leu Gly Gly Gln Asn Gly Gly Leu Asp Asp Ala  
290 295 300  
Ser Trp Asn Ser Glu Gln Leu Ile Val Ser Arg Val Ser Ala Leu Met  
305 310 315 320  
Phe Cys Thr Ser Thr Met Leu Thr Thr Ser Tyr Lys Ser Lys Ile Asn  
325 330 335  
Ile Pro Val Gly Ser Leu Leu Ser Leu Val Glu Arg Val Leu Leu Val  
340 345 350  
Asn Gly Ser Leu Pro Arg Ala Met Ser Pro Phe Met  
355 360

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 355 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..355

(D) OTHER INFORMATION: / Ceres Seq. ID 1481599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Met Cys Asp Leu Arg Leu Lys Pro Asn Ile Leu Arg Asn Leu Leu Ser  
1 5 10 15  
Glu Tyr Val Pro Asn Glu Lys Gln Pro Leu Thr Asn Phe Leu Ser Leu  
20 25 30  
Ser Lys Val Val Ser Thr Ile Ser Thr His Lys Leu Leu Ser Glu Ser  
35 40 45  
Pro Pro Ala Ser Ile Asp Gln Lys Leu His Ala Lys Ser Lys Ser Ala  
50 55 60  
Val Asp Asp Trp Val Ala Arg Leu Ser Ala Leu Ile Ser Ser Asp Met  
65 70 75 80  
Pro Asp Lys Ser Trp Val Gly Ile Cys Leu Ile Gly Val Thr Cys Gln  
85 90 95  
Glu Cys Ser Ser Asp Arg Phe Phe Lys Ser Tyr Ser Val Trp Phe Asn  
100 105 110  
Ser Leu Leu Ser His Leu Lys Asn Pro Ala Ser Ser Arg Ile Val Arg  
115 120 125  
Val Ala Ser Cys Thr Ser Ile Ser Asp Leu Leu Thr Arg Leu Ser Arg  
130 135 140  
Phe Ser Asn Thr Lys Lys Asp Ala Val Ser His Ala Ser Lys Leu Ile  
145 150 155 160  
Leu Pro Ile Ile Lys Leu Leu Asp Glu Asp Ser Ser Glu Ala Leu Leu  
165 170 175  
Glu Gly Ile Val His Leu Leu Ser Thr Ile Val Leu Leu Phe Pro Ala  
180 185 190  
Ala Phe His Ser Asn Tyr Asp Lys Ile Glu Ala Ala Ile Ala Ser Lys  
195 200 205  
Ile Phe Ser Ala Lys Thr Ser Ser Asn Met Leu Lys Lys Phe Ala His  
210 215 220  
Phe Leu Ala Leu Leu Pro Lys Ala Lys Gly Asp Glu Gly Thr Trp Ser  
225 230 235 240  
Leu Met Met Gln Lys Leu Leu Ile Ser Ile Asn Val His Leu Asn Asn  
245 250 255  
Phe Phe Gln Gly Leu Glu Glu Glu Thr Lys Gly Thr Lys Ala Ile Gln  
260 265 270  
Arg Leu Thr Pro Pro Gly Lys Asp Ser Pro Leu Pro Leu Gly Gly Gln  
275 280 285  
Asn Gly Gly Leu Asp Asp Ala Ser Trp Asn Ser Glu Gln Leu Ile Val  
290 295 300  
Ser Arg Val Ser Ala Leu Met Phe Cys Thr Ser Thr Met Leu Thr Thr  
305 310 315 320  
Ser Tyr Lys Ser Lys Ile Asn Ile Pro Val Gly Ser Leu Leu Ser Leu  
325 330 335  
Val Glu Arg Val Leu Leu Val Asn Gly Ser Leu Pro Arg Ala Met Ser  
340 345 350  
Pro Phe Met  
355

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1724
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

|            |            |            |             |             |             |      |
|------------|------------|------------|-------------|-------------|-------------|------|
| attcaacctc | tctacttcag | tttctctgtc | cccatTTTTc  | atctgagagt  | taaaactgta  | 60   |
| acctcaaaat | ctgagataaa | gtcaaaaaaa | aaaccccgagt | ttatgattct  | catttttctct | 120  |
| ttataatcga | aagcttcgat | ttttaacaaa | accagaatc   | tgtgttcttg  | tttttttttt  | 180  |
| tttttggtga | gagttatctt | tttttttttt | ggaatatgtg  | gtgagaatct  | gagtaatggg  | 240  |
| atttacataa | aatattctat | gtaaabacta | aaataatctg  | gaaattatta  | aatttccaaa  | 300  |
| ctttgtgttc | cattttgtgg | actcaaattt | gtttataaag  | atctcaaatc  | agagagattg  | 360  |
| agacgaccaa | gaacaagcag | aagaagaaga | agaattgaga  | gaatgtgggt  | gtgggtcttct | 420  |
| tcaactaaa  | gtcgttcgaa | tctggagagg | tttcttttag  | gaatcactcc  | taagcctcct  | 480  |
| tccttctctc | tccttcagga | acagggaag  | gaggagattg  | agtatttcag  | gcttgatgat  | 540  |
| ctctgggatt | gttatgatga | gatgagtgcg | tatggctttg  | gcacacaggt  | tgatttaaac  | 600  |
| aatggcgaaa | ccgttatgca | gtactacgtc | ccgtacctat  | ccgctatcca  | aatccacact  | 660  |
| aacaaacccg | ccttgctttc | caggaaccag | aatgaggtgg  | ctgaatctga  | gagtagcgag  | 720  |
| ggttggagcg | atagtgaag  | tgaaaagttg | ttgtcaaggt  | caatgagcaa  | tgattcaagc  | 780  |
| aaaacatggg | atgctgtctc | tgaagattcg | gttttcgatc  | cggatgggtc  | accgttgctg  | 840  |
| aaagatagac | ttggtaacct | tgactttaag | tacattgaaa  | gagatcctcc  | gcacaagcgg  | 900  |
| attcccttaa | ccgacaagat | aaacgtattg | gtggagaaat  | atccgggact  | catgacctta  | 960  |
| aggagtgtcg | acatgtctcc | tgcaagttgg | atggctgttg  | cgtgggtaccc | gatataccac  | 1020 |
| atcccaacct | gcagggaacg | gaaagatttg | acgacaggct  | tcctaactta  | tcatactcta  | 1080 |
| tcttcgtctt | ttcaagataa | tgtgggtgaa | ggagatcaaa  | gcaacaacaa  | tgaagaaaca  | 1140 |
| gagttttgtg | aagattccgt | aataaacaag | agaatgccat  | tgctccggtt  | tggtgtaaca  | 1200 |
| acttacaaaa | tgcaaggaga | tctttggggg | aagacggggg  | ttgaccagga  | ccgggttgctt | 1260 |
| tatcttcaaa | gcgctgcgga | ttcatggctg | aaacagctca  | atgttgatca  | ccatgactat  | 1320 |
| aacttcttcc | ttaactcgag | cttctaagaa | tcaatcgggt  | cgttcgtatg  | tttatccttc  | 1380 |
| tccaaacctt | aaacaaaaaa | aaaaagacct | cataaccctt  | tttctttggt  | gttttcaagc  | 1440 |
| tccttttggt | tctctgtggt | ttttgttctt | tttggttttg  | tctggctcgt  | tgtgttggtt  | 1500 |
| taggtagcaa | ccgccatcgc | ggagtttttt | ctccttttgc  | aagccaatca  | tggaagtttc  | 1560 |
| taagaagaaa | acagagcttt | tttttctttt | tttttaacgg  | tgttgagaaa  | acaagaaagt  | 1620 |
| tgttttcttt | tcttggtgga | gagatcatgt | aaattgacct  | tgaacagagg  | actctgtttt  | 1680 |
| gtacttttct | gtctaaaata | tataaaaaaa | tctgtctttc  | ttgt        |             |      |

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..314

(D) OTHER INFORMATION: / Ceres Seq. ID 1481614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Trp | Trp | Trp | Ser | Ser | Thr | Lys | Gly | Arg | Ser | Asn | Leu | Glu | Arg |
| 1   |     |     |     | 5   |     |     | 10  |     |     |     |     | 15  |     |     |
| Phe | Leu | Leu | Gly | Ile | Thr | Pro | Lys | Pro | Pro | Ser | Phe | Ser | Leu | Gln |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Gln | Gly | Lys | Glu | Glu | Ile | Glu | Tyr | Phe | Arg | Leu | Asp | Asp | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     | Trp |
| Asp | Cys | Tyr | Asp | Glu | Met | Ser | Ala | Tyr | Gly | Phe | Gly | Thr | Gln | Val |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     | Asp |
| Leu | Asn | Asn | Gly | Glu | Thr | Val | Met | Gln | Tyr | Tyr | Val | Pro | Tyr | Leu |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Ile | Gln | Ile | His | Thr | Asn | Lys | Pro | Ala | Leu | Leu | Ser | Arg | Asn |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     | Gln |
| Asn | Glu | Val | Ala | Glu | Ser | Glu | Ser | Ser | Glu | Gly | Trp | Ser | Asp | Ser |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     | Glu |
| Ser | Glu | Lys | Leu | Leu | Ser | Arg | Ser | Met | Ser | Asn | Asp | Ser | Ser | Lys |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     | Thr |
| Trp | Asp | Ala | Val | Ser | Glu | Asp | Ser | Val | Phe | Asp | Pro | Asp | Gly | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     | Pro |

Leu Leu Lys Asp Arg Leu Gly Asn Leu Asp Phe Lys Tyr Ile Glu Arg  
145 150 155 160  
Asp Pro Pro His Lys Arg Ile Pro Leu Thr Asp Lys Ile Asn Val Leu  
165 170 175  
Val Glu Lys Tyr Pro Gly Leu Met Thr Leu Arg Ser Val Asp Met Ser  
180 185 190  
Pro Ala Ser Trp Met Ala Val Ala Trp Tyr Pro Ile Tyr His Ile Pro  
195 200 205  
Thr Cys Arg Asn Glu Lys Asp Leu Thr Thr Gly Phe Leu Thr Tyr His  
210 215 220  
Thr Leu Ser Ser Ser Phe Gln Asp Asn Val Val Glu Gly Asp Gln Ser  
225 230 235 240  
Asn Asn Asn Glu Glu Thr Glu Phe Cys Glu Asp Ser Val Ile Asn Lys  
245 250 255  
Arg Met Pro Leu Pro Pro Phe Gly Val Thr Thr Tyr Lys Met Gln Gly  
260 265 270  
Asp Leu Trp Gly Lys Thr Gly Phe Asp Gln Asp Arg Leu Leu Tyr Leu  
275 280 285  
Gln Ser Ala Ala Asp Ser Trp Leu Lys Gln Leu Asn Val Asp His His  
290 295 300  
Asp Tyr Asn Phe Phe Leu Asn Ser Ser Phe  
305 310

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..261

(D) OTHER INFORMATION: / Ceres Seq. ID 1481615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met Ser Ala Tyr Gly Phe Gly Thr Gln Val Asp Leu Asn Asn Gly Glu  
1 5 10 15  
Thr Val Met Gln Tyr Tyr Val Pro Tyr Leu Ser Ala Ile Gln Ile His  
20 25 30  
Thr Asn Lys Pro Ala Leu Leu Ser Arg Asn Gln Asn Glu Val Ala Glu  
35 40 45  
Ser Glu Ser Ser Glu Gly Trp Ser Asp Ser Glu Ser Glu Lys Leu Leu  
50 55 60  
Ser Arg Ser Met Ser Asn Asp Ser Ser Lys Thr Trp Asp Ala Val Ser  
65 70 75 80  
Glu Asp Ser Val Phe Asp Pro Asp Gly Ser Pro Leu Leu Lys Asp Arg  
85 90 95  
Leu Gly Asn Leu Asp Phe Lys Tyr Ile Glu Arg Asp Pro Pro His Lys  
100 105 110  
Arg Ile Pro Leu Thr Asp Lys Ile Asn Val Leu Val Glu Lys Tyr Pro  
115 120 125  
Gly Leu Met Thr Leu Arg Ser Val Asp Met Ser Pro Ala Ser Trp Met  
130 135 140  
Ala Val Ala Trp Tyr Pro Ile Tyr His Ile Pro Thr Cys Arg Asn Glu  
145 150 155 160  
Lys Asp Leu Thr Thr Gly Phe Leu Thr Tyr His Thr Leu Ser Ser Ser  
165 170 175  
Phe Gln Asp Asn Val Val Glu Gly Asp Gln Ser Asn Asn Asn Glu Glu  
180 185 190  
Thr Glu Phe Cys Glu Asp Ser Val Ile Asn Lys Arg Met Pro Leu Pro

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 195                                                             | 200 | 205 |
| Pro Phe Gly Val Thr Thr Tyr Lys Met Gln Gly Asp Leu Trp Gly Lys |     |     |
| 210                                                             | 215 | 220 |
| Thr Gly Phe Asp Gln Asp Arg Leu Leu Tyr Leu Gln Ser Ala Ala Asp |     |     |
| 225                                                             | 230 | 235 |
| Ser Trp Leu Lys Gln Leu Asn Val Asp His His Asp Tyr Asn Phe Phe |     |     |
|                                                                 | 245 | 250 |
| Leu Asn Ser Ser Phe                                             |     | 255 |
| 260                                                             |     |     |

## (2) INFORMATION FOR SEQ ID NO:87:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..243

(D) OTHER INFORMATION: / Ceres Seq. ID 1481616

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Tyr | Tyr | Val | Pro | Tyr | Leu | Ser | Ala | Ile | Gln | Ile | His | Thr | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Pro | Ala | Leu | Leu | Ser | Arg | Asn | Gln | Asn | Glu | Val | Ala | Glu | Ser | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ser | Glu | Gly | Trp | Ser | Asp | Ser | Glu | Ser | Glu | Lys | Leu | Leu | Ser | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Met | Ser | Asn | Asp | Ser | Ser | Lys | Thr | Trp | Asp | Ala | Val | Ser | Glu | Asp |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ser | Val | Phe | Asp | Pro | Asp | Gly | Ser | Pro | Leu | Leu | Lys | Asp | Arg | Leu | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Asn | Leu | Asp | Phe | Lys | Tyr | Ile | Glu | Arg | Asp | Pro | Pro | His | Lys | Arg | Ile |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Leu | Thr | Asp | Lys | Ile | Asn | Val | Leu | Val | Glu | Lys | Tyr | Pro | Gly | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Met | Thr | Leu | Arg | Ser | Val | Asp | Met | Ser | Pro | Ala | Ser | Trp | Met | Ala | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Trp | Tyr | Pro | Ile | Tyr | His | Ile | Pro | Thr | Cys | Arg | Asn | Glu | Lys | Asp |
|     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Leu | Thr | Thr | Gly | Phe | Leu | Thr | Tyr | His | Thr | Leu | Ser | Ser | Ser | Phe | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Asp | Asn | Val | Val | Glu | Gly | Asp | Gln | Ser | Asn | Asn | Asn | Glu | Glu | Thr | Glu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Cys | Glu | Asp | Ser | Val | Ile | Asn | Lys | Arg | Met | Pro | Leu | Pro | Pro | Phe |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |     |
| Gly | Val | Thr | Thr | Tyr | Lys | Met | Gln | Gly | Asp | Leu | Trp | Gly | Lys | Thr | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Phe | Asp | Gln | Asp | Arg | Leu | Leu | Tyr | Leu | Gln | Ser | Ala | Ala | Asp | Ser | Trp |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Lys | Gln | Leu | Asn | Val | Asp | His | His | Asp | Tyr | Asn | Phe | Phe | Leu | Asn |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Ser | Ser | Phe |     |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:88:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1235 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1235

(D) OTHER INFORMATION: / Ceres Seq. ID 1481621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

|         |       |        |       |        |        |         |         |        |       |        |        |        |      |
|---------|-------|--------|-------|--------|--------|---------|---------|--------|-------|--------|--------|--------|------|
| attgacc | caa   | cgctt  | cttct | ccggc  | acgac  | tgttc   | agagt   | tcgatt | tcca  | ttttc  | ggg    | gtc    | 60   |
| gaaag   | gttga | ttttat | tttgg | atttt  | ggatg  | gtagatt | cag     | ttcct  | aaaca | tagga  | aactt  |        | 120  |
| gaatc   | tcaga | gttttt | cag   | ttagg  | gataa  | gagaa   | agaaa   | cacagt | tgga  | gttata | actga  |        | 180  |
| tgaat   | ggagg | aggct  | cag   | agt    | ttgc   | gtt     | cagcatt | gtc    | ctatt | gtgtg  | cagca  | agtac  | 240  |
| gaaact  | atga  | ctatc  | atcac | tacct  | ctgtc  | tcctt   | gaact   | cccaa  | ctgag | atgcg  | taaag  |        | 300  |
| cagcatt | gtc   | tctcc  | ggg   | ct     | ttaat  | gtag    | aaacc   | gcaag  | agcca | tggat  | gttgc  | atctg  | 360  |
| atcccc  | aaaat | cggct  | tgatg | cgg    | tact   | ttt     | gg      | tgg    | caaga | agcaat | tgac   | aaact  | 420  |
| ccaaaa  | agcc  | cataa  | accat | ccag   | ctgc   | ac      | agct    | ctgtc  | ttggg | caata  | tcaga  | aacata | 480  |
| acatc   | agtaa | acctt  | ggcta | aaac   | gctcg  | gtg     | acg     | ctag   | aatcc | gagat  | gcccc  | aaagag | 540  |
| aagtag  | acga  | tatacc | agag  | agcatt | gcg    | g       | ag      | tag    | agaa  | atacg  | cagaa  | gacac  | 600  |
| ccact   | cttct | gtaca  | atata | ctcca  | agcag  | gcg     | gaatt   | ag     | ttca  | acaaca | gctgat | catg   | 660  |
| cagctt  | caca  | cattg  | gtaaa | gccag  | tgg    | ct      | ttg     | ctt    | gct   | gcttaa | aatca  | ttacc  | 720  |
| actgt   | accag | aaacc  | gtcac | cagag  | ttaca  | tccct   | gcaga   | tctc   | gctg  | ag     | cac    | gggt   | 780  |
| tgctc   | gtgaa | acaag  | gtgga | cgatt  | agaaa  | ttctt   | ctgga   | taac   | gatt  | ca     | agaga  | aggac  | 840  |
| taagc   | aatgt | cgtgt  | ttgag | attgc  | atctg  | ttg     | ccaat   | gc     | acat  | ctc    | ctg    | aaag   | 900  |
| aactg   | gcggg | aaagg  | ttcct | gcaga  | agcta  | aacc    | ggtact  | gctt   | catt  | ct     | gtgcc  | ggtac  | 960  |
| aagtt   | cttct | ggatt  | cgtta | aataa  | agtac  | aattc   | gatgt   | gttt   | gat   | ccc    | aggatt | caaa   | 1020 |
| gaggag  | ttct  | tggt   | gttct | ccact  | cttgt  | ttcag   | tttaa   | actc   | aa    | gtg    | tattc  | atgga  | 1080 |
| gagca   | atgtt | ttgaa  | aactt | gtctt  | tatct  | ccctt   | tttctt  | gcct   | ctt   | ttta   | tttct  | ggtt   | 1140 |
| caaag   | acttt | acatta | aact  | ccag   | cttact | tgtatt  | ttctt   | ttgta  | ataat | acaaa  | attac  |        | 1200 |

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..304

(D) OTHER INFORMATION: / Ceres Seq. ID 1481622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Gly | Gly | Gly | Ser | Ser | Ser | Leu | Arg | Ser | Ala | Leu | Ser | Tyr | Cys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Gln | Gln | Val | Arg | Asn | Tyr | Asp | Tyr | His | His | Tyr | Leu | Cys | Leu | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Leu | Pro | Thr | Glu | Met | Arg | Lys | Ala | Ala | Phe | Ala | Leu | Arg | Ala | Phe |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Val | Glu | Thr | Ala | Arg | Ala | Met | Asp | Val | Ala | Ser | Asp | Pro | Lys | Ile |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Gly | Leu | Met | Arg | Leu | Leu | Trp | Trp | Gln | Glu | Ala | Ile | Asp | Lys | Leu | Tyr |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Thr | Lys | Lys | Pro | Ile | Asn | His | Pro | Ala | Ala | Gln | Ala | Leu | Ser | Trp | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ile | Ser | Glu | His | Asn | Ile | Ser | Lys | Pro | Trp | Leu | Lys | Arg | Ser | Val | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Arg | Ile | Arg | Asp | Ala | Gln | Arg | Glu | Val | Asp | Asp | Ile | Pro | Glu | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Ala | Glu | Leu | Glu | Lys | Tyr | Ala | Glu | Asp | Thr | Val | Ser | Thr | Leu | Leu |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Tyr | Asn | Thr | Leu | Gln | Ala | Gly | Gly | Ile | Ser | Ser | Thr | Thr | Ala | Asp | His |
|     |     |     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     | 160 |

Ala Ala Ser His Ile Gly Lys Ala Ser Gly Leu Val Leu Leu Leu Lys  
165 170 175  
Ser Leu Pro Tyr His Cys Thr Arg Asn Arg His Gln Ser Tyr Ile Pro  
180 185 190  
Ala Asp Leu Ala Glu Lys His Gly Leu Leu Val Lys Gln Gly Gly Arg  
195 200 205  
Leu Glu Ile Leu Leu Asp Asn Asp Ser Arg Glu Gly Leu Ser Asn Val  
210 215 220  
Val Phe Glu Ile Ala Ser Val Ala Asn Ala His Leu Leu Lys Ala Arg  
225 230 235 240  
Glu Leu Ala Gly Lys Val Pro Ala Glu Ala Lys Pro Val Leu Leu His  
245 250 255  
Ser Val Pro Val Gln Val Leu Leu Asp Ser Leu Asn Lys Val Gln Phe  
260 265 270  
Asp Val Phe Asp Pro Arg Ile Gln Arg Gly Val Leu Gly Val Pro Pro  
275 280 285  
Leu Leu Phe Gln Phe Lys Leu Lys Trp Tyr Ser Trp Arg Ala Met Phe  
290 295 300

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..267

(D) OTHER INFORMATION: / Ceres Seq. ID 1481623

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met Arg Lys Ala Ala Phe Ala Leu Arg Ala Phe Asn Val Glu Thr Ala  
1 5 10 15  
Arg Ala Met Asp Val Ala Ser Asp Pro Lys Ile Gly Leu Met Arg Leu  
20 25 30  
Leu Trp Trp Gln Glu Ala Ile Asp Lys Leu Tyr Thr Lys Lys Pro Ile  
35 40 45  
Asn His Pro Ala Ala Gln Ala Leu Ser Trp Ala Ile Ser Glu His Asn  
50 55 60  
Ile Ser Lys Pro Trp Leu Lys Arg Ser Val Asp Ala Arg Ile Arg Asp  
65 70 75 80  
Ala Gln Arg Glu Val Asp Asp Ile Pro Glu Ser Ile Ala Glu Leu Glu  
85 90 95  
Lys Tyr Ala Glu Asp Thr Val Ser Thr Leu Leu Tyr Asn Thr Leu Gln  
100 105 110  
Ala Gly Gly Ile Ser Ser Thr Thr Ala Asp His Ala Ala Ser His Ile  
115 120 125  
Gly Lys Ala Ser Gly Leu Val Leu Leu Lys Ser Leu Pro Tyr His  
130 135 140  
Cys Thr Arg Asn Arg His Gln Ser Tyr Ile Pro Ala Asp Leu Ala Glu  
145 150 155 160  
Lys His Gly Leu Leu Val Lys Gln Gly Gly Arg Leu Glu Ile Leu Leu  
165 170 175  
Asp Asn Asp Ser Arg Glu Gly Leu Ser Asn Val Val Phe Glu Ile Ala  
180 185 190  
Ser Val Ala Asn Ala His Leu Leu Lys Ala Arg Glu Leu Ala Gly Lys  
195 200 205  
Val Pro Ala Glu Ala Lys Pro Val Leu Leu His Ser Val Pro Val Gln



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 210                                                             | 215 | 220 |
| Val Leu Leu Asp Ser Leu Asn Lys Val Gln Phe Asp Val Phe Asp Pro |     |     |
| 225                                                             | 230 | 235 |
| Arg Ile Gln Arg Gly Val Leu Gly Val Pro Pro Leu Leu Phe Gln Phe |     | 240 |
|                                                                 | 245 | 250 |
| Lys Leu Lys Trp Tyr Ser Trp Arg Ala Met Phe                     |     | 255 |
| 260                                                             | 265 |     |

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..249

(D) OTHER INFORMATION: / Ceres Seq. ID 1481624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Asp Val Ala Ser Asp Pro Lys Ile Gly Leu Met Arg Leu Leu Trp |     |     |
| 1                                                               | 5   | 10  |
| Trp Gln Glu Ala Ile Asp Lys Leu Tyr Thr Lys Lys Pro Ile Asn His |     | 15  |
|                                                                 | 20  | 25  |
| Pro Ala Ala Gln Ala Leu Ser Trp Ala Ile Ser Glu His Asn Ile Ser |     | 30  |
|                                                                 | 35  | 40  |
| Lys Pro Trp Leu Lys Arg Ser Val Asp Ala Arg Ile Arg Asp Ala Gln |     | 45  |
|                                                                 | 50  | 55  |
| Arg Glu Val Asp Asp Ile Pro Glu Ser Ile Ala Glu Leu Glu Lys Tyr |     | 60  |
| 65                                                              | 70  | 75  |
| Ala Glu Asp Thr Val Ser Thr Leu Leu Tyr Asn Thr Leu Gln Ala Gly |     | 80  |
|                                                                 | 85  | 90  |
| Gly Ile Ser Ser Thr Thr Ala Asp His Ala Ala Ser His Ile Gly Lys |     | 95  |
|                                                                 | 100 | 105 |
| Ala Ser Gly Leu Val Leu Leu Leu Lys Ser Leu Pro Tyr His Cys Thr |     | 110 |
|                                                                 | 115 | 120 |
| Arg Asn Arg His Gln Ser Tyr Ile Pro Ala Asp Leu Ala Glu Lys His |     | 125 |
|                                                                 | 130 | 135 |
| Gly Leu Leu Val Lys Gln Gly Gly Arg Leu Glu Ile Leu Leu Asp Asn |     | 140 |
| 145                                                             | 150 | 155 |
| Asp Ser Arg Glu Gly Leu Ser Asn Val Val Phe Glu Ile Ala Ser Val |     | 160 |
|                                                                 | 165 | 170 |
| Ala Asn Ala His Leu Leu Lys Ala Arg Glu Leu Ala Gly Lys Val Pro |     | 175 |
|                                                                 | 180 | 185 |
| Ala Glu Ala Lys Pro Val Leu Leu His Ser Val Pro Val Gln Val Leu |     | 190 |
|                                                                 | 195 | 200 |
| Leu Asp Ser Leu Asn Lys Val Gln Phe Asp Val Phe Asp Pro Arg Ile |     | 205 |
| 210                                                             | 215 | 220 |
| Gln Arg Gly Val Leu Gly Val Pro Pro Leu Leu Phe Gln Phe Lys Leu |     | 225 |
|                                                                 | 230 | 235 |
| Lys Trp Tyr Ser Trp Arg Ala Met Phe                             |     | 240 |
|                                                                 | 245 |     |

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1232 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1232

(D) OTHER INFORMATION: / Ceres Seq. ID 1481625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

|             |             |            |            |            |             |      |
|-------------|-------------|------------|------------|------------|-------------|------|
| ctctctcgcg  | ttcggttctta | tccacgagct | ctgcaccgtc | gcaatctccg | tcttctccat  | 60   |
| ttagatccaa  | cacagagcct  | tttctacatg | aaattcggca | aagagtttcg | tactcacctc  | 120  |
| gaagaaactt  | taccagagt   | gagagacaag | ttcctttgct | ataaaccttt | aaaaaagctt  | 180  |
| ctcaaataatt | atcctttatta | ctccgccgat | tttgaccg   | ccaattccga | tcacaacgat  | 240  |
| tcgctgcccag | tatttgctga  | tactactaac | atctcttccg | cgcgcgacga | cggcggtgtg  | 300  |
| gttcccggcg  | tcaggccatc  | ggaagatctc | cagggttcgt | ttgtgaggat | acttaacgat  | 360  |
| gaacttgaga  | agttaaacga  | tttttacgtt | gataaggaag | aagatttcgt | tatcagatta  | 420  |
| caggagctca  | aggaaagaat  | cgagcaagtt | aaagaaaaga | atggggaatt | tgcatacagaa | 480  |
| agtgagttca  | gcgaagaaat  | gatggatatt | cggagagacc | ttgttaccat | tcattggcgag | 540  |
| atggtgctcc  | tgaaaaacta  | cagctccctt | aattttgcag | gacttgctca | gattttgaag  | 600  |
| aagtacgata  | aaagaacagg  | tggaacttta | cgtttgccct | tcacacagct | tggtctccat  | 660  |
| caacccttct  | ttactacaga  | gccacttact | aggttagtcc | gtgaatgtga | ggccaatctt  | 720  |
| gagcttcttt  | ttccttcaga  | agcggaagtt | gtagagtctt | ctagcgcagt | gcaagcacac  | 780  |
| tcaagctcac  | atcagcacaa  | ctccccaaga | atctcagctg | agacttcctc | aactctcggc  | 840  |
| aatgaaaatc  | ttgatataata | taagagtaca | ctcgtctgaa | tgagagctat | aagagggtta  | 900  |
| caaaaggcta  | gctcgacgta  | caacccttta | tcattctcat | cgcttcttca | gaacgaggat  | 960  |
| gatgagacgg  | taacagctga  | aaactctcca | aactctggga | acaaagatga | ttcagagaag  | 1020 |
| gaagatactg  | gaccttccca  | ctgatcagaa | gagaatgatg | ctctttttga | tcaagatttt  | 1080 |
| gagaatttgc  | ttcttgattt  | caccctaact | tttcataaaa | ttaacacatt | ttactttact  | 1140 |
| tcttcacctt  | ttgcaggaca  | caacttctgt | atgcatttga | attttagtac | agtcgtttat  | 1200 |
| agattttcaa  | tgaaattttc  | ctccattgtc | gc         |            |             |      |

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 347 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..347

(D) OTHER INFORMATION: / Ceres Seq. ID 1481626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Ser | Arg | Val | Arg | Ser | Tyr | Pro | Arg | Ala | Leu | His | Arg | Arg | Asn | Leu |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Arg | Leu | Leu | His | Leu | Asp | Pro | Thr | Gln | Ser | Leu | Phe | Tyr | Met | Lys | Phe |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gly | Lys | Glu | Phe | Arg | Thr | His | Leu | Glu | Glu | Thr | Leu | Pro | Glu | Trp | Arg |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Asp | Lys | Phe | Leu | Cys | Tyr | Lys | Pro | Leu | Lys | Lys | Leu | Leu | Lys | Tyr | Tyr |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Pro | Tyr | Tyr | Ser | Ala | Asp | Phe | Gly | Pro | Ala | Asn | Ser | Asp | His | Asn | Asp |  |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Ser | Arg | Pro | Val | Phe | Ala | Asp | Thr | Thr | Asn | Ile | Ser | Ser | Ala | Ala | Asp |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Asp | Gly | Gly | Val | Val | Pro | Gly | Val | Arg | Pro | Ser | Glu | Asp | Leu | Gln | Gly |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Ser | Phe | Val | Arg | Ile | Leu | Asn | Asp | Glu | Leu | Glu | Lys | Phe | Asn | Asp | Phe |  |
|     |     |     | 115 |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Tyr | Val | Asp | Lys | Glu | Glu | Asp | Phe | Val | Ile | Arg | Leu | Gln | Glu | Leu | Lys |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Glu | Arg | Ile | Glu | Gln | Val | Lys | Glu | Lys | Asn | Gly | Glu | Phe | Ala | Ser | Glu |  |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ser | Glu | Phe | Ser | Glu | Glu | Met | Met | Asp | Ile | Arg | Arg | Asp | Leu | Val | Thr |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |

Ile His Gly Glu Met Val Leu Leu Lys Asn Tyr Ser Ser Leu Asn Phe  
180 185 190  
Ala Gly Leu Val Lys Ile Leu Lys Lys Tyr Asp Lys Arg Thr Gly Gly  
195 200 205  
Leu Leu Arg Leu Pro Phe Thr Gln Leu Val Leu His Gln Pro Phe Phe  
210 215 220  
Thr Thr Glu Pro Leu Thr Arg Leu Val Arg Glu Cys Glu Ala Asn Leu  
225 230 235 240  
Glu Leu Leu Phe Pro Ser Glu Ala Glu Val Val Glu Ser Ser Ser Ala  
245 250 255  
Val Gln Ala His Ser Ser Ser His Gln His Asn Ser Pro Arg Ile Ser  
260 265 270  
Ala Glu Thr Ser Ser Thr Leu Gly Asn Glu Asn Leu Asp Ile Tyr Lys  
275 280 285  
Ser Thr Leu Ala Ala Met Arg Ala Ile Arg Gly Leu Gln Lys Ala Ser  
290 295 300  
Ser Thr Tyr Asn Pro Leu Ser Phe Ser Ser Leu Leu Gln Asn Glu Asp  
305 310 315 320  
Asp Glu Thr Val Thr Ala Glu Asn Ser Pro Asn Ser Gly Asn Lys Asp  
325 330 335  
Asp Ser Glu Lys Glu Asp Thr Gly Pro Ser His  
340 345

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..318

(D) OTHER INFORMATION: / Ceres Seq. ID 1481627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Met Lys Phe Gly Lys Glu Phe Arg Thr His Leu Glu Glu Thr Leu Pro  
1 5 10 15  
Glu Trp Arg Asp Lys Phe Leu Cys Tyr Lys Pro Leu Lys Lys Leu Leu  
20 25 30  
Lys Tyr Tyr Pro Tyr Tyr Ser Ala Asp Phe Gly Pro Ala Asn Ser Asp  
35 40 45  
His Asn Asp Ser Arg Pro Val Phe Ala Asp Thr Thr Asn Ile Ser Ser  
50 55 60  
Ala Ala Asp Asp Gly Gly Val Val Pro Gly Val Arg Pro Ser Glu Asp  
65 70 75 80  
Leu Gln Gly Ser Phe Val Arg Ile Leu Asn Asp Glu Leu Glu Lys Phe  
85 90 95  
Asn Asp Phe Tyr Val Asp Lys Glu Glu Asp Phe Val Ile Arg Leu Gln  
100 105 110  
Glu Leu Lys Glu Arg Ile Glu Gln Val Lys Glu Lys Asn Gly Glu Phe  
115 120 125  
Ala Ser Glu Ser Glu Phe Ser Glu Glu Met Met Asp Ile Arg Arg Asp  
130 135 140  
Leu Val Thr Ile His Gly Glu Met Val Leu Leu Lys Asn Tyr Ser Ser  
145 150 155 160  
Leu Asn Phe Ala Gly Leu Val Lys Ile Leu Lys Lys Tyr Asp Lys Arg  
165 170 175  
Thr Gly Gly Leu Leu Arg Leu Pro Phe Thr Gln Leu Val Leu His Gln  
180 185 190  
Pro Phe Phe Thr Thr Glu Pro Leu Thr Arg Leu Val Arg Glu Cys Glu

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 195                                                             | 200 | 205 |
| Ala Asn Leu Glu Leu Leu Phe Pro Ser Glu Ala Glu Val Val Glu Ser |     |     |
| 210                                                             | 215 | 220 |
| Ser Ser Ala Val Gln Ala His Ser Ser Ser His Gln His Asn Ser Pro |     |     |
| 225                                                             | 230 | 235 |
| Arg Ile Ser Ala Glu Thr Ser Ser Thr Leu Gly Asn Glu Asn Leu Asp |     | 240 |
|                                                                 | 245 | 250 |
| Ile Tyr Lys Ser Thr Leu Ala Ala Met Arg Ala Ile Arg Gly Leu Gln |     | 255 |
|                                                                 | 260 | 265 |
| Lys Ala Ser Ser Thr Tyr Asn Pro Leu Ser Phe Ser Ser Leu Leu Gln |     | 270 |
|                                                                 | 275 | 280 |
| Asn Glu Asp Asp Glu Thr Val Thr Ala Glu Asn Ser Pro Asn Ser Gly |     | 285 |
|                                                                 | 290 | 295 |
| Asn Lys Asp Asp Ser Glu Lys Glu Asp Thr Gly Pro Ser His         |     | 300 |
| 305                                                             | 310 | 315 |

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..181

(D) OTHER INFORMATION: / Ceres Seq. ID 1481628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Met Asp Ile Arg Arg Asp Leu Val Thr Ile His Gly Glu Met Val |     |     |
| 1                                                               | 5   | 10  |
| Leu Leu Lys Asn Tyr Ser Ser Leu Asn Phe Ala Gly Leu Val Lys Ile |     | 15  |
|                                                                 | 20  | 25  |
| Leu Lys Lys Tyr Asp Lys Arg Thr Gly Gly Leu Leu Arg Leu Pro Phe |     | 30  |
|                                                                 | 35  | 40  |
| Thr Gln Leu Val Leu His Gln Pro Phe Phe Thr Thr Glu Pro Leu Thr |     | 45  |
|                                                                 | 50  | 55  |
| Arg Leu Val Arg Glu Cys Glu Ala Asn Leu Glu Leu Leu Phe Pro Ser |     | 60  |
| 65                                                              | 70  | 75  |
| Glu Ala Glu Val Val Glu Ser Ser Ser Ala Val Gln Ala His Ser Ser |     | 80  |
|                                                                 | 85  | 90  |
| Ser His Gln His Asn Ser Pro Arg Ile Ser Ala Glu Thr Ser Ser Thr |     | 95  |
|                                                                 | 100 | 105 |
| Leu Gly Asn Glu Asn Leu Asp Ile Tyr Lys Ser Thr Leu Ala Ala Met |     | 110 |
|                                                                 | 115 | 120 |
| Arg Ala Ile Arg Gly Leu Gln Lys Ala Ser Ser Thr Tyr Asn Pro Leu |     | 125 |
|                                                                 | 130 | 135 |
| Ser Phe Ser Ser Leu Leu Gln Asn Glu Asp Asp Glu Thr Val Thr Ala |     | 140 |
| 145                                                             | 150 | 155 |
| Glu Asn Ser Pro Asn Ser Gly Asn Lys Asp Asp Ser Glu Lys Glu Asp |     | 160 |
|                                                                 | 165 | 170 |
| Thr Gly Pro Ser His                                             |     | 175 |
|                                                                 | 180 |     |

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1217

(D) OTHER INFORMATION: / Ceres Seq. ID 1481632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| actccaaaat  | gaggacgcgc  | cggcaaacat  | atccgccgat | cgctgaatcc  | ctcacggcga  | 60   |
| ggtccattgt  | tcaggcgctt  | ccggcgctcag | ccacaatatc | aggaaatggt  | ggaccaaaga  | 120  |
| agaagaagaa  | ctgtgttaat  | agaggattgt  | gggataaaca | gattccgacg  | gatctgctgc  | 180  |
| aagagatact  | gtcttgccctc | ggattaaaag  | ccaacataca | tgcttctctc  | gtctgcaaga  | 240  |
| catggcttaa  | agaagctggt  | tctgtcagga  | agtttcagag | tcgtccttgg  | cttttttatc  | 300  |
| cacagagtca  | gagaggagga  | ccaaaagaag  | gagactacgt | tctctttaac  | ccatcacggt  | 360  |
| ctcaaacaca  | tcacctcaag  | tttccagagt  | taacgggcta | cagaaataaa  | ttagcttggt  | 420  |
| ctaaggatgg  | ttgggttgctt | gtggtaaaag  | ataaccccga | tgtgggtcttc | tttcttaacc  | 480  |
| cgttttaccgg | ggaacgcatac | tgcttaccctc | aggtgccaca | aaattccaca  | cgcgattgct  | 540  |
| taactttctc  | agccgctccc  | acatcaacta  | gttgttgctg | catatccttc  | acccctcaaa  | 600  |
| gttttcttta  | cgcagttggt  | aaagttgata  | cttggcgccc | tggtgaatcc  | gtatggacca  | 660  |
| ctcatcactt  | tgatcaaaag  | cgttacgggt  | aggtaatcaa | tagatgtatc  | ttctccaatg  | 720  |
| gtatgttcta  | ttgtctcagt  | accagtgccc  | gcctctcggt | tttcgaccgg  | tctagagaaa  | 780  |
| cctggaatgt  | tcttccagtg  | aaacatgtc   | gggcctttcg | tcgtaaaatt  | atgcttggtga | 840  |
| ggcaagtatt  | catgacagag  | catgaaggag  | acatctttgt | tgtgactaca  | cgcgcgctaa  | 900  |
| acaacagaaa  | actgtttggcc | tttaactaa   | accttcaagg | caatgtgtgg  | gaagagatga  | 960  |
| aagtacctaa  | tggcttgaca  | gtattttcaa  | gtgacgctac | ctctttaaca  | agagctggtc  | 1020 |
| ttccagagga  | ggagaggaac  | attctatatt  | catcgatat  | cgatgatttt  | gtgaaaagct  | 1080 |
| ctcatccaac  | tttctattat  | tatgactgca  | gcgcttggt  | ccagccacct  | catgacaatt  | 1140 |
| ttaatTTTTg  | actatcatcc  | ttaaagtgtt  | ttgtttttga | aaaaacatgt  | tttaatacct  | 1200 |
| tttaaagctt  | ttgatctc    |             |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..382

(D) OTHER INFORMATION: / Ceres Seq. ID 1481633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Lys | Met | Arg | Thr | Arg | Arg | Gln | Thr | Tyr | Pro | Pro | Ile | Ala | Glu | Ser |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Leu | Thr | Ala | Arg | Ser | Ile | Val | Gln | Ala | Leu | Pro | Ala | Ser | Ala | Thr | Ile |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | Gly | Asn | Gly | Gly | Pro | Lys | Lys | Lys | Asn | Cys | Val | Asn | Arg | Gly |     |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Leu | Trp | Asp | Lys | Gln | Ile | Pro | Thr | Asp | Leu | Leu | Gln | Glu | Ile | Leu | Ser |  |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |  |
| Cys | Leu | Gly | Leu | Lys | Ala | Asn | Ile | His | Ala | Ser | Leu | Val | Cys | Lys | Thr |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Trp | Leu | Lys | Glu | Ala | Val | Ser | Val | Arg | Lys | Phe | Gln | Ser | Arg | Pro | Trp |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Leu | Phe | Tyr | Pro | Gln | Ser | Gln | Arg | Gly | Gly | Pro | Lys | Glu | Gly | Asp | Tyr |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Val | Leu | Phe | Asn | Pro | Ser | Arg | Ser | Gln | Thr | His | His | Leu | Lys | Phe | Pro |  |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Glu | Leu | Thr | Gly | Tyr | Arg | Asn | Lys | Leu | Ala | Cys | Ala | Lys | Asp | Gly | Trp |  |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |  |
| Leu | Leu | Val | Val | Lys | Asp | Asn | Pro | Asp | Val | Val | Phe | Phe | Leu | Asn | Pro |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Phe | Thr | Gly | Glu | Arg | Ile | Cys | Leu | Pro | Gln | Val | Pro | Gln | Asn | Ser | Thr |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |

Arg Asp Cys Leu Thr Phe Ser Ala Ala Pro Thr Ser Thr Ser Cys Cys  
180 185 190  
Val Ile Ser Phe Thr Pro Gln Ser Phe Leu Tyr Ala Val Val Lys Val  
195 200 205  
Asp Thr Trp Arg Pro Gly Glu Ser Val Trp Thr Thr His His Phe Asp  
210 215 220  
Gln Lys Arg Tyr Gly Glu Val Ile Asn Arg Cys Ile Phe Ser Asn Gly  
225 230 235 240  
Met Phe Tyr Cys Leu Ser Thr Ser Gly Arg Leu Ser Phe Phe Asp Pro  
245 250 255  
Ser Arg Glu Thr Trp Asn Val Leu Pro Val Lys Pro Cys Arg Ala Phe  
260 265 270  
Arg Arg Lys Ile Met Leu Val Arg Gln Val Phe Met Thr Glu His Glu  
275 280 285  
Gly Asp Ile Phe Val Val Thr Thr Arg Arg Val Asn Asn Arg Lys Leu  
290 295 300  
Leu Ala Phe Lys Leu Asn Leu Gln Gly Asn Val Trp Glu Glu Met Lys  
305 310 315 320  
Val Pro Asn Gly Leu Thr Val Phe Ser Ser Asp Ala Thr Ser Leu Thr  
325 330 335  
Arg Ala Gly Leu Pro Glu Glu Glu Arg Asn Ile Leu Tyr Ser Ser Asp  
340 345 350  
Ile Asp Asp Phe Val Lys Ser Ser His Pro Thr Phe Tyr Tyr Tyr Asp  
355 360 365  
Cys Ser Ala Trp Leu Gln Pro Pro His Asp Asn Phe Asn Phe  
370 375 380

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..380
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Met Arg Thr Arg Arg Gln Thr Tyr Pro Pro Ile Ala Glu Ser Leu Thr  
1 5 10 15  
Ala Arg Ser Ile Val Gln Ala Leu Pro Ala Ser Ala Thr Ile Ser Gly  
20 25 30  
Asn Gly Gly Pro Lys Lys Lys Lys Asn Cys Val Asn Arg Gly Leu Trp  
35 40 45  
Asp Lys Gln Ile Pro Thr Asp Leu Leu Gln Glu Ile Leu Ser Cys Leu  
50 55 60  
Gly Leu Lys Ala Asn Ile His Ala Ser Leu Val Cys Lys Thr Trp Leu  
65 70 75 80  
Lys Glu Ala Val Ser Val Arg Lys Phe Gln Ser Arg Pro Trp Leu Phe  
85 90 95  
Tyr Pro Gln Ser Gln Arg Gly Gly Pro Lys Glu Gly Asp Tyr Val Leu  
100 105 110  
Phe Asn Pro Ser Arg Ser Gln Thr His His Leu Lys Phe Pro Glu Leu  
115 120 125  
Thr Gly Tyr Arg Asn Lys Leu Ala Cys Ala Lys Asp Gly Trp Leu Leu  
130 135 140  
Val Val Lys Asp Asn Pro Asp Val Val Phe Phe Leu Asn Pro Phe Thr  
145 150 155 160  
Gly Glu Arg Ile Cys Leu Pro Gln Val Pro Gln Asn Ser Thr Arg Asp

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Cys | Leu | Thr | Phe | Ser | Ala | Ala | Pro | Thr | Ser | Thr | Ser | Cys | Cys | Val | Ile |  |  |
|     |     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |  |  |
| Ser | Phe | Thr | Pro | Gln | Ser | Phe | Leu | Tyr | Ala | Val | Val | Lys | Val | Asp | Thr |  |  |
|     |     | 195 |     |     |     |     |     | 200 |     |     |     | 205 |     |     |     |  |  |
| Trp | Arg | Pro | Gly | Glu | Ser | Val | Trp | Thr | Thr | His | His | Phe | Asp | Gln | Lys |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Arg | Tyr | Gly | Glu | Val | Ile | Asn | Arg | Cys | Ile | Phe | Ser | Asn | Gly | Met | Phe |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Tyr | Cys | Leu | Ser | Thr | Ser | Gly | Arg | Leu | Ser | Phe | Phe | Asp | Pro | Ser | Arg |  |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |
| Glu | Thr | Trp | Asn | Val | Leu | Pro | Val | Lys | Pro | Cys | Arg | Ala | Phe | Arg | Arg |  |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |
| Lys | Ile | Met | Leu | Val | Arg | Gln | Val | Phe | Met | Thr | Glu | His | Glu | Gly | Asp |  |  |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |  |  |
| Ile | Phe | Val | Val | Thr | Thr | Arg | Arg | Val | Asn | Asn | Arg | Lys | Leu | Leu | Ala |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |
| Phe | Lys | Leu | Asn | Leu | Gln | Gly | Asn | Val | Trp | Glu | Glu | Met | Lys | Val | Pro |  |  |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     |     | 320 |  |  |
| Asn | Gly | Leu | Thr | Val | Phe | Ser | Ser | Asp | Ala | Thr | Ser | Leu | Thr | Arg | Ala |  |  |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |  |  |
| Gly | Leu | Pro | Glu | Glu | Glu | Arg | Asn | Ile | Leu | Tyr | Ser | Ser | Asp | Ile | Asp |  |  |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |  |
| Asp | Phe | Val | Lys | Ser | Ser | His | Pro | Thr | Phe | Tyr | Tyr | Tyr | Asp | Cys | Ser |  |  |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |  |  |
| Ala | Trp | Leu | Gln | Pro | Pro | His | Asp | Asn | Phe | Asn | Phe |     |     |     |     |  |  |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..667
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| mtgacgcttg | gysttcttgc  | accctaccgt | gggattggca | ttggtaagtc | ataaatctgc | 60  |
| tgtgccaaac | ttgaataccg  | acaaaacatg | aataatgaag | aaaactgtta | gcatgttg   | 120 |
| taattctggt | gttttcctta  | cgttttaaca | catgaggcca | gctgtagtat | gtttattctg | 180 |
| tagttctcta | tttgaagtgt  | ctccatttag | agattcaaac | caccaagaaa | tagtccttag | 240 |
| ggttttatgc | atatcgttgt  | tttaccgaga | aactggaatt | agtgactatg | atttcctcct | 300 |
| atatcaagat | ttaagatcga  | attccctgct | tttagaaaga | aaaactcgat | gtctataatt | 360 |
| tgtgtatctt | gtttttttcg  | tcttttgcag | gctcaaactt | attgaatcat | gttcttgaca | 420 |
| tgtgctccaa | gcaaaacatg  | tgtgagatat | acttgcatgt | gcagacaaac | aacgaagacg | 480 |
| caatcaagtt | ctacaagaag  | ttcggctttg | agatcacaga | taccatacaa | aactattaca | 540 |
| tcaacattga | gccaaagagat | tgctacgttg | tcagcaagtc | ctttgctcaa | tctgaagcca | 600 |
| acaaatgatg | aaaaatacca  | aacttgggga | agcatttctt | ccccagtttc | tttgttgcat | 660 |
| tcagttc    |             |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..68  
(D) OTHER INFORMATION: / Ceres Seq. ID 1481636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met Arg Pro Ala Val Val Cys Leu Phe Cys Ser Ser Leu Phe Glu Val  
1 5 10 15  
Ser Pro Phe Arg Asp Ser Asn His Gln Glu Ile Val Leu Arg Val Leu  
20 25 30  
Cys Ile Ser Leu Phe Tyr Arg Glu Thr Gly Ile Ser Asp Tyr Asp Phe  
35 40 45  
Leu Leu Tyr Gln Asp Leu Arg Ser Asn Ser Leu Leu Leu Glu Arg Lys  
50 55 60  
Thr Arg Cys Leu  
65

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..86  
(D) OTHER INFORMATION: / Ceres Seq. ID 1481637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Met Phe Leu Thr Cys Ala Pro Ser Lys Thr Cys Val Arg Tyr Thr Cys  
1 5 10 15  
Met Cys Arg Gln Thr Thr Lys Thr Gln Ser Ser Ser Thr Arg Ser Ser  
20 25 30  
Ala Leu Arg Ser Gln Ile Pro Tyr Lys Thr Ile Thr Ser Thr Leu Ser  
35 40 45  
Gln Glu Ile Ala Thr Leu Ser Ala Ser Pro Leu Leu Asn Leu Lys Pro  
50 55 60  
Thr Asn Asp Glu Lys Tyr Gln Thr Trp Gly Ser His Ser Ser Pro Val  
65 70 75 80  
Ser Leu Leu His Ser Val  
85

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..70  
(D) OTHER INFORMATION: / Ceres Seq. ID 1481638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Met Cys Arg Gln Thr Thr Lys Thr Gln Ser Ser Ser Thr Arg Ser Ser  
1 5 10 15  
Ala Leu Arg Ser Gln Ile Pro Tyr Lys Thr Ile Thr Ser Thr Leu Ser  
20 25 30  
Gln Glu Ile Ala Thr Leu Ser Ala Ser Pro Leu Leu Asn Leu Lys Pro  
35 40 45  
Thr Asn Asp Glu Lys Tyr Gln Thr Trp Gly Ser His Ser Ser Pro Val  
50 55 60  
Ser Leu Leu His Ser Val



65

70

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1177
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

|            |            |             |             |             |             |      |
|------------|------------|-------------|-------------|-------------|-------------|------|
| ctttgcgatg | gtaaaatagt | gttctcagat  | tgggctagca  | atgtgagttc  | tattcttttg  | 60   |
| gtccctgttc | gtgccttgag | tgagaagctt  | gctagagggt  | catcatcagt  | cactccgctg  | 120  |
| aaacaagata | tttttagagg | aatgagaact  | gtagctttga  | aacttgaatt  | tggggttcat  | 180  |
| cataaccaga | tatttgagag | aaccatagct  | gcacatttta  | ccgatccctt  | tgatgtgacc  | 240  |
| acaagggtgg | caaacaaatg | caatgatggc  | actttggtct  | tgcaggttat  | gttacactcc  | 300  |
| ctcgtcaagg | cgaacttgat | agttcttgat  | gtttggcttg  | atcttcaaga  | tggatttatt  | 360  |
| catggacaaa | atgatggaag | accgacttca  | acgttctttc  | cgcttgctgt  | gtctccagga  | 420  |
| tctagagcag | cagtcgtggt | cagtatatgc  | ctagacaaga  | gtatgtcatc  | agaagggaaa  | 480  |
| gatttgcagc | taccagaaag | cattctgaat  | atcaaatatg  | gaatccatgg  | ggatagagca  | 540  |
| gctggagcac | acaggccagt | ggatgcagat  | cactctgaaa  | ctgatactta  | agggagagat  | 600  |
| ttggtgttca | agagtgtcat | tgttttgcag  | cgtccagtac  | ttgatccttg  | cctcacagtt  | 660  |
| ggattcctcc | cacttccttc | tgatgggctt  | agggtcggga  | aacttatcac  | catgcagtgg  | 720  |
| agagtggaaa | ggcttaaaga | tctcaaagaa  | agtgaagccg  | tgaacaaca   | acatgatgag  | 780  |
| gtgttatatg | aagtcaatgc | aaattcggag  | aattggatga  | tcgctggtag  | gaagagaggg  | 840  |
| catgtctctc | tctcagagga | gcaagggttca | agagttagtaa | tctcgatact  | atgtgtcccg  | 900  |
| ttagttgcgg | gttatgtccg | tcctcctcaa  | ctcgggttgc  | caaacgtaga  | agaagcaaatt | 960  |
| gtaagcagca | atccatcggg | tcctcactta  | gtatgtgtct  | tgccctccact | tctcagttct  | 1020 |
| tcctactgcg | tacctgtcaa | gtaatagaat  | ctcactctat  | atTTTTTcca  | agaaaacatt  | 1080 |
| ttttctgtat | ttttattttg | tttgcgatca  | aagaaatatc  | agagtatggg  | atcatcaatg  | 1140 |
| atgagagtga | tttttctttt | gtgacgattt  | tattttcc    |             |             |      |

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Cys | Asp | Gly | Lys | Ile | Val | Phe | Ser | Asp | Trp | Ala | Ser | Asn | Val | Ser |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ser | Ile | Leu | Trp | Val | Pro | Val | Arg | Ala | Leu | Ser | Glu | Lys | Leu | Ala | Arg |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Gly | Ser | Ser | Ser | Val | Thr | Pro | Leu | Lys | Gln | Asp | Ile | Leu | Glu | Gly | Met |  |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |  |
| Arg | Thr | Val | Ala | Leu | Lys | Leu | Glu | Phe | Gly | Val | His | His | Asn | Gln | Ile |  |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |  |
| Phe | Glu | Arg | Thr | Ile | Ala | Ala | His | Phe | Thr | Asp | Pro | Phe | Asp | Val | Thr |  |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |  |
| Thr | Arg | Val | Ala | Asn | Lys | Cys | Asn | Asp | Gly | Thr | Leu | Val | Leu | Gln | Val |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Met | Leu | His | Ser | Leu | Val | Lys | Ala | Asn | Leu | Ile | Val | Leu | Asp | Val | Trp |  |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |  |

Leu Asp Leu Gln Asp Gly Phe Ile His Gly Gln Asn Asp Gly Arg Pro  
115 120 125  
Thr Ser Thr Phe Phe Pro Leu Val Val Ser Pro Gly Ser Arg Ala Ala  
130 135 140  
Val Val Phe Ser Ile Cys Leu Asp Lys Ser Met Ser Ser Glu Gly Lys  
145 150 155 160  
Asp Leu Gln Leu Pro Glu Ser Ile Leu Asn Ile Lys Tyr Gly Ile His  
165 170 175  
Gly Asp Arg Ala Ala Gly Ala His Arg Pro Val Asp Ala Asp His Ser  
180 185 190  
Glu Thr Asp Thr  
195

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1481641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Met Arg Thr Val Ala Leu Lys Leu Glu Phe Gly Val His His Asn Gln  
1 5 10 15  
Ile Phe Glu Arg Thr Ile Ala Ala His Phe Thr Asp Pro Phe Asp Val  
20 25 30  
Thr Thr Arg Val Ala Asn Lys Cys Asn Asp Gly Thr Leu Val Leu Gln  
35 40 45  
Val Met Leu His Ser Leu Val Lys Ala Asn Leu Ile Val Leu Asp Val  
50 55 60  
Trp Leu Asp Leu Gln Asp Gly Phe Ile His Gly Gln Asn Asp Gly Arg  
65 70 75 80  
Pro Thr Ser Thr Phe Phe Pro Leu Val Val Ser Pro Gly Ser Arg Ala  
85 90 95  
Ala Val Val Phe Ser Ile Cys Leu Asp Lys Ser Met Ser Ser Glu Gly  
100 105 110  
Lys Asp Leu Gln Leu Pro Glu Ser Ile Leu Asn Ile Lys Tyr Gly Ile  
115 120 125  
His Gly Asp Arg Ala Ala Gly Ala His Arg Pro Val Asp Ala Asp His  
130 135 140  
Ser Glu Thr Asp Thr  
145

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1481642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Met Gln Trp Arg Val Glu Arg Leu Lys Asp Leu Lys Glu Ser Glu Ala  
1 5 10 15  
Val Glu Gln Gln His Asp Glu Val Leu Tyr Glu Val Asn Ala Asn Ser

(2) INFORMATION FOR SEQ ID NO:107:

(A) LENGTH: 1337 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1337

(D) OTHER INFORMATION: / Ceres Seq. ID 1481647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

|            |             |            |             |            |            |      |
|------------|-------------|------------|-------------|------------|------------|------|
| aaaaaaataa | aaataaaaaa  | tcttcacggt | tcttctctct  | ctctctctct | cgagccacca | 60   |
| aatctgaatt | aggggttttt  | gagaatatct | atcttttgat  | ttcaaattct | tcacccactg | 120  |
| tgtaatttca | ctcgtcagga  | ttcatcagag | gaatcatgat  | tacagattcg | atcaccaacg | 180  |
| cttctgctac | ttcagctccg  | agagattccg | gaaagaagaa  | gaggaacaat | aagtcggcta | 240  |
| agatgaagca | gaacaagctt  | ggtctccgtc | gtgagcaatg  | gctttctcaa | gttgcggtga | 300  |
| gcaataagga | agtttaaagag | gagaggagt  | ttaatcgtag  | tcaaaaagct | gatcatgaga | 360  |
| gttcagataa | gggtgcgtaga | gaagaggata | acaatggtgg  | gaataatctt | cttcatcatg | 420  |
| agagttttat | ggagtcacct  | tcaaatagct | ctgttgggtg  | tacatatctg | agcactaact | 480  |
| tcagtgggag | aagtagcagg  | agtagtagta | gcagcagtg   | cttttgctct | ggtaataata | 540  |
| cagaagagga | aaatgtagac  | gatgatgatg | atgggtgtgt  | ggatgattgg | gaagctgttg | 600  |
| ctgatgcgtt | agcggctgag  | gaagagattg | agaaaaagag  | tcgtctctct | gagtcgtgta | 660  |
| aagagcaagt | gagtgttgga  | caatcagctt | ctaattgtgt  | tgatbcgctg | attagtgtag | 720  |
| catcagatgt | tgtgggtggt  | gaagatccaa | agcaggaatg  | cttgagagtg | tcataagga  | 780  |
| agcagactag | taatatagct  | tggaggctag | attgatgacct | tcgccacag  | gggttaccta | 840  |
| atttggcgaa | cgagcttagt  | tttcgggagt | tagacaagcg  | ttttagctct | gtggcgattc | 900  |
| cgtcttcatg | tcccatatgc  | tacgaagact | tggacttgac  | ggattcgaat | ttcctccctt | 960  |
| gtccttgtgg | atttcggctc  | tgtctgttct | gccacaagac  | catttgcgat | ggagatgggc | 1020 |
| gttgtccagg | ctgcaggaaa  | ccctatgaac | ggaatatggt  | caaggctgag | actagtattc | 1080 |
| aagggtggtg | tctaacaatt  | cggttggtc  | gttcgtctag  | catgttttgc | aagttttaaa | 1140 |
| aggagaggtg | cggttttctc  | aacctggtg  | tcttttgtaa  | ctcgagaact | tgagctctgt | 1200 |
| tttctatgtc | atacatggtt  | ctaagctctg | aacactgtgg  | tgatgatgta | gaatgtgatg | 1260 |
| tgtgaataca | ttaaaggtgg  | tacagaaaa  | gattcaata   | catttagata | gtttcaataa | 1320 |
| tgaatactat | gtttctcc    |            |             |            |            |      |

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..327

(D) OTHER INFORMATION: / Ceres Seq. ID 1481648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Met Ile Thr Asp Ser Ile Thr Asn Ala Ser Ala Thr Ser Ala Pro Arg

|                 |                 |                     |                 |
|-----------------|-----------------|---------------------|-----------------|
| 1               | 5               | 10                  | 15              |
| Asp Ser Gly Lys | Lys Lys Arg Asn | Asn Lys Ser Ala Lys | Met Lys Gln     |
| 20              | 25              | 30                  |                 |
| Asn Lys Leu Gly | Leu Arg Arg Glu | Gln Trp Leu Ser     | Gln Val Ala Val |
| 35              | 40              | 45                  |                 |
| Ser Asn Lys Glu | Val Lys Glu Arg | Ser Val Asn Arg     | Ser Gln Lys     |
| 50              | 55              | 60                  |                 |
| Pro Asp His Glu | Ser Ser Asp Lys | Val Arg Arg Glu     | Glu Asp Asn Asn |
| 65              | 70              | 75                  | 80              |
| Gly Gly Asn Asn | Leu Leu His His | Glu Ser Phe Met     | Glu Ser Pro Ser |
| 85              | 90              | 95                  |                 |
| Asn Ser Ser Val | Gly Gly Thr Tyr | Ser Ser Thr Asn     | Phe Ser Gly Arg |
| 100             | 105             | 110                 |                 |
| Ser Ser Arg Ser | Ser Ser Ser Ser | Ser Ser Gly Phe     | Cys Ser Gly Asn |
| 115             | 120             | 125                 |                 |
| Thr Glu Glu Glu | Asn Val Asp Asp | Asp Asp Gly Cys     | Val Asp Asp     |
| 130             | 135             | 140                 |                 |
| Trp Glu Ala Val | Ala Asp Ala Leu | Ala Glu Glu Glu     | Ile Glu Lys     |
| 145             | 150             | 155                 | 160             |
| Lys Ser Arg Pro | Leu Glu Ser Val | Lys Glu Gln Val     | Ser Val Gly Gln |
| 165             | 170             | 175                 |                 |
| Ser Ala Ser Asn | Val Cys Asp Xaa | Ser Ile Ser Asp     | Ala Ser Asp Val |
| 180             | 185             | 190                 |                 |
| Val Gly Val Glu | Asp Pro Lys Gln | Glu Cys Leu Arg     | Val Ser Ser Arg |
| 195             | 200             | 205                 |                 |
| Lys Gln Thr Ser | Asn Arg Ala Trp | Arg Leu Asp Asp     | Asp Leu Arg Pro |
| 210             | 215             | 220                 |                 |
| Gln Gly Leu Pro | Asn Leu Ala Lys | Gln Leu Ser Phe     | Pro Glu Leu Asp |
| 225             | 230             | 235                 | 240             |
| Lys Arg Phe Ser | Ser Val Ala Ile | Pro Ser Ser Cys     | Pro Ile Cys Tyr |
| 245             | 250             | 255                 |                 |
| Glu Asp Leu Asp | Leu Thr Asp Ser | Asn Phe Leu Pro     | Cys Pro Cys Gly |
| 260             | 265             | 270                 |                 |
| Phe Arg Leu Cys | Leu Phe Cys His | Lys Thr Ile Cys     | Asp Gly Asp Gly |
| 275             | 280             | 285                 |                 |
| Arg Cys Pro Gly | Cys Arg Lys Pro | Tyr Glu Arg Asn     | Met Val Lys Ala |
| 290             | 295             | 300                 |                 |
| Glu Thr Ser Ile | Gln Gly Gly Gly | Leu Thr Ile Arg     | Leu Ala Arg Ser |
| 305             | 310             | 315                 | 320             |
| Ser Ser Met Phe | Cys Lys Phe     |                     |                 |
| 325             |                 |                     |                 |

## (2) INFORMATION FOR SEQ ID NO:109:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 298 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..298

(D) OTHER INFORMATION: / Ceres Seq. ID 1481649

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

|                 |                 |                 |                 |
|-----------------|-----------------|-----------------|-----------------|
| Met Lys Gln Asn | Lys Leu Gly Leu | Arg Arg Glu Gln | Trp Leu Ser Gln |
| 1               | 5               | 10              | 15              |
| Val Ala Val Ser | Asn Lys Glu Val | Lys Glu Glu Arg | Ser Val Asn Arg |
| 20              | 25              | 30              |                 |
| Ser Gln Lys Pro | Asp His Glu Ser | Asp Lys Val Arg | Arg Glu Glu     |
| 35              | 40              | 45              |                 |

Asp Asn Asn Gly Gly Asn Asn Leu Leu His His Glu Ser Phe Met Glu  
50 55 60  
Ser Pro Ser Asn Ser Ser Val Gly Gly Thr Tyr Ser Ser Thr Asn Phe  
65 70 75 80  
Ser Gly Arg Ser Ser Arg Ser Ser Ser Ser Ser Gly Phe Cys Ser  
85 90 95  
Gly Asn Ile Thr Glu Glu Glu Asn Val Asp Asp Asp Asp Asp Gly Cys  
100 105 110  
Val Asp Asp Trp Glu Ala Val Ala Asp Ala Leu Ala Ala Glu Glu Glu  
115 120 125  
Ile Glu Lys Lys Ser Arg Pro Leu Glu Ser Val Lys Glu Gln Val Ser  
130 135 140  
Val Gly Gln Ser Ala Ser Asn Val Cys Asp Xaa Ser Ile Ser Asp Ala  
145 150 155 160  
Ser Asp Val Val Gly Val Glu Asp Pro Lys Gln Glu Cys Leu Arg Val  
165 170 175  
Ser Ser Arg Lys Gln Thr Ser Asn Arg Ala Trp Arg Leu Asp Asp Asp  
180 185 190  
Leu Arg Pro Gln Gly Leu Pro Asn Leu Ala Lys Gln Leu Ser Phe Pro  
195 200 205  
Glu Leu Asp Lys Arg Phe Ser Ser Val Ala Ile Pro Ser Ser Cys Pro  
210 215 220  
Ile Cys Tyr Glu Asp Leu Asp Leu Thr Asp Ser Asn Phe Leu Pro Cys  
225 230 235 240  
Pro Cys Gly Phe Arg Leu Cys Leu Phe Cys His Lys Thr Ile Cys Asp  
245 250 255  
Gly Asp Gly Arg Cys Pro Gly Cys Arg Lys Pro Tyr Glu Arg Asn Met  
260 265 270  
Val Lys Ala Glu Thr Ser Ile Gln Gly Gly Gly Leu Thr Ile Arg Leu  
275 280 285  
Ala Arg Ser Ser Ser Met Phe Cys Lys Phe  
290 295

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1481650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Glu Ser Pro Ser Asn Ser Ser Val Gly Gly Thr Tyr Ser Ser Thr  
1 5 10 15  
Asn Phe Ser Gly Arg Ser Ser Arg Ser Ser Ser Ser Ser Ser Gly Phe  
20 25 30  
Cys Ser Gly Asn Ile Thr Glu Glu Asn Val Asp Asp Asp Asp Asp  
35 40 45  
Gly Cys Val Asp Asp Trp Glu Ala Val Ala Asp Ala Leu Ala Ala Glu  
50 55 60  
Glu Glu Ile Glu Lys Lys Ser Arg Pro Leu Glu Ser Val Lys Glu Gln  
65 70 75 80  
Val Ser Val Gly Gln Ser Ala Ser Asn Val Cys Asp Xaa Ser Ile Ser  
85 90 95  
Asp Ala Ser Asp Val Val Gly Val Glu Asp Pro Lys Gln Glu Cys Leu  
100 105 110  
Arg Val Ser Ser Arg Lys Gln Thr Ser Asn Arg Ala Trp Arg Leu Asp

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 115                                                             | 120 | 125 |
| Asp Asp Leu Arg Pro Gln Gly Leu Pro Asn Leu Ala Lys Gln Leu Ser |     |     |
| 130                                                             | 135 | 140 |
| Phe Pro Glu Leu Asp Lys Arg Phe Ser Ser Val Ala Ile Pro Ser Ser |     |     |
| 145                                                             | 150 | 155 |
| Cys Pro Ile Cys Tyr Glu Asp Leu Asp Leu Thr Asp Ser Asn Phe Leu |     |     |
| 165                                                             | 170 | 175 |
| Pro Cys Pro Cys Gly Phe Arg Leu Cys Leu Phe Cys His Lys Thr Ile |     |     |
| 180                                                             | 185 | 190 |
| Cys Asp Gly Asp Gly Arg Cys Pro Gly Cys Arg Lys Pro Tyr Glu Arg |     |     |
| 195                                                             | 200 | 205 |
| Asn Met Val Lys Ala Glu Thr Ser Ile Gln Gly Gly Gly Leu Thr Ile |     |     |
| 210                                                             | 215 | 220 |
| Arg Leu Ala Arg Ser Ser Ser Met Phe Cys Lys Phe                 |     |     |
| 225                                                             | 230 | 235 |

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1298
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| amatcctmat | cgaaaaacgg | aaattagttt | acaggctgta | atTTTTcttt | caggctctct | 60   |
| ctctttcgtc | gccgaaccag | ttccagaaag | gctgtagcga | ttcaaaattt | cacaaattaa | 120  |
| agtcttcttc | ctctcsgaat | cagagattgt | ctccttctta | gctcagatct | gggagcttct | 180  |
| tgtgatagat | ttggaagaag | atgactgtga | tcgatattct | gactagagtt | gactcgatct | 240  |
| gtaagaagta | cgacaagtac | gatgtcgaca | agcagcgga  | ggccaatatc | tccggcgatg | 300  |
| atgcctttgc | tcgtctctat | ggagctttcg | aaacccaaat | cgagaccgct | ctcgagaaag | 360  |
| ctgaacttgt | tacgaaggag | aaaaacaggg | ctgctgctgt | tgcaatgaat | gctgagatcc | 420  |
| gccggaccac | ggcacgattg | tcagaggaag | ttcccaagtt | gcaaagactt | gctgtcaagc | 480  |
| gggttaaggg | ccttacaacc | gaagagcttg | ctgcgagaaa | tgatttggtg | ctcgctcttc | 540  |
| cagccaggat | tgaagccata | cctgatggga | cagcagggtg | ccctaaaagc | actagtgett | 600  |
| ggactccctc | ctcaacaaca | tctcgtcctg | atatcaaatt | tgattcagat | gggcgttttg | 660  |
| acgatgatta | ctttcaagaa | tcaaataaat | ctagccaatt | caggcaggag | tatgagatgc | 720  |
| ggaaaataaa | acaggaacaa | ggtcttgaca | tgatctccga | agggttagat | gctttgaaga | 780  |
| acatggcttc | tgatatgaac | gaggaactgg | atagacaagt | tccactgatg | gatgaaatcg | 840  |
| acacaaaggt | ggacagagca | acctccgatc | ttaagaacac | caatgttaga | cttaaagata | 900  |
| ccgtgaacca | gctgagatct | agccggaact | tctgtatcga | tattgttttg | ttgtgtattg | 960  |
| ttctgggtat | cgctgcatac | ttatacaatg | tactgaagta | atgagatgaa | ccctacgaaa | 1020 |
| ggacccatta | gtacttatca | cccagtgcaa | tatccagtgt | gtgcttgtgt | cttactcttc | 1080 |
| ttctctgata | tttctacgag | agtttcttct | taatgtcaag | aatattcaag | tcttatcttc | 1140 |
| ctgcatcgac | ttttctccat | gttgttcgtg | tgcatagatt | tcattctgtc | aaatgtgcgt | 1200 |
| caaactaatt | gattgctgtg | tctgcggcag | tgtgctatta | ttttccagcc | aaaatatgat | 1260 |
| tttttattta | ttttaaaatc | aagccaaatt | ttaattcc   |            |            |      |

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266

(D) OTHER INFORMATION: / Ceres Seq. ID 1481669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Thr Val Ile Asp Ile Leu Thr Arg Val Asp Ser Ile Cys Lys Lys  
1 5 10 15  
Tyr Asp Lys Tyr Asp Val Asp Lys Gln Arg Glu Ala Asn Ile Ser Gly  
20 25 30  
Asp Asp Ala Phe Ala Arg Leu Tyr Gly Ala Phe Glu Thr Gln Ile Glu  
35 40 45  
Thr Ala Leu Glu Lys Ala Glu Leu Val Thr Lys Glu Lys Asn Arg Ala  
50 55 60  
Ala Ala Val Ala Met Asn Ala Glu Ile Arg Arg Thr Lys Ala Arg Leu  
65 70 75 80  
Ser Glu Glu Val Pro Lys Leu Gln Arg Leu Ala Val Lys Arg Val Lys  
85 90 95  
Gly Leu Thr Thr Glu Glu Leu Ala Ala Arg Asn Asp Leu Val Leu Ala  
100 105 110  
Leu Pro Ala Arg Ile Glu Ala Ile Pro Asp Gly Thr Ala Gly Gly Pro  
115 120 125  
Lys Ser Thr Ser Ala Trp Thr Pro Ser Ser Thr Thr Ser Arg Pro Asp  
130 135 140  
Ile Lys Phe Asp Ser Asp Gly Arg Phe Asp Asp Asp Tyr Phe Gln Glu  
145 150 155 160  
Ser Asn Glu Ser Ser Gln Phe Arg Gln Glu Tyr Glu Met Arg Lys Ile  
165 170 175  
Lys Gln Glu Gln Gly Leu Asp Met Ile Ser Glu Gly Leu Asp Ala Leu  
180 185 190  
Lys Asn Met Ala Ser Asp Met Asn Glu Glu Leu Asp Arg Gln Val Pro  
195 200 205  
Leu Met Asp Glu Ile Asp Thr Lys Val Asp Arg Ala Thr Ser Asp Leu  
210 215 220  
Lys Asn Thr Asn Val Arg Leu Lys Asp Thr Val Asn Gln Leu Arg Ser  
225 230 235 240  
Ser Arg Asn Phe Cys Ile Asp Ile Val Leu Leu Cys Ile Val Leu Gly  
245 250 255  
Ile Ala Ala Tyr Leu Tyr Asn Val Leu Lys  
260 265

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..198

(D) OTHER INFORMATION: / Ceres Seq. ID 1481670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Asn Ala Glu Ile Arg Arg Thr Lys Ala Arg Leu Ser Glu Glu Val  
1 5 10 15  
Pro Lys Leu Gln Arg Leu Ala Val Lys Arg Val Lys Gly Leu Thr Thr  
20 25 30  
Glu Glu Leu Ala Ala Arg Asn Asp Leu Val Leu Ala Leu Pro Ala Arg  
35 40 45  
Ile Glu Ala Ile Pro Asp Gly Thr Ala Gly Gly Pro Lys Ser Thr Ser  
50 55 60  
Ala Trp Thr Pro Ser Ser Thr Thr Ser Arg Pro Asp Ile Lys Phe Asp  
65 70 75 80  
Ser Asp Gly Arg Phe Asp Asp Asp Tyr Phe Gln Glu Ser Asn Glu Ser

85 90 95  
Ser Gln Phe Arg Gln Glu Tyr Glu Met Arg Lys Ile Lys Gln Glu Gln  
100 105 110  
Gly Leu Asp Met Ile Ser Glu Gly Leu Asp Ala Leu Lys Asn Met Ala  
115 120 125  
Ser Asp Met Asn Glu Glu Leu Asp Arg Gln Val Pro Leu Met Asp Glu  
130 135 140  
Ile Asp Thr Lys Val Asp Arg Ala Thr Ser Asp Leu Lys Asn Thr Asn  
145 150 155 160  
Val Arg Leu Lys Asp Thr Val Asn Gln Leu Arg Ser Ser Arg Asn Phe  
165 170 175  
Cys Ile Asp Ile Val Leu Leu Cys Ile Val Leu Gly Ile Ala Ala Tyr  
180 185 190  
Leu Tyr Asn Val Leu Lys  
195

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 770 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..770
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| cytttcgacc  | tctcctactt | actactactc | agctgcttct | gccttctagg | gttctttctc  | 60  |
| cgttcaccct  | ccgccgcacg | agttgtccag | ctccgccgca | ttcttctgtc | tcccagatca  | 120 |
| ccggctttta  | gcaaatccgg | ctgcttttca | ctctaattcg | taaaccactt | gtgggatttg  | 180 |
| agcatctttt  | acattctcca | aaatctctgc | tttctagggt | tttgtgagtt | ttgggtgggat | 240 |
| gagtagtggtg | ttcagtgatc | agatcctgat | tgataagctc | gctaagctca | atagcagtc   | 300 |
| acagtctatc  | gaaactctgt | cacattggtg | tatattcaat | cggagcaaag | cagaattgat  | 360 |
| cgttacgaca  | tgggagaaac | agtttcacag | tacagagatg | gatcagaaag | tccctctttt  | 420 |
| gtatttggct  | aatgatattc | ttcagaacag | taagcgtcaa | ggtaatgagt | ttgtgcaaga  | 480 |
| gttctggaat  | gttcttccta | aggctcttaa | agacattggt | tctcaaggag | atgataatgg  | 540 |
| caaaagcgct  | gtcgcacgtg | tgatcaagat | atgggaagaa | agaagagtgt | ttggatcacg  | 600 |
| ttcaaagagt  | cttaaagatg | taatgcttgg | agaagatggt | cctctgccac | ttgatatcag  | 660 |
| caaaaagcgg  | gsctcgcgga | tccaaatctt | caaaacggga | gtcaaaatcg | tccagaacga  | 720 |
| aattaacatc  | aagtgggtgt | gtgctgarar | gtagcatcac | catatcattt |             |     |

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Met Ser Ser Val Phe Ser Asp Gln Ile Leu Ile Asp Lys Leu Ala Lys  
1 5 10 15  
Leu Asn Ser Ser Gln Gln Ser Ile Glu Thr Leu Ser His Trp Cys Ile  
20 25 30  
Phe Asn Arg Ser Lys Ala Glu Leu Ile Val Thr Thr Trp Glu Lys Gln  
35 40 45  
Phe His Ser Thr Glu Met Asp Gln Lys Val Pro Leu Leu Tyr Leu Ala



```

 50 55 60
Asn Asp Ile Leu Gln Asn Ser Lys Arg Gln Gly Asn Glu Phe Val Gln
65 70 75 80
Glu Phe Trp Asn Val Leu Pro Lys Ala Leu Lys Asp Ile Val Ser Gln
 85 90 95
Gly Asp Asp Asn Gly Lys Ser Ala Val Ala Arg Val Ile Lys Ile Trp
 100 105 110
Glu Glu Arg Arg Val Phe Gly Ser Arg Ser Lys Ser Leu Lys Asp Val
 115 120 125
Met Leu Gly Glu Asp Val Pro Leu Pro Leu Asp Ile Ser Lys Lys Arg
 130 135 140
Xaa Ser Arg Ile Gln Ile Phe Lys Thr Gly Val Lys Ile Val Gln Asn
145 150 155 160
Glu Ile Asn Ile Lys Trp Trp Cys Ala Xaa Xaa
 165 170

```

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

```

Met Asp Gln Lys Val Pro Leu Leu Tyr Leu Ala Asn Asp Ile Leu Gln
1 5 10 15
Asn Ser Lys Arg Gln Gly Asn Glu Phe Val Gln Glu Phe Trp Asn Val
 20 25 30
Leu Pro Lys Ala Leu Lys Asp Ile Val Ser Gln Gly Asp Asp Asn Gly
 35 40 45
Lys Ser Ala Val Ala Arg Val Ile Lys Ile Trp Glu Glu Arg Arg Val
 50 55 60
Phe Gly Ser Arg Ser Lys Ser Leu Lys Asp Val Met Leu Gly Glu Asp
65 70 75 80
Val Pro Leu Pro Leu Asp Ile Ser Lys Lys Arg Xaa Ser Arg Ile Gln
 85 90 95
Ile Phe Lys Thr Gly Val Lys Ile Val Gln Asn Glu Ile Asn Ile Lys
 100 105 110
Trp Trp Cys Ala Xaa Xaa
 115

```

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1004 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1004
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

```

ctcgcatcgc atcgatcctc ccatctgcgc acccgcaagc ctattctccg cacctcctca 60
ggtgaccggg aagatgatgc cgttgagcca aaccgacttc tcgccgtcgc agttcacctc 120
ctcccagaat gccgccgccg actccaccac gccttccaag atgcgcggcg cgtccagcac 180
catgccgctc accgtgaagc aggtcgtcga cgcgcasagt ctggcacggg cgagaagggc 240

```

|            |             |            |             |             |             |     |
|------------|-------------|------------|-------------|-------------|-------------|-----|
| gctccgttca | tcgtcaatgg  | cgtcgagatg | gctaacattc  | gacttggtggg | gatgggtcaat | 300 |
| gccaaggtgg | agcggacgac  | cgatgtgacc | ttcacgctcg  | acgatggcac  | cggccgcctc  | 360 |
| gatttcatca | gatgggtgaa  | tgatgcttca | gattcttttg  | aaactgctgc  | tattcagaat  | 420 |
| ggtatgtaca | ttgcgggtcat | tggaagcctc | aagggactgc  | aagagaggaa  | gcgtgctact  | 480 |
| gctttctcaa | tcaggcctat  | aaccgatttc | aatgagggtta | cgctgcattt  | cattcagttg  | 540 |
| gttcggatgc | atatagagaa  | cattgaatta | aaggctggca  | gtcctgcacg  | aatcagttct  | 600 |
| tctatgggag | tgctattctc  | aaatggattc | agtgaatcaa  | gcacaccgac  | atctttgaaa  | 660 |
| tccagtcccc | caccgggtgac | cagcgggtca | tccgatactg  | atctgcacac  | gcaggctctg  | 720 |
| aattttttta | atgaaccagc  | gaacctcgag | agtgagcatg  | gggtgcacgt  | tgatgaagta  | 780 |
| ctcaagcggg | tcaaactttt  | gccgaagaag | cagatcacgg  | atgctattga  | ttacaatatg  | 840 |
| gactcggggc | gtctttactc  | aacaattgat | gaattccact  | acaaggcaac  | tttaaccgatt | 900 |
| tgaaggccag | cctgctggaa  | atggcagagg | actaagtatc  | acttgtacta  | aaccaaagtc  | 960 |
| tggaaatgtc | atgttggtgc  | atgaaatgca | tggttggttt  | atgg        |             |     |

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..297

(D) OTHER INFORMATION: / Ceres Seq. ID 1481701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ala | Ser | His | Arg | Ser | Ser | His | Leu | Arg | Thr | Arg | Lys | Pro | Ile | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | Thr | Ser | Ser | Gly | Asp | Arg | Glu | Asp | Asp | Ala | Val | Glu | Pro | Asn | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Leu | Ala | Val | Ala | Val | His | Leu | Leu | Pro | Glu | Cys | Arg | Arg | Arg | Leu |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| His | His | Ala | Phe | Gln | Asp | Ala | Arg | Arg | Val | Gln | His | His | Ala | Ala | His |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Arg | Glu | Ala | Gly | Arg | Arg | Ala | Xaa | Ser | Gly | Thr | Gly | Glu | Lys | Gly |     |
| 65  |     |     |     |     |     |     |     | 70  |     |     |     |     |     | 80  |     |
| Ala | Pro | Phe | Ile | Val | Asn | Gly | Val | Glu | Met | Ala | Asn | Ile | Arg | Leu | Val |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 95  |     |
| Gly | Met | Val | Asn | Ala | Lys | Val | Glu | Arg | Thr | Thr | Asp | Val | Thr | Phe | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Leu | Asp | Asp | Gly | Thr | Gly | Arg | Leu | Asp | Phe | Ile | Arg | Trp | Val | Asn | Asp |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Ala | Ser | Asp | Ser | Phe | Glu | Thr | Ala | Ala | Ile | Gln | Asn | Gly | Met | Tyr | Ile |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 140 |     |
| Ala | Val | Ile | Gly | Ser | Leu | Lys | Gly | Leu | Gln | Glu | Arg | Lys | Arg | Ala | Thr |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 160 |     |
| Ala | Phe | Ser | Ile | Arg | Pro | Ile | Thr | Asp | Phe | Asn | Glu | Val | Thr | Leu | His |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 175 |     |
| Phe | Ile | Gln | Cys | Val | Arg | Met | His | Ile | Glu | Asn | Ile | Glu | Leu | Lys | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Gly | Ser | Pro | Ala | Arg | Ile | Ser | Ser | Ser | Met | Gly | Val | Ser | Phe | Ser | Asn |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |
| Gly | Phe | Ser | Glu | Ser | Ser | Thr | Pro | Thr | Ser | Leu | Lys | Ser | Ser | Pro | Ala |
|     |     |     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |
| Pro | Val | Thr | Ser | Gly | Ser | Ser | Asp | Thr | Asp | Leu | His | Thr | Gln | Val | Leu |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 240 |     |
| Asn | Phe | Phe | Asn | Glu | Pro | Ala | Asn | Leu | Glu | Ser | Glu | His | Gly | Val | His |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 255 |     |
| Val | Asp | Glu | Val | Leu | Lys | Arg | Phe | Lys | Leu | Leu | Pro | Lys | Lys | Gln | Ile |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |

Thr Asp Ala Ile Asp Tyr Asn Met Asp Ser Gly Arg Leu Tyr Ser Thr  
275 280 285  
Ile Asp Glu Phe His Tyr Lys Ala Thr  
290 295

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..208

(D) OTHER INFORMATION: / Ceres Seq. ID 1481702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Met Ala Asn Ile Arg Leu Val Gly Met Val Asn Ala Lys Val Glu Arg  
1 5 10 15  
Thr Thr Asp Val Thr Phe Thr Leu Asp Asp Gly Thr Gly Arg Leu Asp  
20 25 30  
Phe Ile Arg Trp Val Asn Asp Ala Ser Asp Ser Phe Glu Thr Ala Ala  
35 40 45  
Ile Gln Asn Gly Met Tyr Ile Ala Val Ile Gly Ser Leu Lys Gly Leu  
50 55 60  
Gln Glu Arg Lys Arg Ala Thr Ala Phe Ser Ile Arg Pro Ile Thr Asp  
65 70 75 80  
Phe Asn Glu Val Thr Leu His Phe Ile Gln Cys Val Arg Met His Ile  
85 90 95  
Glu Asn Ile Glu Leu Lys Ala Gly Ser Pro Ala Arg Ile Ser Ser Ser  
100 105 110  
Met Gly Val Ser Phe Ser Asn Gly Phe Ser Glu Ser Ser Thr Pro Thr  
115 120 125  
Ser Leu Lys Ser Ser Pro Ala Pro Val Thr Ser Gly Ser Ser Asp Thr  
130 135 140  
Asp Leu His Thr Gln Val Leu Asn Phe Phe Asn Glu Pro Ala Asn Leu  
145 150 155 160  
Glu Ser Glu His Gly Val His Val Asp Glu Val Leu Lys Arg Phe Lys  
165 170 175  
Leu Leu Pro Lys Lys Gln Ile Thr Asp Ala Ile Asp Tyr Asn Met Asp  
180 185 190  
Ser Gly Arg Leu Tyr Ser Thr Ile Asp Glu Phe His Tyr Lys Ala Thr  
195 200 205

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..200

(D) OTHER INFORMATION: / Ceres Seq. ID 1481703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Met Val Asn Ala Lys Val Glu Arg Thr Thr Asp Val Thr Phe Thr Leu  
1 5 10 15  
Asp Asp Gly Thr Gly Arg Leu Asp Phe Ile Arg Trp Val Asn Asp Ala

20 25 30  
Ser Asp Ser Phe Glu Thr Ala Ala Ile Gln Asn Gly Met Tyr Ile Ala  
35 40 45  
Val Ile Gly Ser Leu Lys Gly Leu Gln Glu Arg Lys Arg Ala Thr Ala  
50 55 60  
Phe Ser Ile Arg Pro Ile Thr Asp Phe Asn Glu Val Thr Leu His Phe  
65 70 75 80  
Ile Gln Cys Val Arg Met His Ile Glu Asn Ile Glu Leu Lys Ala Gly  
85 90 95  
Ser Pro Ala Arg Ile Ser Ser Ser Met Gly Val Ser Phe Ser Asn Gly  
100 105 110  
Phe Ser Glu Ser Ser Thr Pro Thr Ser Leu Lys Ser Ser Pro Ala Pro  
115 120 125  
Val Thr Ser Gly Ser Ser Asp Thr Asp Leu His Thr Gln Val Leu Asn  
130 135 140  
Phe Phe Asn Glu Pro Ala Asn Leu Glu Ser Glu His Gly Val His Val  
145 150 155 160  
Asp Glu Val Leu Lys Arg Phe Lys Leu Leu Pro Lys Lys Gln Ile Thr  
165 170 175  
Asp Ala Ile Asp Tyr Asn Met Asp Ser Gly Arg Leu Tyr Ser Thr Ile  
180 185 190  
Asp Glu Phe His Tyr Lys Ala Thr  
195 200

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..500
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| atcattactc | cactccacat  | tcgacaaaat | atatcttaga | caagttaagt  | ttaacgataa | 60  |
| tggattcaag | atatgttacc  | ctatgcattt | tcttagtact | tgcccttacat | ggagatacta | 120 |
| ctttggcaga | aacttgcagg  | cagtatgttg | aagggcagcc | attttgcttt  | aaagcaatgt | 180 |
| gcaaggcaaa | ttgttttatg  | gagggaaaat | tctctgatgg | ttcttatgta  | aagggttaca | 240 |
| gatgtgaatc | aggtggattc  | cactcggtgt | gtgtttgcct | tttgtgcaaa  | aattagttat | 300 |
| ctaaagacaa | gcggatatat  | cttcttatgt | tcctatccat | tatttaggat  | tatagtccaa | 360 |
| ataattatac | aatagcttag  | ttaaatagtt | ttttatttat | agacaaatgt  | agcactagtt | 420 |
| aactagttgt | gatttttttaa | atttctcagc | tataaatcag | gaaatatttt  | ttaacacttc | 480 |
| aataatatat | ctttgttcgc  |            |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ser Leu Leu His Ser Thr Phe Asp Lys Ile Tyr Leu Arg Gln Val Lys  
1 5 10 15  
Phe Asn Asp Asn Gly Phe Lys Ile Cys Tyr Pro Met His Phe Leu Ser

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 20  |     | 25  |     | 30  |     |     |     |     |     |     |     |     |     |     |
| Thr | Cys | Leu | Thr | Trp | Arg | Tyr | Tyr | Phe | Gly | Arg | Asn | Leu | Gln | Ala | Val |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

Cys

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1481706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Tyr | Ser | Thr | Pro | His | Ser | Thr | Lys | Tyr | Ile | Leu | Asp | Lys | Leu | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Thr | Ile | Met | Asp | Ser | Arg | Tyr | Val | Thr | Leu | Cys | Ile | Phe | Leu | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ala | Leu | His | Gly | Asp | Thr | Thr | Leu | Ala | Glu | Thr | Cys | Arg | Gln | Tyr |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Val | Glu | Gly | Gln | Pro | Phe | Cys | Phe | Lys | Ala | Met | Cys | Lys | Ala | Asn | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Met | Glu | Gly | Lys | Phe | Ser | Asp | Gly | Ser | Tyr | Val | Lys | Gly | Tyr | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Cys | Glu | Ser | Gly | Gly | Phe | His | Ser | Val | Cys | Val | Cys | Leu | Leu | Cys | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

Asn

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1481707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Ser | Arg | Tyr | Val | Thr | Leu | Cys | Ile | Phe | Leu | Val | Leu | Ala | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Gly | Asp | Thr | Thr | Leu | Ala | Glu | Thr | Cys | Arg | Gln | Tyr | Val | Glu | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Pro | Phe | Cys | Phe | Lys | Ala | Met | Cys | Lys | Ala | Asn | Cys | Phe | Met | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Lys | Phe | Ser | Asp | Gly | Ser | Tyr | Val | Lys | Gly | Tyr | Arg | Cys | Glu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Gly | Phe | His | Ser | Val | Cys | Val | Cys | Leu | Leu | Cys | Lys | Asn |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 916 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..916

(D) OTHER INFORMATION: / Ceres Seq. ID 1481716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

|             |            |            |            |             |            |     |
|-------------|------------|------------|------------|-------------|------------|-----|
| aattttctgag | caccaaacca | accaagccaa | tcttacgact | gccttgccctt | tggcatgtct | 60  |
| ctaatttcga  | cagcttcgat | actcctcctc | cacgcctgcw | ccctgctcgc  | cgccgcaaga | 120 |
| gtccccgacc  | cggtagaaca | tggcgacgtg | aacacggcga | tgcttaccaa  | cggctcggcc | 180 |
| tcggcgacgc  | cgctcgtccc | tgacagcagc | agcaacggca | acttcgagac  | gtacttctgc | 240 |
| ttcctctgct  | cgggccgcga | cccgtgtgtc | attcaccact | gccccatcta  | ctgggacgag | 300 |
| tgccacctca  | tctgcgacga | tgacatgtcc | accgccactc | ctactccacc  | tgctgttgca | 360 |
| gtgtcgtcgt  | cgctcgtcgt | ccmgccccgt | ccccatggtg | caggtgcagg  | gcgatgatga | 420 |
| ctgttacgtc  | atgaagctct | acatgtccgg | ccgctacgtc | atcgtcgaac  | accggccatg | 480 |
| caaatacatc  | gcctgggtgt | tcctcacntg | cggcgscggg | gagctggcgg  | cggccgaccg | 540 |
| gaaagccgtc  | acggccactg | cgatccaggg | gacctctctg | cctgccgagc  | tatgcggcac | 600 |
| gcaggcggtc  | aatgctccac | cattagcagg | cgctcgtcgt | ccagcagcag  | cagcagcagc | 660 |
| tggttggtgt  | ggtgcgcacc | gacggcgcta | gctgcctagc | tacttatccg  | cgaactaagg | 720 |
| gttaatttta  | gacataaaac | ctgagaggag | gattcaaggg | attaaaatct  | ctttcttatt | 780 |
| ccaaagaaat  | tttagccact | cgaatcctct | ctgattttct | ggctcctaaa  | ttagccctaa | 840 |
| tattaaagga  | ccaacagatg | ccaaacttaa | accatcgatc | tctacaagat  | aactaatatt | 900 |
| ttgatttcca  | aacttt     |            |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1481717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Leu | Ile | Ser | Thr | Ala | Ser | Ile | Leu | Leu | Leu | His | Ala | Cys | Xaa |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Leu | Ala | Ala | Ala | Arg | Val | Pro | Asp | Pro | Val | Glu | His | Gly | Asp | Val |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Asn | Thr | Ala | Met | Leu | Thr | Asn | Gly | Ser | Ala | Ser | Ala | Thr | Pro | Ser | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Asp | Ser | Ser | Ser | Asn | Gly | Asn | Phe | Glu | Thr | Tyr | Phe | Cys | Phe | Leu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Cys | Ser | Gly | Arg | Asp | Pro | Leu | Leu | Ile | His | His | Cys | Pro | Ile | Tyr | Trp |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Glu | Cys | His | Leu | Ile | Cys | Asp | Asp | Asp | Met | Ser | Thr | Ala | Thr | Pro |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Pro | Pro | Ala | Val | Ala | Val | Ser | Ser | Ser | Ser | Ser | Ser | Xaa | Pro | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | His | Gly | Ala | Gly | Ala | Gly | Arg |     |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1481718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

```
Met Thr Cys Pro Pro Pro Leu Leu Leu His Leu Leu Leu Gln Cys Arg
1 5 10 15
Arg Arg Arg Arg Pro Xaa Pro Val Pro Met Val Gln Val Gln Gly Asp
 20 25 30
Asp Asp Cys Tyr Val Met Lys Leu Tyr Met Ser Gly Arg Tyr Val Ile
 35 40 45
Val Glu His Arg Pro Cys Lys Tyr Ile Ala Trp Cys Phe Leu Xaa Cys
 50 55 60
Gly Xaa Gly Glu Leu Ala Ala Ala Asp Arg Lys Ala Val Thr Ala Thr
65 70 75 80
Ala Ile Gln Gly Thr Ser Leu Pro Ala Glu Leu Cys Gly Thr Gln Ala
 85 90 95
Val Asn Ala Pro Pro Leu Ala Gly Val Val Pro Ala Ala Ala Ala
 100 105 110
Ala Ala Gly Gly Ala Gly Ala His Arg Arg Arg
 115 120
```

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1481719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

```
Met Val Gln Val Gln Gly Asp Asp Asp Cys Tyr Val Met Lys Leu Tyr
1 5 10 15
Met Ser Gly Arg Tyr Val Ile Val Glu His Arg Pro Cys Lys Tyr Ile
 20 25 30
Ala Trp Cys Phe Leu Xaa Cys Gly Xaa Gly Glu Leu Ala Ala Ala Asp
 35 40 45
Arg Lys Ala Val Thr Ala Thr Ala Ile Gln Gly Thr Ser Leu Pro Ala
 50 55 60
Glu Leu Cys Gly Thr Gln Ala Val Asn Ala Pro Pro Leu Ala Gly Val
65 70 75 80
Val Val Pro Ala Ala Ala Ala Ala Ala Gly Gly Ala Gly Ala His Arg
 85 90 95
Arg Arg
```

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 553 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..553

(D) OTHER INFORMATION: / Ceres Seq. ID 1481728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```
aaatcgcggt cactgctccg aagtcggaac cttcatcac atcgctctcgt ttccgatttc 60
cccaaattca ggccacaggc gctacaggac ccaggcacca ctcggtcggc ggccaccgcg 120
```

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| tcgccccgcc  | tgctcgattg | gggtcgcggtg | tgcgatagga | agtattgtgt | tgtgtttgca | 180 |
| acgtgatagc  | ttgtactggg | aacaaagggtc | aagatgggag | ccttggacct | acaccttgac | 240 |
| tttgcttctg  | ctcaacatgg | acaagccaag  | ttaaaggaat | atgccaagag | ctctctgttg | 300 |
| tctgatggaa  | actacaatac | agacaagatc  | aatgggtcaa | accctgatga | ctatgagaaa | 360 |
| tttgagaaaag | ggataatgca | ctatgggtgt  | ccacattata | gaaggagatg | ccgcataaga | 420 |
| gctccttgct  | gcaatgaaat | ttttgattgc  | cgacactgcc | acaatgaaac | taagaattcc | 480 |
| attaaaattg  | ataaaatgaa | gaggcatgaa  | cttcacagcc | atgaagtgca | gcaggttgta | 540 |
| tgctcattgt  | gtg        |             |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..61
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ser | Arg | Ser | Leu | Leu | Arg | Ser | Pro | Asn | Leu | His | Thr | His | Arg | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ser | Asp | Phe | Pro | Lys | Phe | Arg | Pro | Gln | Ala | Leu | Gln | Asp | Pro | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Thr | Arg | Ser | Ala | Ala | Thr | Ala | Ser | Pro | Arg | Leu | Leu | Asp | Trp | Gly |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Arg | Val | Cys | Asp | Arg | Lys | Tyr | Cys | Val | Val | Phe | Ala | Thr |     |     |     |
| 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Arg | Gly | His | Cys | Ser | Glu | Val | Arg | Thr | Phe | Ile | His | Ile | Val | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Pro | Ile | Ser | Pro | Asn | Ser | Gly | His | Arg | Arg | Tyr | Arg | Thr | Gln | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Leu | Gly | Arg | Arg | Pro | Pro | Arg | Arg | Pro | Ala | Cys | Ser | Ile | Gly | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Cys | Ala | Ile | Gly | Ser | Ile | Val | Leu | Cys | Leu | Gln | Arg | Asp | Ser | Leu |
| 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Tyr | Trp | Glu | Gln | Arg | Ser | Arg | Trp | Ala | Pro | Trp | Thr | Tyr | Thr | Leu | Thr |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Leu | Leu | Leu | Asn | Met | Asp | Lys | Pro | Ser |     |     |     |     |     |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1481731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ala | Leu | Asp | Leu | His | Leu | Asp | Phe | Ala | Ser | Ala | Gln | His | Gly |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gln | Ala | Lys | Leu | Lys | Glu | Tyr | Ala | Lys | Ser | Ser | Leu | Leu | Ser | Asp | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Tyr | Asn | Thr | Asp | Lys | Ile | Asn | Gly | Ser | Asn | Pro | Asp | Asp | Tyr | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Phe | Glu | Lys | Gly | Ile | Met | His | Tyr | Gly | Cys | Pro | His | Tyr | Arg | Arg |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Cys | Arg | Ile | Arg | Ala | Pro | Cys | Cys | Asn | Glu | Ile | Phe | Asp | Cys | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| His | Cys | His | Asn | Glu | Thr | Lys | Asn | Ser | Ile | Lys | Ile | Asp | Lys | Met | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Arg | His | Glu | Leu | Pro | Arg | His | Glu | Val | Gln | Gln | Val | Val | Cys | Ser | Leu |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |

Cys

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 709 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..709

(D) OTHER INFORMATION: / Ceres Seq. ID 1481732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

|            |             |             |             |            |            |     |
|------------|-------------|-------------|-------------|------------|------------|-----|
| atattcttcg | tgcctgggcg  | ttcccagggtg | ccatgcgagt  | agatcggcaa | ctactccatc | 60  |
| ctcctctccc | tacctggcca  | tctgtcagca  | gccgtgctga  | gcctctgctg | ccctctctct | 120 |
| ggccactcgc | gtgagcccct  | gctggtcggc  | tgtccggaca  | cgacggctat | ggccgagccc | 180 |
| agcgcaagt  | catcctccag  | gactgagccc  | ctgtgcagcc  | actaccgccg | gcaggcctcg | 240 |
| gtgtccggtt | gtgcttcgac  | aagtcacgcg  | cctccgacaa  | acctcgcgcc | cgtcgtgttc | 300 |
| ttgcctctac | gtcaatcgac  | acgcatagaa  | tgcgatccat  | ctccaagctt | cgagggatcg | 360 |
| aagatcaagc | gttggcgacc  | atgtgatcaa  | gctctctgag  | ttctatgagg | ctgaagatcc | 420 |
| tgagcatctg | tttgggtgaag | attgcctttg  | gtgcaatcta  | tgctcaggta | aagagggcgt | 480 |
| cgaggcggat | ctccaggagt  | tccaggacgt  | cgacgggttc  | gaggattagg | ctagcgacct | 540 |
| ccccagtgca | gctgcctgtg  | gtgggttggt  | tacgttggtc  | acgtttcgat | tctgtgtact | 600 |
| ttgatttata | ttatgtaaat  | ggttctagtt  | tgtaatatata | ttacttactc | tttattgtaa | 660 |
| ttcgaagcat | tgtgctatga  | tgagtcattt  | atgtaatcgc  | cgtgtacgc  |            |     |

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..43

(D) OTHER INFORMATION: / Ceres Seq. ID 1481733

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Leu | Arg | Ala | Trp | Ala | Phe | Pro | Gly | Ala | Met | Arg | Val | Asp | Arg | Gln |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |

Leu Leu His Pro Pro Leu Pro Thr Trp Pro Ser Cys Ser Ser Arg Ala  
20 25 30  
Glu Pro Leu Leu Pro Ser Leu Trp Pro Leu Ala  
35 40

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Met Ala Glu Pro Ser Ala Lys Ser Ser Ser Arg Thr Glu Pro Leu Cys  
1 5 10 15  
Ser His Tyr Arg Arg Gln Ala Ser Val Ser Gly Cys Ala Ser Thr Ser  
20 25 30  
His Ala Pro Pro Thr Asn Leu Ala Pro Val Val Phe Leu Pro Leu Arg  
35 40 45  
Gln Ser Thr Arg Ile Glu Cys Asp Pro Ser Pro Ser Phe Glu Gly Ser  
50 55 60  
Lys Ile Lys Arg Trp Arg Pro Cys Asp Gln Ala Leu  
65 70 75

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met Arg Leu Lys Ile Leu Ser Ile Cys Leu Val Lys Ile Ala Phe Gly  
1 5 10 15  
Ala Ile Tyr Ala Gln Val Lys Arg Ala Ser Arg Arg Ile Ser Arg Ser  
20 25 30  
Ser Arg Thr Ser Thr Gly Ser Arg Ile Arg Leu Ala Thr Ser Pro Ser  
35 40 45  
Gln Leu Pro Val Val Gly Cys Leu Arg Trp Leu Arg Phe Asp Ser Val  
50 55 60  
Tyr Phe Asp Leu Tyr Tyr Val Asn Gly Ser Ser Leu  
65 70 75

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..951
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

|            |             |            |             |            |             |     |
|------------|-------------|------------|-------------|------------|-------------|-----|
| attacacaaa | tgtgcgccgc  | catgttctcc | aatctcttcg  | ccaagtttga | ctacggacga  | 60  |
| tcgtctccac | cgaagacgcc  | acacgatgac | ggccgccgta  | gccacatgtc | tgatctttcc  | 120 |
| ctagaaagac | agcctcgacg  | gtcgtccgtc | tccgtccgca  | tgaggcgcc  | cgtggatgat  | 180 |
| gacgacgtca | ctgcgccgcc  | cgtagccgag | gtgatgagca  | cggaccatgg | cggccacgag  | 240 |
| gagtcgtctc | caccgaagac  | gccacacgat | gacggctgcc  | gtagccacat | gtctgatctt  | 300 |
| tccctagaaa | gacagcctcg  | acagtcgtcc | gtctcggtcc  | gcatggaggc | gcccgtggat  | 360 |
| gacgacgacg | tcactkcgcg  | gcccgtagcc | gaggtgatga  | gcatggacca | tggcggccac  | 420 |
| gaggagtcgc | cgacgggtccc | gtgcctcgcg | ttcgcgtccg  | agcacgggta | cagcatcttc  | 480 |
| tccctagcct | acatgcgcgd  | tgttcatcga | cggcgccscac | ggkttcamag | tcaccgccga  | 540 |
| cccagwggga | gcgaaagcga  | aaccgcgkt  | acgtgattct  | tgccaaycgg | ctaacacmcc  | 600 |
| catktggacg | tctggccgtc  | gtgtttgacg | tccgcttctc  | cgaccttdgg | aggccagagc  | 660 |
| scwtggggcg | gctaaagcta  | aacmccggcg | aggttgascc  | aatktggggc | cagccgcaact | 720 |
| ggatcatgcc | trgggataga  | tcggatcgtc | gtcaaggata  | twtcaactag | tacagtttat  | 780 |
| tgtaggtagt | tmcattagtt  | tacatactct | ggctgtcagg  | cmctatttct | acgtaaaagtt | 840 |
| ttttttggca | ttrgggaaa   | atattmcgga | tctataagat  | atthtgrgtt | ttaaaagcta  | 900 |
| ctgataaatc | tacatgtacg  | ttgcaatgcg | aaataaactg  | tgtctatgtt | t           |     |

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..191
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Thr | Gln | Met | Cys | Ala | Ala | Met | Phe | Ser | Asn | Leu | Phe | Ala | Lys | Phe |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asp | Tyr | Gly | Arg | Ser | Ser | Pro | Pro | Lys | Thr | Pro | His | Asp | Asp | Gly | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Arg | Ser | His | Met | Ser | Asp | Leu | Ser | Leu | Glu | Arg | Gln | Pro | Arg | Arg | Ser |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Ser | Val | Ser | Val | Arg | Met | Glu | Ala | Pro | Val | Asp | Asp | Asp | Asp | Val | Thr |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Ala | Ala | Pro | Val | Ala | Glu | Val | Met | Ser | Thr | Asp | His | Gly | Gly | His | Glu |
| 65  |     |     |     |     |     |     |     | 70  |     |     |     |     |     | 75  | 80  |
| Glu | Ser | Ser | Pro | Pro | Lys | Thr | Pro | His | Asp | Asp | Gly | Cys | Arg | Ser | His |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Met | Ser | Asp | Leu | Ser | Leu | Glu | Arg | Gln | Pro | Arg | Gln | Ser | Ser | Val | Ser |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Val | Arg | Met | Glu | Ala | Pro | Val | Asp | Asp | Asp | Asp | Val | Thr | Xaa | Ala | Pro |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Val | Ala | Glu | Val | Met | Ser | Met | Asp | His | Gly | Gly | His | Glu | Glu | Ser | Pro |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Thr | Val | Pro | Cys | Leu | Ala | Phe | Ala | Ser | Glu | His | Gly | Tyr | Ser | Ile | Phe |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ser | Leu | Ala | Tyr | Met | Arg | Xaa | Val | His | Arg | Arg | Arg | Xaa | Arg | Xaa | Xaa |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ser | His | Arg | Arg | Pro | Xaa | Gly | Ser | Glu | Ser | Glu | Thr | Ala | Xaa | Thr |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..188

(D) OTHER INFORMATION: / Ceres Seq. ID 1481742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```
Met Cys Ala Ala Met Phe Ser Asn Leu Phe Ala Lys Phe Asp Tyr Gly
1 5 10 15
Arg Ser Ser Pro Pro Lys Thr Pro His Asp Asp Gly Arg Arg Ser His
20 25 30
Met Ser Asp Leu Ser Leu Glu Arg Gln Pro Arg Arg Ser Ser Val Ser
35 40 45
Val Arg Met Glu Ala Pro Val Asp Asp Asp Asp Val Thr Ala Ala Pro
50 55 60
Val Ala Glu Val Met Ser Thr Asp His Gly Gly His Glu Glu Ser Ser
65 70 75 80
Pro Pro Lys Thr Pro His Asp Asp Gly Cys Arg Ser His Met Ser Asp
85 90 95
Leu Ser Leu Glu Arg Gln Pro Arg Gln Ser Ser Val Ser Val Arg Met
100 105 110
Glu Ala Pro Val Asp Asp Asp Asp Val Thr Xaa Ala Pro Val Ala Glu
115 120 125
Val Met Ser Met Asp His Gly Gly His Glu Glu Ser Pro Thr Val Pro
130 135 140
Cys Leu Ala Phe Ala Ser Glu His Gly Tyr Ser Ile Phe Ser Leu Ala
145 150 155 160
Tyr Met Arg Xaa Val His Arg Arg Arg Xaa Arg Xaa Xaa Ser His Arg
165 170 175
Arg Pro Xaa Gly Ser Glu Ser Glu Thr Ala Xaa Thr
180 185
```

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..184

(D) OTHER INFORMATION: / Ceres Seq. ID 1481743

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```
Met Phe Ser Asn Leu Phe Ala Lys Phe Asp Tyr Gly Arg Ser Ser Pro
1 5 10 15
Pro Lys Thr Pro His Asp Asp Gly Arg Arg Ser His Met Ser Asp Leu
20 25 30
Ser Leu Glu Arg Gln Pro Arg Arg Ser Ser Val Ser Val Arg Met Glu
35 40 45
Ala Pro Val Asp Asp Asp Asp Val Thr Ala Ala Pro Val Ala Glu Val
50 55 60
Met Ser Thr Asp His Gly Gly His Glu Glu Ser Pro Pro Lys Thr
65 70 75 80
Pro His Asp Asp Gly Cys Arg Ser His Met Ser Asp Leu Ser Leu Glu
85 90 95
Arg Gln Pro Arg Gln Ser Ser Val Ser Val Arg Met Glu Ala Pro Val
100 105 110
Asp Asp Asp Asp Val Thr Xaa Ala Pro Val Ala Glu Val Met Ser Met
115 120 125
Asp His Gly Gly His Glu Glu Ser Pro Thr Val Pro Cys Leu Ala Phe
```

130 135 140  
Ala Ser Glu His Gly Tyr Ser Ile Phe Ser Leu Ala Tyr Met Arg Xaa  
145 150 155 160  
Val His Arg Arg Arg Xaa Arg Xaa Xaa Ser His Arg Arg Pro Xaa Gly  
165 170 175  
Ser Glu Ser Glu Thr Ala Xaa Thr  
180

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..432
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| agttctaaac cctaaacctg acgccgccat ggccgcccgc gttcgccaca tcgtgcgccg  | 60  |
| ccgcctctcc acggccgccc ccatactgc accggtcccc actccggcct ccatactcaa   | 120 |
| cccgctctcg ccgagcactc ccctcacctc gcgacataag acccgactcg ccatactccct | 180 |
| cctcaagtct tccccgcccgc ctccccccga ccagatcctc tccatttgcc gcgcgcgcga | 240 |
| ctgacccccg agacacacat cgaccgcacg gcgctgtcgc tagccgcacg aaagctctcc  | 300 |
| tccgctccgg acaccctccg tgacctcgcc tccacmgtcc tcaccccgcg cmamgcaccc  | 360 |
| cacgcmatcg cgctcttcgg ccaggcacam ctctccccg acgssatctc cactttccag   | 420 |
| tcctccccct cc                                                      |     |

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Val Leu Asn Pro Lys Pro Asp Ala Ala Met Ala Ala Val Arg His     |  |
| 1 5 10 15                                                       |  |
| Ile Val Arg Arg Arg Leu Ser Thr Ala Ala Ile Thr Ala Pro Val     |  |
| 20 25 30                                                        |  |
| Pro Thr Pro Ala Ser Ile Leu Asn Pro Ser Ser Pro Ser Thr Pro Leu |  |
| 35 40 45                                                        |  |
| Thr Ser Arg His Lys Thr Arg Leu Ala Ile Ser Leu Leu Lys Ser Ser |  |
| 50 55 60                                                        |  |
| Pro Pro Pro Pro Pro Asp Gln Ile Leu Ser Ile Cys Arg Ala Ala His |  |
| 65 70 75 80                                                     |  |

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1481746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

```
Met Ala Ala Ala Val Arg His Ile Val Arg Arg Arg Leu Ser Thr Ala
1 5 10 15
Ala Ala Ile Thr Ala Pro Val Pro Thr Pro Ala Ser Ile Leu Asn Pro
20 25 30
Ser Ser Pro Ser Thr Pro Leu Thr Ser Arg His Lys Thr Arg Leu Ala
35 40 45
Ile Ser Leu Leu Lys Ser Ser Pro Pro Pro Pro Pro Asp Gln Ile Leu
50 55 60
Ser Ile Cys Arg Ala Ala His
65 70
```

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 557 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..557

(D) OTHER INFORMATION: / Ceres Seq. ID 1481747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

```
agactccggc cacagccgag acgagactag cagcagccgc ttgctcagat cggcagcttc 60
ggcggcgccg gagatggcga ttcggtactg gccgatggcc ggagcagccg ttgggttccg 120
cctcgctctg gttctcttcg gcggggatct ccaccttgcc tctcgccctg aggtctccac 180
ccccctcacc tcccttcgcc gcctggcgga aggctactgg ctgaagcaag cgtccgtgtc 240
accgtactcc ggttctatgt atcacggttc cccattgctc ctgtctgttc ttggtccatt 300
aactagtagc aggcctgacg gacatcatgc tcatatttac tgcagttaga tttttgtggc 360
ttagattttt ctagcagcca tgctcatccg agcgactggg catgaactcg aaatggcacg 420
gaacagaagt ttgaagtcac ttgacctcac aaaggcagtw aaggatacag ttaatgtaag 480
cgctggagat gttgcttctc tcatatattt gtggaaccct tgggcaatag tcacttgtgt 540
gggatcatgt acatcac
```

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..185

(D) OTHER INFORMATION: / Ceres Seq. ID 1481748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

```
Asp Ser Gly His Ser Arg Asp Glu Thr Ser Ser Ser Arg Leu Leu Arg
1 5 10 15
Ser Ala Ala Ser Ala Ala Ala Glu Met Ala Ile Arg Tyr Trp Pro Met
20 25 30
Ala Gly Ala Ala Val Gly Phe Arg Leu Val Leu Val Leu Phe Gly Gly
35 40 45
Asp Leu His Leu Ala Ser Arg Pro Glu Val Ser Thr Pro Leu Thr Ser
50 55 60
Leu Arg Arg Leu Ala Glu Gly Tyr Trp Leu Lys Gln Ala Ser Val Ser
65 70 75 80
Pro Tyr Ser Gly Ser Met Tyr His Gly Ser Pro Leu Leu Leu Ser Val
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Leu | Gly | Pro | Leu | Thr | Ser | Ser | Arg | Pro | Asp | Gly | His | His | Ala | His | Ile |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Tyr | Cys | Ser | Leu | Ile | Phe | Val | Ala | Val | Asp | Phe | Leu | Ala | Ala | Met | Leu |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ile | Arg | Ala | Thr | Gly | His | Glu | Leu | Glu | Met | Ala | Arg | Asn | Arg | Ser | Leu |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Lys | Ser | Leu | Asp | Leu | Thr | Lys | Ala | Xaa | Lys | Asp | Thr | Val | Asn | Val | Ser |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ala | Gly | Asp | Val | Ala | Ser | Leu | Ile | Tyr | Leu | Trp | Asn | Pro | Trp | Ala | Ile |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Val | Thr | Cys | Val | Gly | Ser | Cys | Thr | Ser |     |     |     |     |     |     |     |  |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1481749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Ile | Arg | Tyr | Trp | Pro | Met | Ala | Gly | Ala | Ala | Val | Gly | Phe | Arg |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Leu | Val | Leu | Val | Leu | Phe | Gly | Gly | Asp | Leu | His | Leu | Ala | Ser | Arg | Pro |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Glu | Val | Ser | Thr | Pro | Leu | Thr | Ser | Leu | Arg | Arg | Leu | Ala | Glu | Gly | Tyr |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Trp | Leu | Lys | Gln | Ala | Ser | Val | Ser | Pro | Tyr | Ser | Gly | Ser | Met | Tyr | His |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gly | Ser | Pro | Leu | Leu | Leu | Ser | Val | Leu | Gly | Pro | Leu | Thr | Ser | Ser | Arg |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Pro | Asp | Gly | His | His | Ala | His | Ile | Tyr | Cys | Ser | Leu | Ile | Phe | Val | Ala |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Val | Asp | Phe | Leu | Ala | Ala | Met | Leu | Ile | Arg | Ala | Thr | Gly | His | Glu | Leu |  |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |  |
| Glu | Met | Ala | Arg | Asn | Arg | Ser | Leu | Lys | Ser | Leu | Asp | Leu | Thr | Lys | Ala |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Xaa | Lys | Asp | Thr | Val | Asn | Val | Ser | Ala | Gly | Asp | Val | Ala | Ser | Leu | Ile |  |
|     | 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |  |
| Tyr | Leu | Trp | Asn | Pro | Trp | Ala | Ile | Val | Thr | Cys | Val | Gly | Ser | Cys | Thr |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1481750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Met Ala Gly Ala Ala Val Gly Phe Arg Leu Val Leu Val Leu Phe Gly  
1 5 10 15  
Gly Asp Leu His Leu Ala Ser Arg Pro Glu Val Ser Thr Pro Leu Thr  
20 25 30  
Ser Leu Arg Arg Leu Ala Glu Gly Tyr Trp Leu Lys Gln Ala Ser Val  
35 40 45  
Ser Pro Tyr Ser Gly Ser Met Tyr His Gly Ser Pro Leu Leu Leu Ser  
50 55 60  
Val Leu Gly Pro Leu Thr Ser Ser Arg Pro Asp Gly His His Ala His  
65 70 75 80  
Ile Tyr Cys Ser Leu Ile Phe Val Ala Val Asp Phe Leu Ala Ala Met  
85 90 95  
Leu Ile Arg Ala Thr Gly His Glu Leu Glu Met Ala Arg Asn Arg Ser  
100 105 110  
Leu Lys Ser Leu Asp Leu Thr Lys Ala Xaa Lys Asp Thr Val Asn Val  
115 120 125  
Ser Ala Gly Asp Val Ala Ser Leu Ile Tyr Leu Trp Asn Pro Trp Ala  
130 135 140  
Ile Val Thr Cys Val Gly Ser Cys Thr Ser  
145 150

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..380
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| acaagcaagt ggccaccttt gagtggatgt tggaagaaat agcagccaca agcaagtagt  | 60  |
| cacctgtgtc atcttattcc gatcctagsc cctcccattc ccaawkcctc gsttccctcct | 120 |
| cccttctcta gttctctgat cctcagcact tagcatcaag cttagsacac cggcgagatg  | 180 |
| gcctccamct ccamcttctt gtccamcctc gccagcaggt ccgcgcgcagc cgatagcctg | 240 |
| ygcamgccgt gccgtccttc gccaaagatcg tcaggttctt gccgcgcgar gcgcagatca | 300 |
| gccgcavggn cmgcgcggcg gtgctgccca cgccgarggc ggcggtgtcg ggcacgagaa  | 360 |
| ggcgccgtcg agcaagcacg                                              |     |

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Met Ala Ser Xaa Ser Xaa Phe Leu Ser Xaa Leu Ala Ser Arg Ser Ala  
1 5 10 15  
Ala Ala Asp Ser Leu Xaa Xaa Pro Cys Arg Pro Ser Pro Arg Ser Ser  
20 25 30  
Gly Ser Cys Pro Arg Xaa Arg Arg Ser Ala Ala Xaa Xaa Ala Arg Arg  
35 40 45  
Cys Cys Pro Arg Arg Xaa Arg Arg Cys Arg Ala Arg Glu Gly Ala Val  
50 55 60



Glu Gln Ala

65

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..482
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ctgttcttcc | acctgctggc | tgwcctggc  | tccctggcg  | cccaaacc   | cccgcctgc  | 60  |
| cgtccccgca | gccgcagcct | gctctcggt  | cccgcgcgcg | tctaccgcgt | cctgcggctg | 120 |
| cggtgttgcg | tcacctcggg | ttcgcttaa  | cttcacaa   | cctgcgcgtc | ctggtgctcc | 180 |
| gccgcccctc | cctttgtact | cgcgctggag | ctgcagatcc | accgcgacct | ggcgaccaat | 240 |
| tcctcctccc | gctgaagaat | tggcgacctt | ggcctccgcm | cccgcggcgc | gaggagtcaa | 300 |
| ctgtggtagc | aaccaccgcg | gaggctgcaa | gcttcggtaa | gggaggaaag | ttgacttgtt | 360 |
| ggaagccggt | ccagggccgc | gatgacgtcg | acagccgcgc | ggcgtcgtcg | tcggcggcga | 420 |
| agagcgagtc | ctacctgcgg | gccgacaaga | tcgacctcga | gagcctggac | atccagctgg | 480 |

ag

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Ser | Ser | Thr | Cys | Trp | Leu | Xaa | Leu | Pro | Pro | Leu | Arg | Pro | Lys | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Arg | Leu | Ala | Val | Pro | Ala | Ala | Ala | Ala | Cys | Ser | Arg | Leu | Pro | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ser | Thr | Ala | Ser | Cys | Gly | Cys | Gly | Val | Ala | Ser | Pro | Arg | Val | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Asn | Phe | His | Asn | Pro | Arg | Arg | Pro | Gly | Ala | Pro | Pro | Pro | Leu | Pro |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Tyr | Ser | Arg | Trp | Ser | Cys | Arg | Ser | Thr | Ala | Thr | Trp | Arg | Pro | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Pro | Pro | Ala | Glu | Glu | Leu | Ala | Thr | Leu | Ala | Ser | Xaa | Pro | Ala | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Arg | Gly | Val | Asn | Cys | Gly | Ser | Asn | His | Arg | Gly | Gly | Cys | Lys | Leu | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1481766

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

```
Val Leu Pro Pro Ala Gly Cys Xaa Cys Leu Pro Cys Ala Pro Asn Pro
1 5 10 15
Pro Ala Ser Pro Ser Pro Gln Pro Gln Pro Ala Leu Gly Ser Arg Arg
20 25 30
Arg Leu Pro Arg Pro Ala Ala Ala Val Leu Arg His Leu Gly Phe Ala
35 40 45
Leu Thr Ser Thr Ile Leu Ala Val Leu Val Leu Arg Arg Pro Ser Leu
50 55 60
Cys Thr Arg Ala Gly Ala Ala Asp Pro Pro Arg Pro Gly Asp Gln Phe
65 70 75 80
Leu Leu Pro Leu Lys Asn Trp Arg Pro Trp Pro Pro Xaa Pro Arg Arg
85 90 95
Glu Glu Ser Thr Val Val Ala Thr Thr Ala Glu Ala Ala Ser Phe Gly
100 105 110
Lys Gly Gly Lys Leu Thr Cys Trp Lys Pro Val Gln Gly Arg Asp Asp
115 120 125
Val Asp Ser Arg Arg Ala Ser Ser Ser Ala Ala Lys Ser Glu Ser Tyr
130 135 140
Leu Arg Ala Asp Lys Ile Asp Leu Glu Ser Leu Asp Ile Gln Leu Glu
145 150 155 160
```

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 376 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..376

(D) OTHER INFORMATION: / Ceres Seq. ID 1481770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

```
ggactcacga agcagcacac tctgcactct cggcaacaac tgacggccgg aggaagaagg 60
cgcagacgac aagcagaagc ttgtgccatc gatcaatggc ggcggtgaca aagatctacg 120
tcgtgtacta ctgcacgtac gghcacgtgg cgargctggc ggaggagatc aagaagggcg 180
ccgactccgt ggacggcgctc gaggcaacca tctggcargw agcgggaracg ctgccggavg 240
argcgctggc gaagatgcrc gcaccggcga ggagcgagga gcaccgggtg atctcgggca 300
arcagctggg ggacgcrac ggcacccctgt tcggcttccc rgcrccggttc ggcacgatgg 360
crgcgcatga gaaggc
```

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1481771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

```
Thr His Glu Ala Ala His Ser Ala Leu Ser Ala Thr Thr Asp Gly Arg
1 5 10 15
```

Arg Lys Lys Ala Gln Thr Thr Ser Arg Ser Leu Cys His Arg Ser Met  
20 25 30  
Ala Ala Val Thr Lys Ile Tyr Val Val Tyr Tyr Ser Thr Tyr Xaa His  
35 40 45  
Val Ala Xaa Leu Ala Glu Glu Ile Lys Lys Gly Ala Asp Ser Val Asp  
50 55 60  
Gly Val Glu Ala Thr Ile Trp Xaa Xaa Ala Xaa Thr Leu Pro Xaa Xaa  
65 70 75 80  
Ala Leu Ala Lys Met Xaa Ala Pro Ala Arg Ser Glu Glu His Pro Val  
85 90 95  
Ile Ser Gly Xaa Gln Leu Val Asp Xaa Asp Gly Ile Leu Phe Gly Phe  
100 105 110  
Xaa Xaa Arg Phe Gly Met Met Xaa Ala Gln Met Lys  
115 120

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Met Ala Ala Val Thr Lys Ile Tyr Val Val Tyr Tyr Ser Thr Tyr Xaa  
1 5 10 15  
His Val Ala Xaa Leu Ala Glu Glu Ile Lys Lys Gly Ala Asp Ser Val  
20 25 30  
Asp Gly Val Glu Ala Thr Ile Trp Xaa Xaa Ala Xaa Thr Leu Pro Xaa  
35 40 45  
Xaa Ala Leu Ala Lys Met Xaa Ala Pro Ala Arg Ser Glu Glu His Pro  
50 55 60  
Val Ile Ser Gly Xaa Gln Leu Val Asp Xaa Asp Gly Ile Leu Phe Gly  
65 70 75 80  
Phe Xaa Xaa Arg Phe Gly Met Met Xaa Ala Gln Met Lys  
85 90

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..448
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| attgagtata ggtttgctct cctacacttt tttgagaaag acattgaagg atgacatagt   | 60  |
| tgttccaatg cttgatttta agatccaaga tggggacatt gtaccgttgg tgtatgggtc   | 120 |
| acaggggtgat tgggatagta gtctgaagat agtacttgat tgggtcccctt tttcttcgaa | 180 |
| ggaagaactt ctgcagcagt ttcaggatgt tggtagtcat ggaactaaag tggtagtgta   | 240 |
| caatttatgg atgaatgatg atggcctttt ggaacttgac tttgaggatg atgatgagga   | 300 |
| catattactt agagatcaag gtagcgcaag tsvggggggt ctcaaagagt cagaaagaaa   | 360 |
| ttgttaagca acacatatcc cacaggctca gakttttcat tgcgagctta tacctccatc   | 420 |
| ctttacctca ggaagtttga taatttcc                                      |     |

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 121 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..121  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1481776  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:  
Leu Ser Ile Gly Leu Leu Ser Tyr Thr Phe Leu Arg Lys Thr Leu Lys  
1                  5                  10                  15  
Asp Asp Ile Val Val Pro Met Leu Asp Phe Lys Ile Gln Asp Gly Asp  
                  20                  25                  30  
Ile Val Pro Leu Val Tyr Gly Ser Gln Gly Asp Trp Asp Ser Ser Leu  
                  35                  40                  45  
Lys Ile Val Leu Asp Trp Ser Pro Phe Ser Ser Lys Glu Glu Leu Leu  
50                  55                  60  
Gln Gln Phe Gln Asp Val Gly Ser His Gly Thr Lys Val Val Val Tyr  
65                  70                  75                  80  
Asn Leu Trp Met Asn Asp Asp Gly Leu Leu Glu Leu Asp Phe Glu Asp  
                  85                  90                  95  
Asp Asp Glu Asp Ile Leu Leu Arg Asp Gln Gly Ser Ala Ser Xaa Gly  
100                  105                  110  
Val Leu Lys Glu Ser Glu Arg Asn Cys  
115                  120  
(2) INFORMATION FOR SEQ ID NO:158:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 99 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..99  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1481777  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:  
Met Leu Asp Phe Lys Ile Gln Asp Gly Asp Ile Val Pro Leu Val Tyr  
1                  5                  10                  15  
Gly Ser Gln Gly Asp Trp Asp Ser Ser Leu Lys Ile Val Leu Asp Trp  
                  20                  25                  30  
Ser Pro Phe Ser Ser Lys Glu Glu Leu Leu Gln Gln Phe Gln Asp Val  
35                  40                  45  
Gly Ser His Gly Thr Lys Val Val Val Tyr Asn Leu Trp Met Asn Asp  
50                  55                  60  
Asp Gly Leu Leu Glu Leu Asp Phe Glu Asp Asp Asp Glu Asp Ile Leu  
65                  70                  75                  80  
Leu Arg Asp Gln Gly Ser Ala Ser Xaa Gly Val Leu Lys Glu Ser Glu  
85                  90                  95  
Arg Asn Cys

(2) INFORMATION FOR SEQ ID NO:159:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 61 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..61

(D) OTHER INFORMATION: / Ceres Seq. ID 1481778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

```
Met Met Met Ala Phe Trp Asn Leu Thr Leu Arg Met Met Met Arg Thr
1 5 10 15
Tyr Tyr Leu Glu Ile Lys Val Ala Gln Xaa Xaa Gly Phe Ser Lys Ser
 20 25 30
Gln Lys Glu Ile Val Lys Gln His Ile Ser His Arg Leu Arg Xaa Phe
 35 40 45
Ile Ala Ser Leu Tyr Leu His Pro Leu Pro Gln Glu Val
 50 55 60
```

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 657 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..657

(D) OTHER INFORMATION: / Ceres Seq. ID 1481779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```
attatggatt agcgctgca taacagacca ccagggaatt ccgctctcac ctcatgggg 60
tcctgggtggg cgaataagca ccaagccctc cgcttgatc grccatcgtg cgcgtccctt 120
gctcgcgctcg agagatttcc aacgccgagc tagcgcacag ggaagggaga gaaaagtgag 180
tgccaccgcg gggacgaggg aaactcgact caccacctat cgctccttgg agttgtgtcc 240
tggggattct ccgggcttgg aggaggaagg ttgaagcagc tcttccgggg attcgtgttc 300
aacgttgttg gaattcctcg ccaccaggaa ctaccctgcc gtggaccgcg ggtccgctg 360
gccaagactg tcctcgctgc tagccttgac gagcaagcca cacatgatcg agtgcttcag 420
taggtggaga ctgctgagca ggagctcatt gaagcccccc acaggagaag aacatgtgg 480
tcaagaggag ccacacaatg aggagtcca cttgatctag gtgtcgtttc ccagttgact 540
ttatggcgcc aaggatggac atttgctcgt tttatattat tattttgtaa gacttccgct 600
atgtaataag tactctgatt atattgtgac atttatctct atacactctg ttattgt
```

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..90

(D) OTHER INFORMATION: / Ceres Seq. ID 1481780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```
Leu Trp Ile Ser Ala Cys Ile Thr Asp His Gln Gly Ile Pro Leu Ser
1 5 10 15
Pro His Trp Gly Pro Gly Gly Arg Ile Ser Thr Lys Pro Ser Ala Trp
 20 25 30
Ile Xaa His Arg Ala Arg Pro Leu Leu Ala Ser Arg Asp Phe Gln Arg
 35 40 45
Arg Ala Ser Ala Gln Gly Arg Glu Arg Lys Val Ser Ala Thr Ala Gly
 50 55 60
Thr Arg Glu Thr Arg Leu Thr Thr Tyr Arg Ser Leu Glu Leu Cys Pro
 65 70 75 80
```

Gly Asp Ser Pro Gly Leu Glu Glu Glu Gly  
85 90

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..413
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ctgctcgtc  | tctccctctc | gtcgtcttct | ttcctggtcg | cgccgccctt | catcaggtct | 60  |
| cctccgcctt | agccggtgaa | gagcgaccag | gcccaataaa | taatcaccat | ggctcatcaa | 120 |
| aagcgtgaag | gcagctacgc | cgatgatgat | agtacatcca | agcgcatcaa | aggcaccgac | 180 |
| actgcttctg | aaacggggga | cagtgtagag | tctagtgttt | cacagcaa   | ggatgctgaa | 240 |
| gctaggagga | cctgccaaaa | ggaaagcgaa | caccatcgga | caaatgcgtt | tcagatgggg | 300 |
| aatgcgctgc | aaactctaag | gttttggggt | aagcagaaga | kggtattgac | tgttgctgag | 360 |
| gctgatcgcg | cggacgacaa | gggttgacag | cacactatgg | aggacgcctg | ggk        |     |

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | His | Gln | Lys | Arg | Glu | Gly | Ser | Tyr | Ala | Asp | Asp | Asp | Ser | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Lys | Arg | Ile | Lys | Gly | Thr | Asp | Thr | Ala | Ser | Glu | Thr | Gly | Asp | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Glu | Ser | Ser | Val | Ser | Gln | Gln | Met | Asp | Ala | Glu | Ala | Arg | Arg | Thr |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Cys | Gln | Lys | Glu | Ser | Glu | His | His | Arg | Thr | Asn | Ala | Phe | Gln | Met | Gly |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Asn | Ala | Leu | Gln | Thr | Leu | Arg | Phe | Trp | Gly | Lys | Gln | Lys | Xaa | Val | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Val | Val | Glu | Ala | Asp | Ala | Ala | Asp | Asp | Lys | Gly | Cys | Arg | His | Thr |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | Glu | Asp | Ala | Trp |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 100 |

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..61
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Met Asp Ala Glu Ala Arg Arg Thr Cys Gln Lys Glu Ser Glu His His  
1 5 10 15  
Arg Thr Asn Ala Phe Gln Met Gly Asn Ala Leu Gln Thr Leu Arg Phe  
20 25 30  
Trp Gly Lys Gln Lys Xaa Val Leu Thr Val Val Glu Ala Asp Ala Ala  
35 40 45  
Asp Asp Lys Gly Cys Arg His Thr Met Glu Asp Ala Trp  
50 55 60

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..460
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atcaaggaac agtgcaaaact agaagaaacc tccgtcatca gcgacctctc cccaacggcg | 60  |
| ccgacgatgg cgcaacagca gacgcagcta accactggct cgggcatcct ggatgccgtc  | 120 |
| ccgctcttcg tcgtcatcct cctcgcgcc cagtccttg ccctcgtgtt ctggatgtac    | 180 |
| aagctggctt ccgagaagca accaccccg aggaagacac agtgacggcg ccgatctacg   | 240 |
| ccatcggcga gtccttcgct agcctcttta tcggttccat tttcatgtga accagtaccc  | 300 |
| tccagaacat tcaggccgct aattattcag agatatccat atagtctttc aatttgtttt  | 360 |
| atttatactt attgcatttt gggtattgtt tgataacaac ttagcgatat tctatgaatc  | 420 |
| actatccggt tgggtgataa ataatgttc ctagttttag                         |     |

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Ile Lys Glu Gln Cys Lys Leu Glu Glu Thr Ser Val Ile Ser Asp Leu  
1 5 10 15  
Ser Pro Thr Ala Pro Thr Met Ala Gln Gln Thr Gln Leu Thr Thr  
20 25 30  
Gly Ser Gly Ile Leu Asp Ala Val Pro Leu Phe Val Val Ile Leu Leu  
35 40 45  
Ala Ala His Val Leu Ala Leu Val Phe Trp Met Tyr Lys Leu Ala Ser  
50 55 60  
Glu Lys Gln Pro Pro Arg Arg Lys Thr Gln  
65 70

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1481794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Gln Gly Thr Val Gln Thr Arg Arg Asn Leu Arg His Gln Arg Pro Leu  
1 5 10 15  
Pro Asn Gly Ala Asp Asp Gly Ala Thr Ala Asp Ala Ala Asn His Trp  
20 25 30  
Leu Gly His Pro Gly Cys Arg Pro Ala Leu Arg Arg His Pro Pro Arg  
35 40 45  
Gly Pro Arg Pro Gly Pro Arg Val Leu Asp Val Gln Ala Gly Phe Arg  
50 55 60  
Glu Ala Thr Thr Pro Glu Glu Asp Thr Val Thr Ala Pro Ile Tyr Ala  
65 70 75 80  
Ile Gly Glu Ser Phe Ala Ser Leu Phe Ile Gly Ser Ile Phe Met  
85 90 95

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..52

(D) OTHER INFORMATION: / Ceres Seq. ID 1481795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Met Ala Gln Gln Gln Thr Gln Leu Thr Thr Gly Ser Gly Ile Leu Asp  
1 5 10 15  
Ala Val Pro Leu Phe Val Val Ile Leu Leu Ala Ala His Val Leu Ala  
20 25 30  
Leu Val Phe Trp Met Tyr Lys Leu Ala Ser Glu Lys Gln Pro Pro Arg  
35 40 45  
Arg Lys Thr Gln  
50

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 761 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..761

(D) OTHER INFORMATION: / Ceres Seq. ID 1481796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| aggacaacga | gacgtctgam | ggcgtgargc | tgagaccaa  | ggagaacaga | nacggarang  | 60  |
| agcdcr gcg | cccgggcgcc | ggagcctgga | gggtagggga | agagaagaga | agaggcgatg  | 120 |
| gcgtcaatcg | ggtcctccaa | catcggattc | cagctgctga | agaagtctgg | ttggaaggag  | 180 |
| ggcactggcc | ttrgagcgca | ggagcagggg | aggttggaa  | ctgtagagac | tcgtgttaag  | 240 |
| aataacaagc | gtggtatagg | ttctaaagaa | ccaaaaccac | aacctaaagg | tgaggatgac  | 300 |
| attgaaacac | atcctcaaaa | gccaagcag  | gaaatgcaat | caaagaaaag | ggcaaaaatta | 360 |
| gctgcaaaga | ggataagaaa | actgcaagaa | gaggagaagc | gcttgaaaga | gaaggaattc  | 420 |
| gragatggct | tttttcaggg | aatttttggc | ctgataatgt | ggtaaggcag | aaacttcaac  | 480 |
| acttgacaat | gtagctgctg | acttttgsct | gatatagtgg | atgtataggc | ttgcaaaacg  | 540 |
| cttggcctac | aaaatgttac | cccatcatt  | ccgtggatga | tttcacacat | gatttgtggc  | 600 |
| tagggttggc | acaaagctgt | tcatccatgt | agtggacaaa | tctagtgtag | aattgcccac  | 660 |
| gctatgtgat | cttgtaattt | ttatacatta | taaatcttgt | ttttttttgt | tcatataact  | 720 |



gtgctcaata ttttgccttg ccaatgcaaa tattttaaattc t

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Asn | Glu | Thr | Ser | Xaa | Gly | Val | Xaa | Leu | Arg | Pro | Lys | Glu | Asn | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Xaa | Gly | Xaa | Glu | Xaa | Xaa | Gly | Pro | Gly | Ala | Gly | Ala | Trp | Arg | Val | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Glu | Lys | Arg | Arg | Gly | Asp | Gly | Val | Asn | Arg | Val | Leu | Gln | His | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Pro | Ala | Ala | Glu | Glu | Val | Trp | Leu | Glu | Gly | Gly | His | Trp | Pro | Xaa |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Ser | Ala | Gly | Ala | Gly | Lys | Val | Gly | Thr | Cys | Arg | Asp | Ser | Cys |     |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Ile | Gly | Ser | Ser | Asn | Ile | Gly | Phe | Gln | Leu | Leu | Lys | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Gly | Trp | Lys | Glu | Gly | Thr | Gly | Leu | Xaa | Ala | Gln | Glu | Gln | Gly | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Glu | Pro | Val | Glu | Thr | Arg | Val | Lys | Asn | Asn | Lys | Arg | Gly | Ile | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Lys | Glu | Pro | Lys | Pro | Gln | Pro | Lys | Val | Glu | Asp | Asp | Ile | Glu | Thr |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| His | Pro | Gln | Lys | Pro | Lys | Gln | Glu | Met | Gln | Ser | Lys | Lys | Arg | Ala | Lys |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Ala | Ala | Lys | Arg | Ile | Arg | Lys | Leu | Gln | Glu | Glu | Glu | Lys | Arg | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Glu | Lys | Glu | Phe | Xaa | Asp | Gly | Phe | Phe | Gln | Gly | Ile | Phe | Gly | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Met | Trp |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..712

(D) OTHER INFORMATION: / Ceres Seq. ID 1481799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

|             |            |            |            |             |            |     |
|-------------|------------|------------|------------|-------------|------------|-----|
| gtttatcttg  | gacaaaggaa | ctaagtgaat | ggactatggt | tacttgagta  | gattgaagag | 60  |
| tggttatggt  | tctaaaacaa | atatagtgtg | ctaatttgca | agatgctacc  | attatgacat | 120 |
| tgtctgctac  | tgaaatctgc | ttgtcacgcc | agaaatagac | atgctttatt  | tttgttttct | 180 |
| atccttgcca  | atTTTTccgg | caattgaaat | tgttactgtg | tcaattctta  | cagtttgcat | 240 |
| agtttggtga  | atgtactttt | acttttaccg | tagtacaatg | ctaattgtaga | atactgtaac | 300 |
| cagtttgcac  | ttgcaggttc | tcttctcaga | catcaatgct | tatgagggtg  | agcttggtac | 360 |
| tgatgaagag  | aagcactgct | tctgccgtga | gtcagacttg | ttagctgtag  | ttgaatgaat | 420 |
| tttaccatga  | aaatttcgga | cttacctggg | aatgctccaa | cggcatgaac  | ttatcttgcc | 480 |
| cccactttgt  | tgtatgccat | ttgaacgttc | gttaattcag | cttctagatg  | attgttagtt | 540 |
| accgttgatt  | tttggtcgcc | ataaactgga | attatgttaa | tgcccatttt  | ctttacagag | 600 |
| gctcttgctc  | acgtttggaa | tacgaaactg | tgctgaaccg | aacttgaaat  | gtttacattg | 660 |
| cccactctgat | gtttctgctt | ctgaacattc | tttaggcaac | atcctaatta  | tt         |     |

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 794 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..794

(D) OTHER INFORMATION: / Ceres Seq. ID 1481800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| atgcatcttc  | ctagtcctag | ccgcagctcc | tcatcttcc   | gcgcgcgctc | cttctctgtc | 60  |
| tcccatggcc  | gagcgtcttc | cctgctcttc | tctcctttat  | ctccctctcc | atgccggcgc | 120 |
| ttccctagct  | cgttttccca | tctccctgct | ccttcccatg  | gtgcgcaggg | cgctctcccc | 180 |
| tgcactccct  | ccctagctcc | ccaccgctcg | ccttcccttc  | cttccctagc | gcccgtmtcc | 240 |
| agctcgggtc  | gcactcgccg | tccctgcccc | tcgctgtttt  | tgtggccagc | cgagctcgcc | 300 |
| cagccccctg  | cctctccacc | tcataaacgc | cctcagccat  | ggatgtcgaa | tccccctctc | 360 |
| ttagtgccct  | tctttgcagc | ccctgcgtcg | ccgtgcatgt  | aagggtgttt | gtctaaatgc | 420 |
| tcaagaggag  | tgctcgtgtc | tggacagccc | ttttggcgtc  | gtcgggtgtt | tgatgttttg | 480 |
| cgcataccgt  | ctacgacacc | gtcgaccctc | agtgatatatt | cgttcttgct | ttgtcgtttt | 540 |
| atcgatcgac  | gtctatttgc | taatgtgaag | tgtgtgtatg  | tgccctatgt | tgttgaggag | 600 |
| cgacatctgt  | ggaatctggg | tgaagaagaa | acagagcacg  | tccgacgctt | actagctgct | 660 |
| ggtgaaagga  | ttgaatcggc | tatcatggtc | gttttagtgtc | gatcgagtca | accttagctg | 720 |
| tggtaaagcta | ccattatttc | tgctatttag | ccgatgtatg  | agttagatgg | ataaaatagt | 780 |
| tacgatgatt  | ttcc       |            |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1481801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Leu | Pro | Ser | Pro | Ser | Arg | Ser | Ser | Ser | Ser | Ser | Cys | Ala | Arg |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Phe | Ser | Val | Ser | His | Gly | Arg | Ala | Ser | Ser | Leu | Leu | Leu | Ser | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ser | Pro | Ser | Pro | Cys | Arg | Arg | Phe | Pro | Ser | Ser | Phe | Ser | His | Leu |

35 40 45  
Pro Ala Pro Ser His Gly Ala Gln Gly Val Leu Pro Ser Thr Pro Ser  
50 55 60  
Leu Ala Pro His Arg Ser Pro Ser Ser Pro Ser  
65 70 75

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1481802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Met His Leu Pro Ser Pro Ser Arg Ser Ser Ser Ser Cys Ala Arg  
1 5 10 15  
Ser Phe Ser Val Ser His Gly Arg Ala Ser Ser Leu Leu Leu Ser Pro  
20 25 30  
Leu Ser Pro Ser Pro Cys Arg Arg Phe Pro Ser Ser Phe Ser His Leu  
35 40 45  
Pro Ala Pro Ser His Gly Ala Gln Gly Val Leu Pro Ser Thr Pro Ser  
50 55 60  
Leu Ala Pro His Arg Ser Pro Ser Ser Pro Ser  
65 70 75

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1481803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Cys Ile Phe Leu Val Leu Ala Ala Ala Pro His Leu Pro Ala Arg Ala  
1 5 10 15  
Pro Ser Leu Ser Pro Met Ala Glu Arg Pro Pro Cys Ser Ser Leu Leu  
20 25 30  
Tyr Leu Pro Leu His Ala Gly Ala Ser Leu Ala Arg Phe Pro Ile Ser  
35 40 45  
Leu Leu Leu Pro Met Val Arg Arg Ala Ser Ser Pro Arg Leu Pro Pro  
50 55 60

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1481808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

|        |      |        |      |        |       |        |      |        |       |        |      |     |
|--------|------|--------|------|--------|-------|--------|------|--------|-------|--------|------|-----|
| atataa | acaa | gcctat | gtta | gcctgt | ctacg | cactgt | gttc | gtgcat | gttt  | tcattt | gacc | 60  |
| ttgttt | ccat | gatgct | tcga | cgtgtt | acgc  | gtgctc | gtgc | ttcttg | ctgt  | gtcatc | actg | 120 |
| gtccac | attt | tcttgt | ggaa | agtgtt | ccct  | tgtacg | agct | tatgaa | acca  | gtgtgc | acaa | 180 |
| gcgacg | gacg | gatttg | tacc | atccag | naac  | gnatag | tgan | tcggtt | tttac | taactc | ctg  |     |

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1481809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Asn | Lys | Pro | Met | Leu | Ala | Cys | Tyr | Ala | Leu | Cys | Ser | Cys | Met | Phe |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ser | Phe | Asp | Leu | Val | Ser | Met | Met | Leu | Arg | Arg | Val | Thr | Arg | Ala | Arg |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ala | Ser | Cys | Cys | Val | Ile | Thr | Gly | Pro | His | Phe | Leu | Val | Glu | Ser | Val |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Pro | Leu | Tyr | Glu | Leu | Met | Lys | Pro | Val | Cys | Thr | Ser | Asp | Gly | Arg | Ile |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Cys | Thr | Ile | Gln | Xaa | Xaa | Ile | Val | Xaa | Pro | Phe | Tyr |     |     |     |     |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1481810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Leu | Ala | Cys | Tyr | Ala | Leu | Cys | Ser | Cys | Met | Phe | Ser | Phe | Asp | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Val | Ser | Met | Met | Leu | Arg | Arg | Val | Thr | Arg | Ala | Arg | Ala | Ser | Cys | Cys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Ile | Thr | Gly | Pro | His | Phe | Leu | Val | Glu | Ser | Val | Pro | Leu | Tyr | Glu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Leu | Met | Lys | Pro | Val | Cys | Thr | Ser | Asp | Gly | Arg | Ile | Cys | Thr | Ile | Gln |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Xaa | Xaa | Ile | Val | Xaa | Pro | Phe | Tyr |     |     |     |     |     |     |     |     |  |
| 65  |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1481811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Ser | Phe | Asp | Leu | Val | Ser | Met | Met | Leu | Arg | Arg | Val | Thr | Arg |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Arg | Ala | Ser | Cys | Cys | Val | Ile | Thr | Gly | Pro | His | Phe | Leu | Val | Glu |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ser | Val | Pro | Leu | Tyr | Glu | Leu | Met | Lys | Pro | Val | Cys | Thr | Ser | Asp | Gly |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Arg | Ile | Cys | Thr | Ile | Gln | Xaa | Xaa | Ile | Val | Xaa | Pro | Phe | Tyr |     |     |
| 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 433 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..433

(D) OTHER INFORMATION: / Ceres Seq. ID 1481815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

|             |             |             |             |            |             |     |
|-------------|-------------|-------------|-------------|------------|-------------|-----|
| gatggaatca  | atttcctcga  | tcatttttagc | tgacagcaata | tgaatcatga | tccatcaatt  | 60  |
| gctgcagaaa  | gtaagcaaaa  | caatgaagat  | gaaccttttaa | gggaaatgaa | gaataaaaaag | 120 |
| aagaaatgga  | agcaaggtac  | tagtagcatt  | gaaccaaaatg | acattctaga | atctttttccc | 180 |
| tcagagaaaag | ctagcttaac  | tggtcatttt  | ggtaccagca  | aagctattgt | gccatctgtt  | 240 |
| gcaaaagaaa  | gcatgaacat  | agaaaatgag  | aatgtgaatg  | acggcaagga | gaagaagaga  | 300 |
| aagggaagaa  | ctaataatgga | agtagctact  | gctgaaaagg  | acaattctaa | ttgtgataat  | 360 |
| caaggaattg  | atattagtac  | ccaagaatca  | cttaktkctt  | ttgtacaaaa | tgaaagggrtg | 420 |
| ggtcaggaaa  | atg         |             |             |            |             |     |

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1481816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Gly | Ile | Asn | Phe | Leu | Asp | His | Phe | Ser | Cys | Ser | Asn | Met | Asn | His |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |     |
| Asp | Pro | Ser | Ile | Ala | Ala | Glu | Ser | Lys | Gln | Asn | Asn | Glu | Asp | Glu | Pro |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Leu | Arg | Glu | Met | Lys | Asn | Lys | Lys | Lys | Lys | Trp | Lys | Gln | Gly | Thr | Ser |
|     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
| Ser | Ile | Glu | Pro | Asn | Asp | Ile | Leu | Glu | Ser | Phe | Pro | Ser | Glu | Lys | Ala |
| 50  |     |     |     |     | 55  |     |     | 60  |     |     |     |     |     |     |     |
| Ser | Leu | Thr | Gly | His | Phe | Gly | Thr | Ser | Lys | Ala | Ile | Val | Pro | Ser | Val |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |     |
| Ala | Lys | Glu | Ser | Met | Asn | Ile | Glu | Asn | Glu | Asn | Val | Asn | Asp | Gly | Lys |
|     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |
| Glu | Lys | Lys | Arg | Lys | Gly | Lys | Ala | Asn | Met | Glu | Val | Pro | Thr | Ala | Glu |
|     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Lys | Asp | Asn | Ser | Asn | Cys | Asp | Asn | Gln | Gly | Ile | Asp | Ile | Ser | Thr | Gln |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

Glu Ser Leu Xaa Xaa Phe Val Gln Asn Glu Arg Xaa Gly Gln Glu Asn  
130 135 140

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1481817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Met Asn His Asp Pro Ser Ile Ala Ala Glu Ser Lys Gln Asn Asn Glu  
1 5 10 15  
Asp Glu Pro Leu Arg Glu Met Lys Asn Lys Lys Lys Lys Trp Lys Gln  
20 25 30  
Gly Thr Ser Ser Ile Glu Pro Asn Asp Ile Leu Glu Ser Phe Pro Ser  
35 40 45  
Glu Lys Ala Ser Leu Thr Gly His Phe Gly Thr Ser Lys Ala Ile Val  
50 55 60  
Pro Ser Val Ala Lys Glu Ser Met Asn Ile Glu Asn Glu Asn Val Asn  
65 70 75 80  
Asp Gly Lys Glu Lys Lys Arg Lys Gly Lys Ala Asn Met Glu Val Pro  
85 90 95  
Thr Ala Glu Lys Asp Asn Ser Asn Cys Asp Asn Gln Gly Ile Asp Ile  
100 105 110  
Ser Thr Gln Glu Ser Leu Xaa Xaa Phe Val Gln Asn Glu Arg Xaa Gly  
115 120 125  
Gln Glu Asn  
130

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1481818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Met Lys Asn Lys Lys Lys Lys Trp Lys Gln Gly Thr Ser Ser Ile Glu  
1 5 10 15  
Pro Asn Asp Ile Leu Glu Ser Phe Pro Ser Glu Lys Ala Ser Leu Thr  
20 25 30  
Gly His Phe Gly Thr Ser Lys Ala Ile Val Pro Ser Val Ala Lys Glu  
35 40 45  
Ser Met Asn Ile Glu Asn Glu Asn Val Asn Asp Gly Lys Glu Lys Lys  
50 55 60  
Arg Lys Gly Lys Ala Asn Met Glu Val Pro Thr Ala Glu Lys Asp Asn  
65 70 75 80  
Ser Asn Cys Asp Asn Gln Gly Ile Asp Ile Ser Thr Gln Glu Ser Leu  
85 90 95  
Xaa Xaa Phe Val Gln Asn Glu Arg Xaa Gly Gln Glu Asn

100 105  
(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..495
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| anrgggaggg | ctgcggttg  | ggaagagaga | gatagaagag | aatcagggta | atgcagatgg | 60  |
| gatcgatgga | attcgtagcg | ccggcggttg | aggagctttt | gccggaactt | tccctcgagg | 120 |
| agcagccacg | gttgacagaa | caatcccgcg | agcgtgaccg | catccggaag | cgacgtaaca | 180 |
| agcactctcc | tcctccccgt | ccgtcgttga | tctcgttaca | gtacgtgatg | gatatgggat | 240 |
| cgatgggaat | ggatttcgtg | gcgcggcggt | tggaggagct | gctgccggat | ctttcccgcg | 300 |
| aggagcagct | acggttgcaa | aacaaatccc | gcgggcgtga | ccgcattctc | aagccacgta | 360 |
| acaagcacgc | tcctcgtccc | cgtccgtcgc | cgttctcgga | atgggacggc | aacatcttca | 420 |
| aaattcccca | ggtcctccac | gctctcgsc  | actacaatgc | caggcaccct | ggtggcgagt | 480 |
| tcgatgttgt | gaagc      |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gln | Met | Gly | Ser | Met | Glu | Phe | Val | Ala | Pro | Ala | Leu | Glu | Glu | Leu |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Leu | Pro | Glu | Leu | Ser | Leu | Glu | Glu | Gln | Pro | Arg | Leu | Gln | Asn | Gln | Ser |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg | Glu | Arg | Asp | Arg | Ile | Arg | Lys | Arg | Arg | Asn | Lys | His | Ser | Pro | Pro |  |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| Pro | Arg | Pro | Ser | Leu | Ile | Ser | Val | Gln | Tyr | Val | Met | Asp | Met | Gly | Ser |  |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |  |
| Met | Gly | Met | Asp | Phe | Val | Ala | Pro | Ala | Leu | Glu | Glu | Leu | Leu | Pro | Asp |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Leu | Ser | Arg | Glu | Glu | Gln | Leu | Arg | Leu | Gln | Asn | Lys | Ser | Arg | Gly | Arg |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Asp | Arg | Ile | Ser | Lys | Pro | Arg | Asn | Lys | His | Ala | Pro | Arg | Pro | Arg | Pro |  |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ser | Pro | Phe | Ser | Glu | Trp | Asp | Gly | Asn | Ile | Phe | Lys | Ile | Pro | Gln | Val |  |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |  |
| Leu | His | Ala | Leu | Xaa | His | Tyr | Asn | Ala | Arg | His | Pro | Gly | Gly | Glu | Phe |  |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |  |
| Asp | Val | Val | Lys |     |     |     |     |     |     |     |     |     |     |     |     |  |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..146  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1481821  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Met Gly Ser Met Glu Phe Val Ala Pro Ala Leu Glu Glu Leu Leu Pro  
1                  5                  10                  15  
Glu Leu Ser Leu Glu Glu Gln Pro Arg Leu Gln Asn Gln Ser Arg Glu  
                  20                  25                  30  
Arg Asp Arg Ile Arg Lys Arg Arg Asn Lys His Ser Pro Pro Pro Arg  
                  35                  40                  45  
Pro Ser Leu Ile Ser Val Gln Tyr Val Met Asp Met Gly Ser Met Gly  
                  50                  55                  60  
Met Asp Phe Val Ala Pro Ala Leu Glu Glu Leu Leu Pro Asp Leu Ser  
65                  70                  75                  80  
Arg Glu Glu Gln Leu Arg Leu Gln Asn Lys Ser Arg Gly Arg Asp Arg  
                  85                  90                  95  
Ile Ser Lys Pro Arg Asn Lys His Ala Pro Arg Pro Arg Pro Ser Pro  
                  100                  105                  110  
Phe Ser Glu Trp Asp Gly Asn Ile Phe Lys Ile Pro Gln Val Leu His  
                  115                  120                  125  
Ala Leu Xaa His Tyr Asn Ala Arg His Pro Gly Gly Glu Phe Asp Val  
130                  135                  140  
Val Lys  
145

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 143 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..143  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1481822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Met Glu Phe Val Ala Pro Ala Leu Glu Glu Leu Leu Pro Glu Leu Ser  
1                  5                  10                  15  
Leu Glu Glu Gln Pro Arg Leu Gln Asn Gln Ser Arg Glu Arg Asp Arg  
                  20                  25                  30  
Ile Arg Lys Arg Arg Asn Lys His Ser Pro Pro Pro Arg Pro Ser Leu  
                  35                  40                  45  
Ile Ser Val Gln Tyr Val Met Asp Met Gly Ser Met Gly Met Asp Phe  
                  50                  55                  60  
Val Ala Pro Ala Leu Glu Glu Leu Leu Pro Asp Leu Ser Arg Glu Glu  
65                  70                  75                  80  
Gln Leu Arg Leu Gln Asn Lys Ser Arg Gly Arg Asp Arg Ile Ser Lys  
                  85                  90                  95  
Pro Arg Asn Lys His Ala Pro Arg Pro Arg Pro Ser Pro Phe Ser Glu  
                  100                  105                  110  
Trp Asp Gly Asn Ile Phe Lys Ile Pro Gln Val Leu His Ala Leu Xaa  
                  115                  120                  125  
His Tyr Asn Ala Arg His Pro Gly Gly Glu Phe Asp Val Val Lys  
130                  135                  140

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:



|             |             |            |             |             |            |     |
|-------------|-------------|------------|-------------|-------------|------------|-----|
| agtcctccact | ctcgtccccc  | ctccctccaa | agtcctccaa  | ctaccacccc  | acttccccac | 60  |
| caccactaca  | tggcggcggc  | gctcgcctcc | tcccgcctact | gctggagccg  | cccgtcgtcg | 120 |
| ccgccccaac  | cgacccgcgg  | ccgcgcctcc | gtcactagct  | gcgcgcctctc | cggacgagag | 180 |
| aaaagaaact  | ccttttagctg | gagagagtg  | gcaatttctg  | ttgcattgtc  | agttggacta | 240 |
| atcactgggtg | caccaacgtt  | tggaccaccg | gcctatgctt  | cttctcttga  | acctgttctt | 300 |
| ccagatgtgt  | ctgttcttat  | ctctggacct | cccattaaag  | atccagggtgc | tttattgaga | 360 |
| tatgcttttac | caatagataa  | taaagctatt | cgggtgaagtt | caaaagccgc  | tggaggatat | 420 |
| cactgasagc  | ctcaaggttg  | stggkgttag | aggcttggat  | tcagttgaaa  | gaaaatgtca | 480 |
| qasaagcadc  | qaaagcackg  |            |             |             |            |     |

[illegible]

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1481825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

```
Val Pro Thr Leu Val Pro Ala Pro Ser Lys Val Gln Thr Leu Pro Pro
1 5 10 15
His Phe Pro Thr Thr Thr Thr Trp Arg Arg Arg Ser Pro Pro Pro Ala
20 25 30
Thr Ala Gly Ala Ala Arg Arg Cys Arg Pro Asn Arg Pro Ala Ala Ala
35 40 45
Ala Pro Ser Leu Ala Ala Arg Ser Pro Asp Glu Arg Lys Glu Thr Pro
50 55 60
Leu Ala Gly Glu Ser Val Gln Phe Leu Leu His Cys Gln Leu Asp
65 70 75
```

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1481826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

```
Met Ala Ala Ala Leu Ala Ser Ser Arg Tyr Cys Trp Ser Arg Pro Ser
1 5 10 15
Leu Pro Pro Gln Pro Thr Arg Gly Arg Ser Val Thr Ser Cys Ala
20 25 30
Leu Ser Gly Arg Glu Lys Arg Asn Ser Phe Ser Trp Arg Glu Cys Ala
35 40 45
Ile Ser Val Ala Leu Ser Val Gly Leu Ile Thr Gly Ala Pro Thr Phe
50 55 60
Gly Pro Pro Ala Tyr Ala Ser Ser Leu Glu Pro Val Leu Pro Asp Val
65 70 75 80
Ser Val Leu Ile Ser Gly Pro Pro Ile Lys Asp Pro Gly Ala Leu Leu
85 90 95
Arg Tyr Ala Leu Pro Ile Asp Asn Lys Ala Ile Arg
100 105
```

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..876

(D) OTHER INFORMATION: / Ceres Seq. ID 1481827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

```
gaaggcacac tgccggcgct ctatcttccg ctctctctcc tactcgcgct cggcaaggcg 60
gcgggcgsst caggctcggg ctacggcgctc acggcatccc ctccgcctct cgccagtcgc 120
ctcgcgccat cgctccgggt cacaccggcc ggtgactctg ctaaaaatgg tgttcctttc 180
aaatgaagac gcctggatcc atgatgaaga catcatggat gatgttgatt cagatgttga 240
agaatcagac tcagaagggtg attcagggtga agaagctcag gctaagcctg cagacaaagc 300
gatatacaac aaggaggcta ttcttgaaaa acttgaagac atagcctggc ccaagaatgt 360
ggactggatg cacaaactca ctggtgagca tgatcaaggg gagaaagttg atgtgaacga 420
tgatcttgcc cgcgaacttg cgttttacac ccaagctttg gatggcacia ggcaggcctt 480
tgagaagctg cagtcgatga aggtccggtt cctcagacca acagattact acgctgagat 540
```

```
ggtgaagact gatgcacaca tgcacaagat caaggggagg ttgttgtcag agaagaagag 600
gattgaggaa gctgaggagc ggaggaaggc tagggagtcc aggaagaaag caaaggaggt 660
tcaggctgag aagaagaagg agagggctaa gcagaagaag gagcagattg agtcagtcaa 720
gaagtggaga aagcagagac aacaaggggg attcaccaag ggaaatgatg atgtgccaga 780
ccttaatttt gaaggagaag aaggatttaa acaatcaaag aaaaagaggc ccggtgtttc 840
tcctggtgac aggtctggtg gtcttgccctt ctcttc
```

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..291

(D) OTHER INFORMATION: / Ceres Seq. ID 1481828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

```
Lys Ala His Cys Arg Arg Ser Ile Phe Arg Ser Leu Ser Tyr Ser Arg
1 5 10 15
Ser Ala Arg Arg Arg Arg Xaa Gln Ala Arg Ala Thr Ala Ser Arg His
20 25 30
Pro Leu Arg Leu Ser Pro Val Ala Ser Arg His Arg Leu Arg Ser His
35 40 45
Arg Pro Val Thr Leu Leu Lys Met Val Phe Leu Ser Asn Glu Asp Ala
50 55 60
Trp Ile His Asp Glu Asp Ile Met Asp Asp Val Asp Ser Asp Val Glu
65 70 75 80
Glu Ser Asp Ser Glu Gly Asp Ser Gly Glu Glu Ala Gln Ala Lys Pro
85 90 95
Ala Asp Lys Ala Ile Tyr Asn Lys Glu Ala Ile Leu Glu Lys Leu Glu
100 105 110
Asp Ile Ala Trp Pro Lys Asn Val Asp Trp Met His Lys Leu Thr Val
115 120 125
Glu His Asp Gln Gly Glu Lys Val Asp Val Asn Asp Asp Leu Ala Arg
130 135 140
Glu Leu Ala Phe Tyr Thr Gln Ala Leu Asp Gly Thr Arg Gln Ala Phe
145 150 155 160
Glu Lys Leu Gln Ser Met Lys Val Arg Phe Leu Arg Pro Thr Asp Tyr
165 170 175
Tyr Ala Glu Met Val Lys Thr Asp Ala His Met His Lys Ile Lys Gly
180 185 190
Arg Leu Leu Ser Glu Lys Lys Arg Ile Glu Glu Ala Glu Glu Arg Arg
195 200 205
Lys Ala Arg Glu Ser Arg Lys Lys Ala Lys Glu Val Gln Ala Glu Lys
210 215 220
Lys Lys Glu Arg Ala Lys Gln Lys Lys Glu Gln Ile Glu Ser Val Lys
225 230 235 240
Lys Trp Arg Lys Gln Arg Gln Gln Gly Gly Phe Thr Lys Gly Asn Asp
245 250 255
Asp Val Pro Asp Leu Asn Phe Glu Gly Glu Glu Gly Phe Lys Gln Ser
260 265 270
Lys Lys Lys Arg Pro Gly Val Ser Pro Gly Asp Arg Ser Gly Gly Leu
275 280 285
Ala Phe Ser
290
```

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..236  
(D) OTHER INFORMATION: / Ceres Seq. ID 1481829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

```
Met Val Phe Leu Ser Asn Glu Asp Ala Trp Ile His Asp Glu Asp Ile
1 5 10 15
Met Asp Asp Val Asp Ser Asp Val Glu Glu Ser Asp Ser Glu Gly Asp
 20 25 30
Ser Gly Glu Glu Ala Gln Ala Lys Pro Ala Asp Lys Ala Ile Tyr Asn
 35 40 45
Lys Glu Ala Ile Leu Glu Lys Leu Glu Asp Ile Ala Trp Pro Lys Asn
 50 55 60
Val Asp Trp Met His Lys Leu Thr Val Glu His Asp Gln Gly Glu Lys
65 70 75 80
Val Asp Val Asn Asp Asp Leu Ala Arg Glu Leu Ala Phe Tyr Thr Gln
 85 90 95
Ala Leu Asp Gly Thr Arg Gln Ala Phe Glu Lys Leu Gln Ser Met Lys
 100 105 110
Val Arg Phe Leu Arg Pro Thr Asp Tyr Tyr Ala Glu Met Val Lys Thr
 115 120 125
Asp Ala His Met His Lys Ile Lys Gly Arg Leu Leu Ser Glu Lys Lys
 130 135 140
Arg Ile Glu Glu Ala Glu Glu Arg Arg Lys Ala Arg Glu Ser Arg Lys
 145 150 155 160
Lys Ala Lys Glu Val Gln Ala Glu Lys Lys Lys Glu Arg Ala Lys Gln
 165 170 175
Lys Lys Glu Gln Ile Glu Ser Val Lys Lys Trp Arg Lys Gln Arg Gln
 180 185 190
Gln Gly Gly Phe Thr Lys Gly Asn Asp Asp Val Pro Asp Leu Asn Phe
 195 200 205
Glu Gly Glu Glu Gly Phe Lys Gln Ser Lys Lys Lys Arg Pro Gly Val
 210 215 220
Ser Pro Gly Asp Arg Ser Gly Gly Leu Ala Phe Ser
 225 230 235
```

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 220 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..220

(D) OTHER INFORMATION: / Ceres Seq. ID 1481830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

```
Met Asp Asp Val Asp Ser Asp Val Glu Glu Ser Asp Ser Glu Gly Asp
1 5 10 15
Ser Gly Glu Glu Ala Gln Ala Lys Pro Ala Asp Lys Ala Ile Tyr Asn
 20 25 30
Lys Glu Ala Ile Leu Glu Lys Leu Glu Asp Ile Ala Trp Pro Lys Asn
 35 40 45
Val Asp Trp Met His Lys Leu Thr Val Glu His Asp Gln Gly Glu Lys
 50 55 60
```

Val Asp Val Asn Asp Asp Leu Ala Arg Glu Leu Ala Phe Tyr Thr Gln  
65 70 75 80  
Ala Leu Asp Gly Thr Arg Gln Ala Phe Glu Lys Leu Gln Ser Met Lys  
85 90 95  
Val Arg Phe Leu Arg Pro Thr Asp Tyr Tyr Ala Glu Met Val Lys Thr  
100 105 110  
Asp Ala His Met His Lys Ile Lys Gly Arg Leu Leu Ser Glu Lys Lys  
115 120 125  
Arg Ile Glu Glu Ala Glu Glu Arg Arg Lys Ala Arg Glu Ser Arg Lys  
130 135 140  
Lys Ala Lys Glu Val Gln Ala Glu Lys Lys Lys Glu Arg Ala Lys Gln  
145 150 155 160  
Lys Lys Glu Gln Ile Glu Ser Val Lys Lys Trp Arg Lys Gln Arg Gln  
165 170 175  
Gln Gly Gly Phe Thr Lys Gly Asn Asp Asp Val Pro Asp Leu Asn Phe  
180 185 190  
Glu Gly Glu Glu Gly Phe Lys Gln Ser Lys Lys Lys Arg Pro Gly Val  
195 200 205  
Ser Pro Gly Asp Arg Ser Gly Gly Leu Ala Phe Ser  
210 215 220

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..530
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| aagctcgtct cgcaccagaa acccgcggaat caatcccga tcccgatcga ccggcgggcgc  | 60  |
| gggaggcgat gccggacaag gcggtggacg acgtcatgga ggccgcgggtg gggggcccact | 120 |
| tcagcggcct ccgcctcgag gcgctgcgcc tctccacctc tgcgccctct tccccttct    | 180 |
| cctccccgcg cgccgcggcg cacacgcact ccaacggagc cgtctacgcc aacggcacca   | 240 |
| ccgagcttcc ctctcctgcc gctgcccggc agccattcgt catcggggtt tctggaggga   | 300 |
| cggcgctcggg gaagacgacg gtgtgcgaca tgatcatcca gcagctgcac gaccaccgtg  | 360 |
| tcgtgctcgt taaccaggat tcgtttttacc gtggccttac tgctgaagag tctgcacacg  | 420 |
| cacaagacta taattttgat caccctgatg catttgatac agagcaactt ctagaatgca   | 480 |
| tggggcagct gaaatgtgct caacctgtaa atgttcctat atatgatttc              |     |

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..176
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481832

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Ala Arg Leu Ala Pro Glu Thr Arg Glu Ser Ile Pro Asn Pro Asp Arg  
1 5 10 15  
Pro Ala Ala Arg Glu Ala Met Pro Asp Lys Ala Val Asp Asp Val Met  
20 25 30  
Glu Ala Ala Val Gly Ala His Phe Ser Gly Leu Arg Leu Glu Ala Leu  
35 40 45

```

Arg Leu Ser Thr Ser Ala Pro Ser Ser Pro Ser Ser Ser Pro Ala Ala
 50 55 60
Ala Ala His Thr His Ser Asn Gly Ala Val Tyr Ala Asn Gly Thr Thr
 65 70 75 80
Glu Leu Pro Ser Pro Ala Ala Ala Arg Gln Pro Phe Val Ile Gly Val
 85 90 95
Ser Gly Gly Thr Ala Ser Gly Lys Thr Thr Val Cys Asp Met Ile Ile
 100 105 110
Gln Gln Leu His Asp His Arg Val Val Leu Val Asn Gln Asp Ser Phe
 115 120 125
Tyr Arg Gly Leu Thr Ala Glu Glu Ser Ala His Ala Gln Asp Tyr Asn
 130 135 140
Phe Asp His Pro Asp Ala Phe Asp Thr Glu Gln Leu Leu Glu Cys Met
 145 150 155 160
Gly Gln Leu Lys Cys Ala Gln Pro Val Asn Val Pro Ile Tyr Asp Phe
 165 170 175

```

## (2) INFORMATION FOR SEQ ID NO:199:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1481833

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

```

Met Pro Asp Lys Ala Val Asp Asp Val Met Glu Ala Ala Val Gly Ala
 1 5 10 15
His Phe Ser Gly Leu Arg Leu Glu Ala Leu Arg Leu Ser Thr Ser Ala
 20 25 30
Pro Ser Ser Pro Ser Ser Ser Pro Ala Ala Ala Ala His Thr His Ser
 35 40 45
Asn Gly Ala Val Tyr Ala Asn Gly Thr Thr Glu Leu Pro Ser Pro Ala
 50 55 60
Ala Ala Arg Gln Pro Phe Val Ile Gly Val Ser Gly Gly Thr Ala Ser
 65 70 75 80
Gly Lys Thr Thr Val Cys Asp Met Ile Ile Gln Gln Leu His Asp His
 85 90 95
Arg Val Val Leu Val Asn Gln Asp Ser Phe Tyr Arg Gly Leu Thr Ala
 100 105 110
Glu Glu Ser Ala His Ala Gln Asp Tyr Asn Phe Asp His Pro Asp Ala
 115 120 125
Phe Asp Thr Glu Gln Leu Leu Glu Cys Met Gly Gln Leu Lys Cys Ala
 130 135 140
Gln Pro Val Asn Val Pro Ile Tyr Asp Phe
 145 150

```

## (2) INFORMATION FOR SEQ ID NO:200:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1481834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

```
Met Glu Ala Ala Val Gly Ala His Phe Ser Gly Leu Arg Leu Glu Ala
1 5 10 15
Leu Arg Leu Ser Thr Ser Ala Pro Ser Ser Pro Ser Ser Ser Pro Ala
20 25 30
Ala Ala Ala His Thr His Ser Asn Gly Ala Val Tyr Ala Asn Gly Thr
35 40 45
Thr Glu Leu Pro Ser Pro Ala Ala Arg Gln Pro Phe Val Ile Gly
50 55 60
Val Ser Gly Gly Thr Ala Ser Gly Lys Thr Thr Val Cys Asp Met Ile
65 70 75 80
Ile Gln Gln Leu His Asp His Arg Val Val Leu Val Asn Gln Asp Ser
85 90 95
Phe Tyr Arg Gly Leu Thr Ala Glu Glu Ser Ala His Ala Gln Asp Tyr
100 105 110
Asn Phe Asp His Pro Asp Ala Phe Asp Thr Glu Gln Leu Leu Glu Cys
115 120 125
Met Gly Gln Leu Lys Cys Ala Gln Pro Val Asn Val Pro Ile Tyr Asp
130 135 140
Phe
145
```

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1087 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1087

(D) OTHER INFORMATION: / Ceres Seq. ID 1481839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

```
aatcaagctg actcgggtgc tccgccgtgt tacctgccag ctcaaggaac gattccaagc 60
tcgatattctg ctgtttcaga tcataatccg gtcctaaatcc gtaactcagg ttctgaaact 120
cgtccccatt tccaaatcct atacactcca ccgggaaact cggctgactt aactcgctct 180
cactctgaga gacaacgcag accttcttcg ccggaggctg atcgggtgat cgtggcgatg 240
acggcggagg agtataatta ggaggaggag gatggtgcag atctgggaag ttgagcttgg 300
ctttatcacc acggatctgc ttggccgcaa catcataagc catggcagct tcctccgccg 360
tggtgaacgt accaagccaa actctaacac cttttcgtgg atctcgaatc tcagccgccc 420
attttcccca tggacgctta cgtatccctc tataaacatt cttcctcttc ctccgttttc 480
ccggctctgt tcctgctcc ttcttctactg cctcctcttt cacgttaact tcaaaatttt 540
caccgatttc cccaaagttc aaaatttaca attttaaccc cacacagata attaaataat 600
cctgataaat tacattacca aaaccacaaa tatttttttt ttatcatctt ccgtaagtgc 660
cagaaatatt attttacctt ttgtctaaaa aggttagaaa aaactatatg tttgtgtttt 720
tgaatgattt tgtatttttt tttatgattm ataggagagt acataccttg gttgggtgga 780
tgaggttttg aggtggaata gaaaccccag aagtcgctcg cggcggaagc atcgagctct 840
gaccagagtt cctcagccgt gagtttacgg cccttggcct tggtgacgag aggggcataa 900
tcggaaataa tagcaccgcc acacattttc tctgtttgtt gctgtgggtt tctttcaaga 960
gaaagtttcc tacggtggag ctgaaatgcc tttataggcg caaaataaat gttttatggt 1020
aataaagtgt gagtgaaatg aattacttta tattagaata ataattctaa tagttttatg 1080
ttccttg
```

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..86
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1481840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Asn Gln Ala Asp Ser Val Ala Pro Pro Cys Tyr Arg Pro Ala Gln Gly  
1 5 10 15  
Thr Ile Pro Ser Ser Ile Ser Ala Val Ser Asp His Asn Pro Ala Gln  
20 25 30  
Ile Arg Asn Ser Gly Ser Glu Thr Arg Pro His Phe Gln Ile Leu Tyr  
35 40 45  
Thr Pro Pro Gly Asn Ser Ala Asp Leu Thr Arg Ser His Ser Glu Arg  
50 55 60  
Gln Arg Arg Pro Ser Ser Pro Glu Ala Asp Arg Leu Ile Val Ala Met  
65 70 75 80  
Thr Ala Glu Glu Tyr Asn  
85

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 56 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..56
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1481841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Ile Lys Leu Thr Arg Leu Leu Arg Arg Val Thr Val Gln Leu Lys Glu  
1 5 10 15  
Arg Phe Gln Ala Arg Tyr Leu Leu Phe Gln Ile Ile Ile Arg Leu Lys  
20 25 30  
Ser Val Thr Gln Val Leu Lys Leu Val Pro Ile Ser Lys Ser Tyr Thr  
35 40 45  
Leu His Arg Glu Thr Arg Leu Thr  
50 55

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 101 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..101
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1481842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Met Val Gln Ile Trp Glu Val Glu Leu Gly Phe Ile Thr Thr Asp Leu  
1 5 10 15  
Leu Gly Arg Asn Ile Ile Ser His Gly Ser Phe Leu Arg Arg Val Glu  
20 25 30  
Arg Thr Lys Pro Asn Ser Asn Thr Phe Ser Trp Ile Ser Asn Leu Ser  
35 40 45  
Arg Pro Phe Ser Pro Trp Thr Leu Thr Tyr Pro Ser Ile Asn Ile Leu  
50 55 60



Pro Leu Pro Pro Phe Pro Arg Leu Cys Cys Leu Leu Leu Leu His Cys  
65 70 75 80  
Leu Leu Phe His Val Asn Phe Lys Ile Phe Thr Gly Phe Pro Lys Val  
85 90 95  
Gln Asn Leu Gln Phe  
100

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

|            |             |            |             |             |            |      |
|------------|-------------|------------|-------------|-------------|------------|------|
| gaggtttctt | gggaacagga  | tcgcttctac | agatatttca  | cccatgtcaa  | gtttaacagt | 60   |
| gagaagggtg | tcgcgcgaag  | atatacaact | ggttcagaat  | ctaattgaac  | gatgcctcca | 120  |
| gctttacatg | aaccagaaag  | aagttgttga | cactcttcta  | gaacaggcta  | agatcgaacc | 180  |
| tggttttaca | gaactagttt  | ggcagaagct | tgaagaagag  | aaccgcgaat  | ttttcaaggc | 240  |
| atattatctg | aggctcatgg  | tgaagcacca | gataatggaa  | tataacgaac  | tgcttgagca | 300  |
| gcagataaac | cacatgcgcc  | agatgcaccc | aactgcaggg  | gcttctgttc  | gaaacaggaa | 360  |
| tggttctcat | gttccaccaa  | tgaatcagca | acaattactc  | tatgaacgca  | aggaaccaga | 420  |
| tcaatcctct | cctaattctgt | caagtccata | cctcaatgga  | ggctcagcaa  | ttaacacaaa | 480  |
| tataccttct | tatgtggact  | tttcatccca | ttctagaaga  | gttgatcctt  | caccaaactc | 540  |
| gctctccttg | caggccacaa  | atatgccttt | gatgcaagga  | atgatcaagt  | ctgagactgc | 600  |
| atatcaaaac | tgtgctccat  | acatgtatgg | tggtgaagca  | cagtccacag  | ttggagatgt | 660  |
| caccatcgca | tctttcagca  | atgattccag | caaccaatcc  | ctgaatgatc  | ctcttgctga | 720  |
| tccagatgct | cctacatttg  | gctcgttagg | acaaattcct  | cagaacttca  | gcctctctga | 780  |
| tctgacagct | gatttttccc  | agagttcaga | tattctggag  | agctacgagg  | gatcaccgtt | 840  |
| cctattggct | gatgctgaaa  | atttcctgga | ctctagcgaa  | agggtagaac  | atcaaggaga | 900  |
| ccacgaaaga | ttgaggacca  | tatcatcagg | cttcagttac  | gaaaacttcc  | gaagcaatta | 960  |
| ggtttattac | acatggaaact | tcgtagtcat | gcttttacgt  | ctgcaactac  | ttgcaggatt | 1020 |
| taatcccacg | atcagtgtac  | atagatatcc | ttacctttcg  | aaagacaatt  | ttgggggttc | 1080 |
| gggtgattac | taatattatt  | attctcaagt | gtagagaaaat | ttgggttttta | gtaataaata | 1140 |
| tttaagaacc | tgttgatttt  |            |             |             |            |      |

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..319
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Phe | Leu | Gly | Asn | Arg | Ile | Ala | Ser | Thr | Asp | Ile | Ser | Pro | Met | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Leu | Thr | Val | Arg | Arg | Val | Ser | Arg | Glu | Asp | Ile | Gln | Leu | Val | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Leu | Ile | Glu | Arg | Cys | Leu | Gln | Leu | Tyr | Met | Asn | Gln | Lys | Glu | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Asp | Thr | Leu | Leu | Glu | Gln | Ala | Lys | Ile | Glu | Pro | Gly | Phe | Thr | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Val | Trp | Gln | Lys | Leu | Glu | Glu | Glu | Asn | Arg | Glu | Phe | Phe | Lys | Ala |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Tyr | Tyr | Leu | Arg | Leu | Met | Val | Lys | His | Gln | Ile | Met | Glu | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |
| Leu | Leu | Glu | Gln | Gln | Ile | Asn | His | Met | Arg | Gln | Met | His | Pro |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |
| Gly | Ala | Ser | Val | Arg | Asn | Arg | Asn | Gly | Ser | His | Val | Pro | Pro |
|     |     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |
| Gln | Gln | Gln | Leu | Leu | Tyr | Glu | Arg | Lys | Glu | Pro | Asp | Gln | Ser |
|     |     |     |     |     |     |     |     |     |     |     |     |     | 140 |
| Asn | Leu | Ser | Ser | Pro | Tyr | Leu | Asn | Gly | Gly | Ser | Ala | Ile | Asn |
|     |     |     |     |     |     |     |     |     |     |     |     |     | 160 |
| Ile | Pro | Ser | Tyr | Val | Asp | Phe | Ser | Ser | His | Ser | Arg | Arg | Val |
|     |     |     |     |     |     |     |     |     |     |     |     |     | 175 |
| Ser | Pro | Asn | Ser | Leu | Ser | Leu | Gln | Ala | Thr | Asn | Met | Pro | Leu |
|     |     |     |     |     |     |     |     |     |     |     |     |     | 190 |
| Gly | Met | Ile | Lys | Ser | Glu | Thr | Ala | Tyr | Gln | Asn | Cys | Ala | Pro |
|     |     |     |     |     |     |     |     |     |     |     |     |     | 205 |
| Tyr | Gly | Gly | Glu | Ala | Gln | Ser | Thr | Val | Gly | Asp | Val | Thr | Ile |
|     |     |     |     |     |     |     |     |     |     |     |     |     | 220 |
| Phe | Ser | Asn | Asp | Ser | Ser | Asn | Gln | Ser | Leu | Asn | Asp | Pro | Leu |
|     |     |     |     |     |     |     |     |     |     |     |     |     | 240 |
| Pro | Asp | Ala | Pro | Thr | Phe | Gly | Ser | Leu | Gly | Gln | Ile | Pro | Gln |
|     |     |     |     |     |     |     |     |     |     |     |     |     | 255 |
| Ser | Leu | Ser | Asp | Leu | Thr | Ala | Asp | Phe | Ser | Gln | Ser | Ser | Asp |
|     |     |     |     |     |     |     |     |     |     |     |     |     | 270 |
| Glu | Ser | Tyr | Glu | Gly | Ser | Pro | Phe | Leu | Leu | Ala | Asp | Ala | Glu |
|     |     |     |     |     |     |     |     |     |     |     |     |     | 285 |
| Leu | Asp | Ser | Ser | Glu | Arg | Val | Glu | His | Gln | Gly | Asp | His | Glu |
|     |     |     |     |     |     |     |     |     |     |     |     |     | 300 |
| Arg | Thr | Ile | Ser | Ser | Gly | Phe | Ser | Tyr | Glu | Asn | Phe | Arg | Ser |
|     |     |     |     |     |     |     |     |     |     |     |     |     | 315 |

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..305

(D) OTHER INFORMATION: / Ceres Seq. ID 1481849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ser | Leu | Thr | Val | Arg | Arg | Val | Ser | Arg | Glu | Asp | Ile | Gln | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Gln | Asn | Leu | Ile | Glu | Arg | Cys | Leu | Gln | Leu | Tyr | Met | Asn | Gln | Lys |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Val | Val | Asp | Thr | Leu | Leu | Glu | Gln | Ala | Lys | Ile | Glu | Pro | Gly | Phe |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Thr | Glu | Leu | Val | Trp | Gln | Lys | Leu | Glu | Glu | Glu | Asn | Arg | Glu | Phe | Phe |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Lys | Ala | Tyr | Tyr | Leu | Arg | Leu | Met | Val | Lys | His | Gln | Ile | Met | Glu | Tyr |
|     |     |     |     | 65  |     |     |     | 70  |     |     | 75  |     |     | 80  |     |
| Asn | Glu | Leu | Leu | Glu | Gln | Gln | Ile | Asn | His | Met | Arg | Gln | Met | His | Pro |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Thr | Ala | Gly | Ala | Ser | Val | Arg | Asn | Arg | Asn | Gly | Ser | His | Val | Pro | Pro |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Met | Asn | Gln | Gln | Leu | Leu | Tyr | Glu | Arg | Lys | Glu | Pro | Asp | Gln | Ser |     |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |

Ser Pro Asn Leu Ser Ser Pro Tyr Leu Asn Gly Gly Ser Ala Ile Asn  
130 135 140  
Thr Asn Ile Pro Ser Tyr Val Asp Phe Ser Ser His Ser Arg Arg Val  
145 150 155 160  
Asp Pro Ser Pro Asn Ser Leu Ser Leu Gln Ala Thr Asn Met Pro Leu  
165 170 175  
Met Gln Gly Met Ile Lys Ser Glu Thr Ala Tyr Gln Asn Cys Ala Pro  
180 185 190  
Tyr Met Tyr Gly Gly Glu Ala Gln Ser Thr Val Gly Asp Val Thr Ile  
195 200 205  
Ala Ser Phe Ser Asn Asp Ser Ser Asn Gln Ser Leu Asn Asp Pro Leu  
210 215 220  
Val Asp Pro Asp Ala Pro Thr Phe Gly Ser Leu Gly Gln Ile Pro Gln  
225 230 235 240  
Asn Phe Ser Leu Ser Asp Leu Thr Ala Asp Phe Ser Gln Ser Ser Asp  
245 250 255  
Ile Leu Glu Ser Tyr Glu Gly Ser Pro Phe Leu Leu Ala Asp Ala Glu  
260 265 270  
Asn Phe Leu Asp Ser Ser Glu Arg Val Glu His Gln Gly Asp His Glu  
275 280 285  
Arg Leu Arg Thr Ile Ser Ser Gly Phe Ser Tyr Glu Asn Phe Arg Ser  
290 295 300

Asn  
305

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 277 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..277

(D) OTHER INFORMATION: / Ceres Seq. ID 1481850

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Met Asn Gln Lys Glu Val Val Asp Thr Leu Leu Glu Gln Ala Lys Ile  
1 5 10 15  
Glu Pro Gly Phe Thr Glu Leu Val Trp Gln Lys Leu Glu Glu Glu Asn  
20 25 30  
Arg Glu Phe Phe Lys Ala Tyr Tyr Leu Arg Leu Met Val Lys His Gln  
35 40 45  
Ile Met Glu Tyr Asn Glu Leu Leu Glu Gln Gln Ile Asn His Met Arg  
50 55 60  
Gln Met His Pro Thr Ala Gly Ala Ser Val Arg Asn Arg Asn Gly Ser  
65 70 75 80  
His Val Pro Pro Met Asn Gln Gln Gln Leu Leu Tyr Glu Arg Lys Glu  
85 90 95  
Pro Asp Gln Ser Ser Pro Asn Leu Ser Ser Pro Tyr Leu Asn Gly Gly  
100 105 110  
Ser Ala Ile Asn Thr Asn Ile Pro Ser Tyr Val Asp Phe Ser Ser His  
115 120 125  
Ser Arg Arg Val Asp Pro Ser Pro Asn Ser Leu Ser Leu Gln Ala Thr  
130 135 140  
Asn Met Pro Leu Met Gln Gly Met Ile Lys Ser Glu Thr Ala Tyr Gln  
145 150 155 160  
Asn Cys Ala Pro Tyr Met Tyr Gly Gly Glu Ala Gln Ser Thr Val Gly  
165 170 175  
Asp Val Thr Ile Ala Ser Phe Ser Asn Asp Ser Ser Asn Gln Ser Leu

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 180 |     | 185 |     | 190 |     |     |     |     |     |     |     |     |     |     |
| Asn | Asp | Pro | Leu | Val | Asp | Pro | Asp | Ala | Pro | Thr | Phe | Gly | Ser | Leu | Gly |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gln | Ile | Pro | Gln | Asn | Phe | Ser | Leu | Ser | Asp | Leu | Thr | Ala | Asp | Phe | Ser |
|     | 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Gln | Ser | Ser | Asp | Ile | Leu | Glu | Ser | Tyr | Glu | Gly | Ser | Pro | Phe | Leu | Leu |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ala | Asp | Ala | Glu | Asn | Phe | Leu | Asp | Ser | Ser | Glu | Arg | Val | Glu | His | Gln |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Asp | His | Glu | Arg | Leu | Arg | Thr | Ile | Ser | Ser | Gly | Phe | Ser | Tyr | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Asn | Phe | Arg | Ser | Asn |     |     |     |     |     |     |     |     |     |     |     |
|     | 275 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..806
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| cagcttaaca | cttgatgagg  | ttcaaaatca | cttggggagt | tctggtaaag | ctctgggaag | 60  |
| catgaacctt | gatgagcttt  | tgaagagtgt | ctgttctgtt | gaagctaata | agccatcgtc | 120 |
| tatggctgtc | aatgggtggag | cagctgctca | ggagggtcct | tctcgccagg | ggagtttgac | 180 |
| tttgccctcg | gatctcagca  | aaaagactgt | tgatgaggtt | tggaaagaca | ttcagcagaa | 240 |
| taagaatgga | ggtagtgtc   | atgagaggag | ggataagcag | cctacacttg | gggaaatgac | 300 |
| gcttgaagac | ctgttggtga  | aagcaggagt | ggtcactgag | actatccctg | gttcgaacca | 360 |
| tgatggtoct | gttgggtggtg | gtagtgtctg | ttcaggtgct | ggtttagggc | aaaacattac | 420 |
| tcaagttggc | ccatggattc  | aatatcatca | gctcccatca | atgccacagc | ctcaagcatt | 480 |
| tatgccctat | ccggtttcag  | atatgcaagc | aatggtgtct | cagtcttctt | tgatgggtgg | 540 |
| tttgtcagat | acacaaactc  | ctggaaggaa | gagggtagct | tcaggagaag | ttgtagagaa | 600 |
| gactgtgaca | ccattgcttg  | catagctgca | acaggtaaa  | gtccactcaa | caattgggct | 660 |
| actcacctca | gtgatccact  | ccacaccacc | atcatcgata | ccttctcttc | atcttaaaat | 720 |
| cattatcatg | tgagattcta  | tttgtaactt | atgtaaaaac | agagctatga | tgatactgaa | 780 |
| tcgactttgg | gcttttgctt  | gtttgg     |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..207
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Thr | Leu | Asp | Glu | Val | Gln | Asn | His | Leu | Gly | Ser | Ser | Gly | Lys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Leu | Gly | Ser | Met | Asn | Leu | Asp | Glu | Leu | Leu | Lys | Ser | Val | Cys | Ser |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Val | Glu | Ala | Asn | Gln | Pro | Ser | Ser | Met | Ala | Val | Asn | Gly | Gly | Ala | Ala |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ala | Gln | Glu | Gly | Leu | Ser | Arg | Gln | Gly | Ser | Leu | Thr | Leu | Pro | Arg | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

Leu Ser Lys Lys Thr Val Asp Glu Val Trp Lys Asp Ile Gln Gln Asn  
65 70 75 80  
Lys Asn Gly Gly Ser Ala His Glu Arg Arg Asp Lys Gln Pro Thr Leu  
85 90 95  
Gly Glu Met Thr Leu Glu Asp Leu Leu Leu Lys Ala Gly Val Val Thr  
100 105 110  
Glu Thr Ile Pro Gly Ser Asn His Asp Gly Pro Val Gly Gly Ser  
115 120 125  
Ala Gly Ser Gly Ala Gly Leu Gly Gln Asn Ile Thr Gln Val Gly Pro  
130 135 140  
Trp Ile Gln Tyr His Gln Leu Pro Ser Met Pro Gln Pro Gln Ala Phe  
145 150 155 160  
Met Pro Tyr Pro Val Ser Asp Met Gln Ala Met Val Ser Gln Ser Ser  
165 170 175  
Leu Met Gly Gly Leu Ser Asp Thr Gln Thr Pro Gly Arg Lys Arg Val  
180 185 190  
Ala Ser Gly Glu Val Val Glu Lys Thr Val Thr Pro Leu Leu Ala  
195 200 205

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..187
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Met Asn Leu Asp Glu Leu Leu Lys Ser Val Cys Ser Val Glu Ala Asn  
1 5 10 15  
Gln Pro Ser Ser Met Ala Val Asn Gly Gly Ala Ala Ala Gln Glu Gly  
20 25 30  
Leu Ser Arg Gln Gly Ser Leu Thr Leu Pro Arg Asp Leu Ser Lys Lys  
35 40 45  
Thr Val Asp Glu Val Trp Lys Asp Ile Gln Gln Asn Lys Asn Gly Gly  
50 55 60  
Ser Ala His Glu Arg Arg Asp Lys Gln Pro Thr Leu Gly Glu Met Thr  
65 70 75 80  
Leu Glu Asp Leu Leu Lys Ala Gly Val Val Thr Glu Thr Ile Pro  
85 90 95  
Gly Ser Asn His Asp Gly Pro Val Gly Gly Gly Ser Ala Gly Ser Gly  
100 105 110  
Ala Gly Leu Gly Gln Asn Ile Thr Gln Val Gly Pro Trp Ile Gln Tyr  
115 120 125  
His Gln Leu Pro Ser Met Pro Gln Pro Gln Ala Phe Met Pro Tyr Pro  
130 135 140  
Val Ser Asp Met Gln Ala Met Val Ser Gln Ser Ser Leu Met Gly Gly  
145 150 155 160  
Leu Ser Asp Thr Gln Thr Pro Gly Arg Lys Arg Val Ala Ser Gly Glu  
165 170 175  
Val Val Glu Lys Thr Val Thr Pro Leu Leu Ala  
180 185

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..167  
(D) OTHER INFORMATION: / Ceres Seq. ID 1481854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

```
Met Ala Val Asn Gly Gly Ala Ala Ala Gln Glu Gly Leu Ser Arg Gln
1 5 10 15
Gly Ser Leu Thr Leu Pro Arg Asp Leu Ser Lys Lys Thr Val Asp Glu
20 25 30
Val Trp Lys Asp Ile Gln Gln Asn Lys Asn Gly Gly Ser Ala His Glu
35 40 45
Arg Arg Asp Lys Gln Pro Thr Leu Gly Glu Met Thr Leu Glu Asp Leu
50 55 60
Leu Leu Lys Ala Gly Val Val Thr Glu Thr Ile Pro Gly Ser Asn His
65 70 75 80
Asp Gly Pro Val Gly Gly Gly Ser Ala Gly Ser Gly Ala Gly Leu Gly
85 90 95
Gln Asn Ile Thr Gln Val Gly Pro Trp Ile Gln Tyr His Gln Leu Pro
100 105 110
Ser Met Pro Gln Pro Gln Ala Phe Met Pro Tyr Pro Val Ser Asp Met
115 120 125
Gln Ala Met Val Ser Gln Ser Ser Leu Met Gly Gly Leu Ser Asp Thr
130 135 140
Gln Thr Pro Gly Arg Lys Arg Val Ala Ser Gly Glu Val Val Glu Lys
145 150 155 160
Thr Val Thr Pro Leu Leu Ala
165
```

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 391 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..391  
(D) OTHER INFORMATION: / Ceres Seq. ID 1481859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

```
acatatgctg tccgtcacccg cgcgcgcctc ctgccccttc ttcacccttt cctcccggac 60
ccggcgtctc cgtgcccgtg cgtcccttct ccggcctgcg gtctcctcca ccggccaccg 120
ctgcctcgca attgggcaag gcaatcagac cgctcccatc aaccgccctg accgcgcgag 180
gaagatcaaa cgcggaggcc gtccgtccct cccgcgttat cgtgatgcca ggccctgcgcg 240
cagccgagca ggacgcgcgtc tcgctgggtgc ggcgcgtcgc ccgsgctctc aaccgccgct 300
tcaccgacat cgtcgcactg ctcttcagcc acaagggcgc tggatcgctc ggcgcmgtcg 360
cggggttcgc matcgccgtc gtgttcgcgt g
```

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..130  
(D) OTHER INFORMATION: / Ceres Seq. ID 1481860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```
His Met Leu Ser Val Thr Ala Arg Ala Ser Leu Pro Phe Phe Thr Leu
1 5 10 15
Ser Ser Arg Thr Arg Arg Leu Arg Ala Arg Ala Xaa Leu Leu Arg Pro
 20 25 30
Ala Val Ser Ser Thr Gly His Arg Cys Leu Ala Ile Gly Gln Gly Asn
 35 40 45
Gln Thr Ala Pro Ile Asn Arg Pro Asp Arg Ala Arg Lys Ile Lys Arg
 50 55 60
Gly Gly Arg Pro Ser Leu Pro Arg Tyr Arg Asp Ala Arg Pro Arg Arg
65 70 75 80
Ser Arg Ala Gly Arg Arg Leu Ala Gly Ala Ala Arg Arg Pro Xaa Ser
 85 90 95
Gln Pro Pro Leu His Arg His Arg Arg Thr Ala Leu Gln Pro Gln Gly
 100 105 110
Arg Trp Ile Ala Arg Arg Xaa Arg Gly Val Arg Xaa Arg Arg Arg Val
 115 120 125
Arg Val
 130
```

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```
Ile Cys Cys Pro Ser Pro Arg Ala Pro Pro Cys Pro Ser Ser Pro Phe
1 5 10 15
Pro Pro Gly Pro Gly Val Ser Val Pro Val Arg Xaa Phe Ser Gly Leu
 20 25 30
Arg Ser Pro Pro Pro Ala Thr Ala Ala Ser Gln Leu Gly Lys Ala Ile
 35 40 45
Arg Pro Leu Pro Ser Thr Ala Leu Thr Ala Arg Gly Arg Ser Asn Ala
 50 55 60
Glu Ala Val Arg Pro Ser Arg Val Ile Val Met Pro Gly Leu Ala Ala
65 70 75 80
Ala Glu Gln Asp Ala Val Ser Leu Val Arg Arg Val Ala Xaa Ala Leu
 85 90 95
Asn Arg Arg Phe Thr Asp Ile Val Ala Leu Leu Phe Ser His Lys Gly
 100 105 110
Ala Gly Ser Leu Gly Xaa Val Ala Gly Phe Xaa Ile Ala Val Val Phe
 115 120 125
Ala
```

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1481862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

```
Met Leu Ser Val Thr Ala Arg Ala Ser Leu Pro Phe Phe Thr Leu Ser
1 5 10 15
Ser Arg Thr Arg Arg Leu Arg Ala Arg Ala Xaa Leu Leu Arg Pro Ala
 20 25 30
Val Ser Ser Thr Gly His Arg Cys Leu Ala Ile Gly Gln Gly Asn Gln
 35 40 45
Thr Ala Pro Ile Asn Arg Pro Asp Arg Ala Arg Lys Ile Lys Arg Gly
 50 55 60
Gly Arg Pro Ser Leu Pro Arg Tyr Arg Asp Ala Arg Pro Arg Arg Ser
 65 70 75 80
Arg Ala Gly Arg Arg Leu Ala Gly Ala Ala Arg Arg Pro Xaa Ser Gln
 85 90 95
Pro Pro Leu His Arg His Arg Arg Thr Ala Leu Gln Pro Gln Gly Arg
 100 105 110
Trp Ile Ala Arg Arg Xaa Arg Gly Val Arg Xaa Arg Arg Val Arg
 115 120 125
Val
```

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..589
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

```
agcagccgct cccgactttt accttcctac ctggtgctgt agcatccgcc gcctcccgca 60
gaacccgaag atggcgctcgt cggcgtcgac cctcgaaatc gaggcccgcg acgtgggttaa 120
gatagtgtg cagttctgca aggagaattc gctgcagcag acgttccaga cgctgcaaaa 180
cgagtgccag gtctccctca acactgttga cagcatcgac accttcattg ccgacatcaa 240
cgccgggcgt tgggatgctg tgcttcccca ggctgcacag ctcaagctgc cagcaagaa 300
gctcaggagc ctctatgagc agattgtgtt ggagatggct gagctccgtg agcttgacac 360
ggcccgctgcc atcctccgcc agacgcaggt catgggtgtt atgaagcagg agcagcctga 420
rcggtacctc cgccttgagc acctccttgt ccgcacatac ttgacccca atgaggccta 480
ccaagaatcb accaaggaga agcggcgagc actgattgct caagctgttg ctttcagaag 540
tctcagtagt acsgccatct cgtcttatgg cactgattgg tcaggcttg
```

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

```
Ala Ala Ala Pro Asp Phe Tyr Leu Pro Thr Trp Cys Cys Ser Ile Arg
1 5 10 15
Arg Leu Pro Gln Asn Pro Lys Met Ala Ser Ser Ala Ser Thr Leu Glu
 20 25 30
Ile Glu Ala Arg Asp Val Val Lys Ile Val Leu Gln Phe Cys Lys Glu
```



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 35                                                              | 40  | 45  |
| Asn Ser Leu Gln Gln Thr Phe Gln Thr Leu Gln Asn Glu Cys Gln Val |     |     |
| 50                                                              | 55  | 60  |
| Ser Leu Asn Thr Val Asp Ser Ile Asp Thr Phe Ile Ala Asp Ile Asn |     |     |
| 65                                                              | 70  | 75  |
| Ala Gly Arg Trp Asp Ala Val Leu Pro Gln Val Ala Gln Leu Lys Leu |     |     |
| 85                                                              | 90  | 95  |
| Pro Arg Lys Lys Leu Glu Asp Leu Tyr Glu Gln Ile Val Leu Glu Met |     |     |
| 100                                                             | 105 | 110 |
| Ala Glu Leu Arg Glu Leu Asp Thr Ala Arg Ala Ile Leu Arg Gln Thr |     |     |
| 115                                                             | 120 | 125 |
| Gln Val Met Gly Val Met Lys Gln Glu Gln Pro Xaa Arg Tyr Leu Arg |     |     |
| 130                                                             | 135 | 140 |
| Leu Glu His Leu Leu Val Arg Thr Tyr Phe Asp Pro Asn Glu Ala Tyr |     |     |
| 145                                                             | 150 | 155 |
| Gln Glu Xaa Thr Lys Glu Lys Arg Arg Ala Leu Ile Ala Gln Ala Val |     |     |
| 165                                                             | 170 | 175 |
| Ala Phe Arg Ser Leu Ser Ser Xaa Ala Ile Ser Ser Tyr Gly Thr Asp |     |     |
| 180                                                             | 185 | 190 |
| Trp Ser Gly Leu                                                 |     |     |
| 195                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1481865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Ala Ser Ser Ala Ser Thr Leu Glu Ile Glu Ala Arg Asp Val Val |     |     |
| 1                                                               | 5   | 10  |
| Lys Ile Val Leu Gln Phe Cys Lys Glu Asn Ser Leu Gln Gln Thr Phe |     |     |
| 20                                                              | 25  | 30  |
| Gln Thr Leu Gln Asn Glu Cys Gln Val Ser Leu Asn Thr Val Asp Ser |     |     |
| 35                                                              | 40  | 45  |
| Ile Asp Thr Phe Ile Ala Asp Ile Asn Ala Gly Arg Trp Asp Ala Val |     |     |
| 50                                                              | 55  | 60  |
| Leu Pro Gln Val Ala Gln Leu Lys Leu Pro Arg Lys Lys Leu Glu Asp |     |     |
| 65                                                              | 70  | 75  |
| Leu Tyr Glu Gln Ile Val Leu Glu Met Ala Glu Leu Arg Glu Leu Asp |     |     |
| 85                                                              | 90  | 95  |
| Thr Ala Arg Ala Ile Leu Arg Gln Thr Gln Val Met Gly Val Met Lys |     |     |
| 100                                                             | 105 | 110 |
| Gln Glu Gln Pro Xaa Arg Tyr Leu Arg Leu Glu His Leu Leu Val Arg |     |     |
| 115                                                             | 120 | 125 |
| Thr Tyr Phe Asp Pro Asn Glu Ala Tyr Gln Glu Xaa Thr Lys Glu Lys |     |     |
| 130                                                             | 135 | 140 |
| Arg Arg Ala Leu Ile Ala Gln Ala Val Ala Phe Arg Ser Leu Ser Ser |     |     |
| 145                                                             | 150 | 155 |
| Xaa Ala Ile Ser Ser Tyr Gly Thr Asp Trp Ser Gly Leu             |     |     |
| 165                                                             | 170 |     |

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 554 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..554
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1481873
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| agaatttgat  | ttgcaaaaac | aaactaagt   | gtggcaaaga | gcgatccaaa | tatgccaaat | 60  |
| tatagtcaaa  | aacaatttgg | tcttcaattg  | cattgatttt | gcacttcttg | tgttgctttt | 120 |
| tgatgtgttg  | gcataaatca | ccaaaaaggg  | ggagattata | aggcaaagt  | gcccttgggc | 180 |
| cattttctaaa | atgttttgg  | gattaagtgc  | ccaacacgtt | tgaataagtt | cttatggggc | 240 |
| aaataaagt   | agaagtga   | atcaaggcac  | aatgtatgtt | tctagactta | gtacatcggt | 300 |
| ttttgaaggc  | taatgtgtt  | tctctaagt   | cttgaaacag | tgataaaa   | gaagaaaagg | 360 |
| attgcaaaag  | agttggctat | gtgcagcaaa  | ctccagttcg | gcttggcaca | ccgaactgtc | 420 |
| cgggtggtgca | ccggactgtc | cgggtgcgcca | rgctggtctc | cggtgaaatg | gccactctcg | 480 |
| ggactcaaca  | acgcgtatgg | ctaaaaatca  | ccggaccgtc | cggtgagtca | tctacgacga | 540 |
| actcattgct  | ctcg       |             |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 44 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..44
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1481874
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Glu | Phe | Asp | Leu | Gln | Lys | Gln | Thr | Lys | Trp | Trp | Gln | Arg | Ala | Ile | Gln |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Ile | Cys | Gln | Ile | Ile | Val | Lys | Asn | Asn | Leu | Val | Phe | Asn | Cys | Ile | Asp |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Phe | Ala | Leu | Leu | Val | Leu | Leu | Phe | Asp | Val | Leu | Ala |     |     |     |     |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..41
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1481875
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Cys | Ser | Lys | Leu | Gln | Phe | Gly | Leu | Ala | His | Arg | Thr | Val | Arg | Trp |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Cys | Thr | Gly | Leu | Ser | Gly | Ala | Pro | Xaa | Trp | Ser | Pro | Val | Lys | Trp | Pro |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Leu | Ser | Gly | Leu | Asn | Asn | Ala | Tyr | Gly |     |     |     |     |     |     |     |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 478 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

(2) INFORMATION FOR SEQ ID NO:224:

(A) LENGTH: 127 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1481886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

(2) INFORMATION FOR SEQ ID NO:225:

(A) LENGTH: 112 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1481887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Xaa | Arg | Leu | Lys | Ile | Gly | Xaa | Gly | Gly | Gly | Pro | Trp | Met | Gln | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ser | Asp | Phe | His | Gly | Arg | Gln | Val | Xaa | Glu | Tyr | Asp | Pro | Asp | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gly | Thr | Asp | Glu | Glu | Arg | Thr | Arg | Trp | Ser | Ser | Phe | Ala | Gly | Arg | Ser |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Gln | Arg | Thr | Ala | Ser | Glu | Glu | Gly | Ile | Ala | Gly | Pro | Pro | Asn | Ala | Tyr |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Ala | Val | Arg | Trp | Thr | Lys | Ile | Cys | Xaa | Cys | Xaa | Ser | Xaa | Cys | Xaa | His |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Gln | Asp | Arg | Xaa | Gly | Trp | Arg | Arg | Gly | Ala | Ala | Asp | Gly | Gly | Glu | Val |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Xaa | Gly | Ile | Ala | Xaa | Ala | Ser | Xaa | Gly | Xaa | His | Gly | Cys | Ser | Pro | Ser |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1481888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Gly | Arg | Phe | Xaa | Ser | Thr | Thr | Arg | Thr | Pro | Ala | Pro | Thr | Arg |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ser | Ala | Gln | Gly | Gly | Ala | Ala | Ser | Pro | Gly | Val | His | Arg | Glu | Pro | Leu |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |
| Pro | Lys | Arg | Glu | Ser | Gln | Asp | Leu | Leu | Met | Arg | Met | Gln | Phe | Ala | Gly |  |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Gln | Lys | Tyr | Xaa | His | Xaa | Asp | Xaa | Pro | Xaa | Ala | Thr | Lys | Ile | Xaa | Glu |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Asp | Gly | Asp | Glu | Val | Pro | Leu | Thr | Glu | Glu | Arg | Leu | Xaa | Glu | Ser | Leu |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Xaa | Arg | Xaa | Leu | Gly | Xaa | Met | Ala | Ala | Leu | Gln | Ala | Glu | Asp | Gly | His |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Trp | Pro | Pro | Gly | Asp | Tyr | Ser | Xaa | Val | Met | Tyr | Leu | Met | Pro | Phe | Trp |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |
| Ile | Phe | Ala | Leu | His | Ile | Thr | Gly | Thr | Val | Asp |     |     |     |     |     |  |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 545 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..545

(D) OTHER INFORMATION: / Ceres Seq. ID 1481893

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| atagccttar | ccggcgcgga | gaagaaatcg | tatcctcgcc | agctcttcac  | caacagattc  | 60  |
| gtctcctcgc | ctccgcccgg | tttcgaccag | aacgcccgcg | ccagcccacc  | agtaattcct  | 120 |
| ccgggcactg | gtctccacct | cctctgggat | caccacccaa | gaaaaggggtg | cgcgggcgcat | 180 |
| aggcgaccac | tgagatttta | ttctctatat | aacatttggc | tgtaagtggg  | ttataatctc  | 240 |
| tataactctt | aaataagtgc | aaatatctca | atgtcaagtg | tttcaaattc  | tattgctgtg  | 300 |
| ggtcttccaa | gctatgggct | atatctagag | acaaggtttc | tcacgcagac  | ctataggaac  | 360 |
| ttcgcacaga | aatcctctta | caagtattcc | agaatccgtg | cagtgcaggg  | aaatggtggg  | 420 |

cgtcgaaggc tgggtgacat aatccgaatc attccagaac tctcaaggga ctattttaaa 480  
agtcgatcga ggcgagctct ttttggtggc atctcgttgc ttggcggctt ttacgttgca 540  
cagac

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1481894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ala | Leu | Xaa | Arg | Arg | Glu | Lys | Lys | Ser | Tyr | Pro | Arg | Gln | Leu | Phe |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Thr | Asn | Arg | Phe | Val | Ser | Ser | Pro | Pro | Gly | Phe | Asp | Gln | Asn | Ala |     |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ala | Ala | Ser | Pro | Pro | Val | Ile | Pro | Pro | Gly | Thr | Gly | Leu | His | Leu | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Trp | Asp | His | His | Pro | Arg | Lys | Gly | Cys | Ala | Ala | His | Arg | Arg | Pro | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Phe | Tyr | Ser | Leu | Tyr | Asn | Ile | Trp | Leu |     |     |     |     |     |     |
| 65  |     |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1481895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Xaa | Pro | Ala | Arg | Glu | Glu | Ile | Val | Ser | Ser | Pro | Ala | Leu | His |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gln | Gln | Ile | Arg | Leu | Leu | Ala | Ser | Ala | Gly | Phe | Arg | Pro | Glu | Arg | Arg |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Arg | Gln | Pro | Thr | Ser | Asn | Ser | Ser | Gly | His | Trp | Ser | Pro | Pro | Pro | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Gly | Ser | Pro | Pro | Lys | Lys | Arg | Val | Arg | Gly | Ala |     |     |     |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1481896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ser | Val | Ser | Asn | Ser | Ile | Ala | Val | Gly | Leu | Pro | Ser | Tyr | Gly |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |

Leu Tyr Leu Glu Thr Arg Phe Leu Thr Gln Thr Tyr Arg Asn Phe Ala  
20 25 30  
Gln Lys Ser Ser Tyr Lys Tyr Ser Arg Ile Arg Ala Val Gln Gly Asn  
35 40 45  
Gly Gly Arg Arg Arg Leu Val Asp Ile Ile Arg Ile Ile Pro Glu Leu  
50 55 60  
Ser Arg Asp Tyr Phe Lys Ser Arg Ser Arg Arg Ala Leu Phe Gly Gly  
65 70 75 80  
Ile Ser Leu Leu Gly Gly Phe Tyr Val Ala Gln  
85 90

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..391
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

|          |             |              |                |                  |            |     |
|----------|-------------|--------------|----------------|------------------|------------|-----|
| tatgtgga | ccatagct    | tat tggggg   | cgaa gggctt    | atga gcgtcatttc  | aaggaatggc | 60  |
| gtcatcag | ca tgggatg  | cgca tgccttg | sca ttcccca    | atata ctaagaattt | caatgaaatt | 120 |
| acatccat | cg aggagg   | cgaa agcgct  | ctctgg gagaaa  | attc aagcacgaca  | aggggtgaat | 180 |
| aagtggcg | gc cagacct  | aga ggaagag  | tat gaagatc    | cagg aaggcaacat  | ctacaacaag | 240 |
| aagacct  | aca ctgacct | gca gcgtca   | aggc ctgatct   | agg gctcctgctg   | gttaaagttg | 300 |
| tcgggatt | tg ttcaga   | actt atctcat | gta gttgtaactc | tgaaaaatatt      | ggcccatctg | 360 |
| gcatacat | ttt tatgta  | ataa catgatt | ctc c          |                  |            |     |

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

Tyr Val Glu Thr Ile Ala Ile Gly Gly Glu Gly Leu Met Ser Val Ile  
1 5 10 15  
Ser Arg Asn Gly Val Ile Ser Met Gly Cys Asp Ala Leu Xaa Phe Pro  
20 25 30  
Asn Thr Lys Asn Phe Asn Glu Ile Thr Ser Ile Glu Glu Ala Lys Ala  
35 40 45  
Leu Trp Glu Lys Ile Gln Ala Arg Gln Gly Val Asn Lys Trp Arg Pro  
50 55 60  
Asp Leu Glu Glu Glu Tyr Glu Asp Gln Glu Gly Asn Ile Tyr Asn Lys  
65 70 75 80  
Lys Thr Tyr Thr Asp Leu Gln Arg Gln Gly Leu Ile  
85 90

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..80  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1481899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Val | Ile | Ser | Arg | Asn | Gly | Val | Ile | Ser | Met | Gly | Cys | Asp | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Xaa | Phe | Pro | Asn | Thr | Lys | Asn | Phe | Asn | Glu | Ile | Thr | Ser | Ile | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Ala | Lys | Ala | Leu | Trp | Glu | Lys | Ile | Gln | Ala | Arg | Gln | Gly | Val | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Trp | Arg | Pro | Asp | Leu | Glu | Glu | Glu | Tyr | Glu | Asp | Gln | Glu | Gly | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ile | Tyr | Asn | Lys | Lys | Thr | Tyr | Thr | Asp | Leu | Gln | Arg | Gln | Gly | Leu | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 69 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..69  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1481900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Cys | Asp | Ala | Leu | Xaa | Phe | Pro | Asn | Thr | Lys | Asn | Phe | Asn | Glu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Thr | Ser | Ile | Glu | Glu | Ala | Lys | Ala | Leu | Trp | Glu | Lys | Ile | Gln | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Gln | Gly | Val | Asn | Lys | Trp | Arg | Pro | Asp | Leu | Glu | Glu | Glu | Tyr | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Gln | Glu | Gly | Asn | Ile | Tyr | Asn | Lys | Lys | Thr | Tyr | Thr | Asp | Leu | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Gln | Gly | Leu | Ile |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:235:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 722 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..722  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1481901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

|            |             |            |             |            |             |     |
|------------|-------------|------------|-------------|------------|-------------|-----|
| aatttattct | caaaccttat  | gagtgagatc | tctcttaatc  | attctctctt | tcttctctcc  | 60  |
| tctgtgatgt | gaggtttcga  | agatcccttc | ctgattccctc | atcaaactca | gatcagtagc  | 120 |
| ggacccaagt | catttccttta | gagagatata | tggcagaggt  | gaaggatcaa | ttagagatta  | 180 |
| agttccggct | taacgatggg  | tctgatatcg | gtcctaaatt  | gtttcctgat | gctactaccg  | 240 |
| ttgctacatt | gaaagaaacc  | gttggtgctc | agtgggccaag | agataaggag | aacggggccaa | 300 |
| agacagtgaa | agatgttaaa  | ctgataagcg | cgggtagaat  | attggagaac | aacaaaacgg  | 360 |
| ttggagattg | caggagtccc  | gtcggcaatt | tctcaggtgc  | tgtcaccaca | atgcatgtta  | 420 |

taattcaaca tcaagttact gaaaaagaaa agaagaagaa gaagcctaaa ggtgatctga 480  
aacagaacaa atgtgtctgt ttatgttttg gagctcgttg ttaacaattg tgcaagacaa 540  
gtagagagag ttaaaaaagc ttgggagatt cacattctgt tcttgagcct tcttcaatac 600  
cttttgcctt tgttccttgt aattcttttt tctgacatga catgacatga ttggcttttt 660  
gatcgcttga gggttggttt ctattgtatt tcggattcgc aacaccgtgg aaattattag 720  
gt

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Met Ala Glu Val Asp Gln Leu Glu Ile Lys Phe Arg Leu Asn Asp  
1 5 10 15  
Gly Ser Asp Ile Gly Pro Lys Leu Phe Pro Asp Ala Thr Thr Val Ala  
20 25 30  
Thr Leu Lys Glu Thr Val Val Ala Gln Trp Pro Arg Asp Lys Glu Asn  
35 40 45  
Gly Pro Lys Thr Val Lys Asp Val Lys Leu Ile Ser Ala Gly Arg Ile  
50 55 60  
Leu Glu Asn Asn Lys Thr Val Gly Asp Cys Arg Ser Pro Val Gly Asn  
65 70 75 80  
Phe Ser Gly Ala Val Thr Thr Met His Val Ile Ile Gln His Gln Val  
85 90 95  
Thr Glu Lys Glu Lys Lys Lys Lys Lys Pro Lys Gly Asp Leu Lys Gln  
100 105 110  
Asn Lys Cys Val Cys Leu Cys Phe Gly Ala Arg Cys  
115 120

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 647 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..647
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

cccccttta ctacacactt cttctttttt cttcagaaag aaagaaagac agagagagag 60  
agagaagatg gtgttaggaa agcgtcatgg atcactgatc aagagaacaa ctagcatgaa 120  
gatgatcaca ctcgatacac ccacgatcta tgacgcattc cagccgtccg atcatctaac 180  
ctttcatcaa caccctcaca atccgatggg ggtgatggct agtaactacg atgatttctt 240  
gaagacttgk agtctctgca atcgaagtct ctgccatcat cgtgacattt acatgtatag 300  
agggaacaac gcatttttga gcttagaattg cagggagaag caaattaagc tggacgagaa 360  
aaaagcgaag accggcttcg taacatcgaa gaaaccaatt cgtatttagt tgatcatcta 420  
tgatctaata tgataacgat agtttttctt tatgagtaaa atgaatatgt tttkcgctwt 480  
cgtgtacaag aatgatgaaa ataaagagag aaaaaatgag actaaatgag tgtagtgatc 540  
atatagtaat gggacttcat aagcatgatt tgatttgttc gtgtgatttg tttctttgtg 600  
atgtgtaata tgtaatgtaa tatcaatggt gatgtatatt caggtgg

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..135
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1481904
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Pro Pro Leu Leu His Thr Ser Ser Phe Phe Arg Lys Lys Glu Arg  
1 5 10 15  
Gln Arg Glu Arg Glu Lys Met Val Leu Gly Lys Arg His Gly Ser Leu  
20 25 30  
Ile Lys Arg Thr Thr Ser Met Lys Met Ile Thr Leu Asp Thr Pro Thr  
35 40 45  
Ile Tyr Asp Ala Ser Gln Pro Ser Asp His Leu Thr Phe His Gln His  
50 55 60  
Pro His Asn Pro Met Val Val Met Ala Ser Asn Tyr Asp Asp Phe Leu  
65 70 75 80  
Lys Thr Xaa Ser Leu Cys Asn Arg Ser Leu Cys His His Arg Asp Ile  
85 90 95  
Tyr Met Tyr Arg Gly Asn Asn Ala Phe Cys Ser Leu Glu Cys Arg Glu  
100 105 110  
Lys Gln Ile Lys Leu Asp Glu Lys Lys Ala Lys Thr Gly Phe Val Thr  
115 120 125  
Ser Lys Lys Pro Ile Arg Ile  
130 135

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..113
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1481905
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

Met Val Leu Gly Lys Arg His Gly Ser Leu Ile Lys Arg Thr Thr Ser  
1 5 10 15  
Met Lys Met Ile Thr Leu Asp Thr Pro Thr Ile Tyr Asp Ala Ser Gln  
20 25 30  
Pro Ser Asp His Leu Thr Phe His Gln His Pro His Asn Pro Met Val  
35 40 45  
Val Met Ala Ser Asn Tyr Asp Asp Phe Leu Lys Thr Xaa Ser Leu Cys  
50 55 60  
Asn Arg Ser Leu Cys His His Arg Asp Ile Tyr Met Tyr Arg Gly Asn  
65 70 75 80  
Asn Ala Phe Cys Ser Leu Glu Cys Arg Glu Lys Gln Ile Lys Leu Asp  
85 90 95  
Glu Lys Lys Ala Lys Thr Gly Phe Val Thr Ser Lys Lys Pro Ile Arg  
100 105 110  
Ile

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 97 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..97  
(D) OTHER INFORMATION: / Ceres Seq. ID 1481906  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:  
Met Lys Met Ile Thr Leu Asp Thr Pro Thr Ile Tyr Asp Ala Ser Gln  
1 5 10 15  
Pro Ser Asp His Leu Thr Phe His Gln His Pro His Asn Pro Met Val  
20 25 30  
Val Met Ala Ser Asn Tyr Asp Asp Phe Leu Lys Thr Xaa Ser Leu Cys  
35 40 45  
Asn Arg Ser Leu Cys His His Arg Asp Ile Tyr Met Tyr Arg Gly Asn  
50 55 60  
Asn Ala Phe Cys Ser Leu Glu Cys Arg Glu Lys Gln Ile Lys Leu Asp  
65 70 75 80  
Glu Lys Lys Ala Lys Thr Gly Phe Val Thr Ser Lys Lys Pro Ile Arg  
85 90 95  
Ile

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..800  
(D) OTHER INFORMATION: / Ceres Seq. ID 1481907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| acttttcatta gtttccaatt taacaaatca aaatcagaag aagaagaaga tgaccagctc | 60  |
| tgatcctcaa tctcacaacg tcttcgtcta cggtagcatt ctagaaccg cgcgcgcgc    | 120 |
| cgtgatcctt gatcgcacag ccgatacagt cccgcgcgtt ctccatggct agtacgctct  | 180 |
| ctcaccctct cgatgatcgt ttattcaatc ggagattaac aaaagattta tgggttttta  | 240 |
| acagtcacag atataaactc aaaggacttc catatccatg tattgtttct tctgattctg  | 300 |
| gaaaagtcaa cggaaagggt ataactggag tgtctgatgc tgagttaaat aatttcgatg  | 360 |
| tgattgaagg taatgattat gagagagtaa ctggtgaagt tgtaagaatg gataattctg  | 420 |
| agaaggtgaa agttgaaact tatgtttggg ttaataaaga tgatcctaga atgtatggag  | 480 |
| aatgggattt cgaggaatgg agagtgggtc acgcggagaa attcgtggag acttttagaa  | 540 |
| aaatgttgga atggaacaag aatccaaatg ggaagagcat ggaggaggct gtaggatcat  | 600 |
| tattatcgtc aggggattaa ttcttgatga gcttggttaa tcttagcaga agagagtaag  | 660 |
| tgagtaagta aagagtgggt tttgaataat gtgttggttg aacttgaaac agagtcttct  | 720 |
| atgtgatttt gtttgtgttg ttatggatat cttgttgga ctttttctga tttcagttgg   | 780 |
| aaacaggtgc gtttgcgggc                                              |     |

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1481908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Met Ala Ser Thr Leu Ser His Pro Leu Asp Asp Arg Leu Phe Asn Arg  
1 5 10 15  
Arg Leu Thr Lys Asp Leu Trp Val Phe Asn Ser His Arg Tyr Lys Leu  
20 25 30  
Lys Gly Leu Pro Tyr Pro Cys Ile Val Ser Ser Asp Ser Gly Lys Val  
35 40 45  
Asn Gly Lys Val Ile Thr Gly Val Ser Asp Ala Glu Leu Asn Asn Phe  
50 55 60  
Asp Val Ile Glu Gly Asn Asp Tyr Glu Arg Val Thr Val Glu Val Val  
65 70 75 80  
Arg Met Asp Asn Ser Glu Lys Val Lys Val Glu Thr Tyr Val Trp Val  
85 90 95  
Asn Lys Asp Asp Pro Arg Met Tyr Gly Glu Trp Asp Phe Glu Glu Trp  
100 105 110  
Arg Val Val His Ala Glu Lys Phe Val Glu Thr Phe Arg Lys Met Leu  
115 120 125  
Glu Trp Asn Lys Asn Pro Asn Gly Lys Ser Met Glu Glu Ala Val Gly  
130 135 140  
Ser Leu Leu Ser Ser Gly Asp  
145 150

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..675

(D) OTHER INFORMATION: / Ceres Seq. ID 1481913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

aactcagtcg tctcaatgcc gtgtaacaac ttcatcgtct ttttcagttc aacaacttca 60  
tcgtcttttt cagttcaacc tccgacatct ctctgtctcca ggtgattgat cccatcgaag 120  
ggtctatgga agagaacaac aacgccggga gcgattccga ctctaattcc gtcgaagatt 180  
cacaagacta ttacgaaccg atctcagccg tcgatttata taactccaac gacgatgaag 240  
aagacagtta tcttccgatac ggtggagatg gtctctctaa cggccattgt atgattccgg 300  
atgcagaggt aggaatctct tctattagta taaacgataa cacagacagc gaagaagaga 360  
cagagacgga gactggaccg gagatccgta gagcgtttga ggaggacgaa cggcggagaa 420  
ggtcgccggt agtggaggag aatgccgtta gggttatgga ggcaatgcga gccatctcat 480  
tccctggaac ggctcctgat tgggcctccg atgttaatga ggatcgttgg attgatcagc 540  
tgcgaaagatt gagaaccact tctcaataag ctttctccaa tctcगतagt tgttttcgtt 600  
taagatcttt ctcaatgttg ttcaatgtga cttcttttaa acattcaata taaaaccag 660  
agaatttcac cactc

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1481914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Met Glu Glu Asn Asn Asn Ala Gly Ser Asp Ser Asp Ser Asn Ser Val

1 5 10 15  
Glu Asp Ser Gln Asp Tyr Tyr Glu Pro Ile Ser Ala Val Asp Leu Tyr  
20 25 30  
Asn Ser Asn Asp Asp Glu Glu Asp Ser Tyr Leu Pro Ile Gly Gly Asp  
35 40 45  
Gly Leu Ser Asn Gly His Cys Met Ile Pro Asp Ala Glu Val Gly Ile  
50 55 60  
Ser Ser Ile Ser Ile Asn Asp Asn Thr Asp Ser Glu Glu Glu Thr Glu  
65 70 75 80  
Thr Glu Thr Gly Pro Glu Ile Arg Arg Ala Phe Glu Glu Asp Glu Arg  
85 90 95  
Arg Arg Arg Ser Pro Leu Val Glu Glu Asn Ala Val Arg Val Met Glu  
100 105 110  
Ala Met Arg Ala Ile Ser Phe Pro Gly Thr Ala Pro Asp Trp Ala Ser  
115 120 125  
Asp Val Asn Glu Asp Arg Trp Ile Asp Gln Leu Arg Arg Leu Arg Thr  
130 135 140  
Thr Ser Gln  
145

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1481915

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

Met Ile Pro Asp Ala Glu Val Gly Ile Ser Ser Ile Ser Ile Asn Asp  
1 5 10 15  
Asn Thr Asp Ser Glu Glu Glu Thr Glu Thr Glu Thr Gly Pro Glu Ile  
20 25 30  
Arg Arg Ala Phe Glu Glu Asp Glu Arg Arg Arg Arg Ser Pro Leu Val  
35 40 45  
Glu Glu Asn Ala Val Arg Val Met Glu Ala Met Arg Ala Ile Ser Phe  
50 55 60  
Pro Gly Thr Ala Pro Asp Trp Ala Ser Asp Val Asn Glu Asp Arg Trp  
65 70 75 80  
Ile Asp Gln Leu Arg Arg Leu Arg Thr Thr Ser Gln  
85 90

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 729 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..729

(D) OTHER INFORMATION: / Ceres Seq. ID 1481916

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

acgatttttta tctgatttga caccaaagta tcttttagcc ttaattcggtt acgttgtaaa 60  
gaaactgata caatcccttc tattcggatt atatagaccc aatatgtaca gatccgcgag 120  
ctggaaccgt gtgacggagg attactcggg gccttggtcc gcaccaaagg gattatggaa 180  
gggcttagac gaagacgagg ccggctccat acgatccac tggccaaaag atgactaaga 240

|            |             |            |             |            |             |     |
|------------|-------------|------------|-------------|------------|-------------|-----|
| aagagaagtc | acgtaccaag  | tttgctgaaa | acgccgttca  | cataatccct | tttgtccttc  | 300 |
| ttgcttgtgc | tctcgtcctt  | tggttcttct | ctaattccaga | tgtagatggt | gggggtgaaag | 360 |
| gggacttcat | tgcggctagg  | attgaaggat | taacgatcga  | aggagacatt | gacaatgaca  | 420 |
| gcgacggamc | tcagaccgga  | ttcttaggag | ccgccacaga  | ggtcggacat | tcaaaaaata  | 480 |
| aactaaaacg | cgaggctaata | aaacgcaatc | ggaggataca  | agcttcaagg | aaagtgatga  | 540 |
| aaggttttta | ttaatcacct  | ttttgtttga | taaagtgtta  | cgagataaac | tttcaaaaacg | 600 |
| aattattctt | ttttttcttt  | ctattttgat | tgcgcatggt  | agttgatcag | gagatgtgtt  | 660 |
| tctttggtta | aacttttata  | tttagttctt | cacattatct  | tcaagatcca | caagaactac  | 720 |
| tttcactct  |             |            |             |            |             |     |

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481917

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Phe | Leu | Ser | Asp | Leu | Thr | Pro | Lys | Tyr | Leu | Leu | Ala | Leu | Ile | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Val | Val | Lys | Lys | Leu | Ile | Gln | Ser | Leu | Leu | Phe | Gly | Leu | Tyr | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Asn | Met | Tyr | Arg | Ser | Ala | Ser | Trp | Asn | Arg | Val | Thr | Glu | Asp | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Val | Pro | Trp | Ser | Ala | Pro | Lys | Gly | Leu | Trp | Lys | Gly | Leu | Asp | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Glu | Ala | Gly | Ser | Ile | Arg | Ser | His | Trp | Pro | Lys | Asp | Asp |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Lys | Lys | Glu | Lys | Ser | Arg | Thr | Lys | Phe | Ala | Glu | Asn | Ala | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Ile | Ile | Pro | Phe | Val | Leu | Leu | Ala | Cys | Ala | Leu | Val | Leu | Trp | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Ser | Asn | Pro | Asp | Val | Asp | Val | Gly | Val | Lys | Gly | Asp | Phe | Ile | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Arg | Ile | Glu | Gly | Leu | Thr | Ile | Glu | Gly | Asp | Ile | Asp | Asn | Asp | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Gly | Xaa | Gln | Thr | Gly | Phe | Leu | Gly | Ala | Ala | Thr | Glu | Val | Gly | His |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Lys | Asn | Lys | Leu | Lys | Arg | Glu | Ala | Asn | Lys | Arg | Asn | Arg | Arg | Ile |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Ala | Ser | Arg | Lys | Val | Met | Lys | Gly | Phe | Tyr |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..674

(D) OTHER INFORMATION: / Ceres Seq. ID 1481919

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| ctgaacgaag | ctctctctct  | gattggccgg | atctgccgga | gagaaaaatg | acgacgagta  | 60  |
| ttcacatcac | agctctcgac  | ggaatcgta  | acgtgaactc | actcttcaca | ctcgccgtat  | 120 |
| tcacgggatt | agcttggaac  | cctaccgata | cagacaacag | cctcgtaacc | gaccctaatt  | 180 |
| gcgtccccac | agctcgatg   | gctgagaatc | tcgtcgctt  | ccatgtgtac | tctttcgcat  | 240 |
| cattcctatt | ctcaagtctc  | atcgctctag | gtctcaaaca | agcaatgagg | ctcaacatag  | 300 |
| cttcttcggt | tcacatctct  | actcgaatcg | atcctgtggt | ttactatgtg | aacaagacgg  | 360 |
| ctcttagatt | tgggatgggt  | acatccgggt | tgggatcggt | ttgtggatgt | gggtttctca  | 420 |
| tgttggtttt | gattaatggt  | gttcagatca | agcttgggac | tttgggctgt | ggtgctagtgt | 480 |
| gtcatactta | tgcagctggt  | gtgccgcttt | gtgattctgg | ttccttctgc | acttttcac   | 540 |
| tatgtttctc | ttatgttata  | tgcttttact | cgttagagac | atgggttttg | attccatggt  | 600 |
| tgatgcaatt | aggggttatgt | ttgtatgatg | atgatatgat | ggaaatgaga | atgattctat  | 660 |
| gytttgatat | gggt        |            |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..224

(D) OTHER INFORMATION: / Ceres Seq. ID 1481920

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Arg | Ser | Ser | Leu | Ser | Asp | Trp | Pro | Asp | Leu | Pro | Glu | Arg | Lys | Met |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Thr | Thr | Ser | Ile | His | Ile | Thr | Ala | Leu | Asp | Gly | Ile | Val | Asn | Val | Asn |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Leu | Phe | Thr | Leu | Ala | Val | Phe | Ile | Gly | Leu | Ala | Trp | Asn | Pro | Thr |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Asp | Pro | Asp | Asn | Ser | Leu | Val | Thr | Asp | Pro | Asn | Cys | Val | Pro | Thr | Ala |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Arg | Met | Ala | Glu | Asn | Leu | Val | Ala | Phe | His | Val | Tyr | Ser | Phe | Ala | Ser |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Phe | Leu | Phe | Ser | Ser | Leu | Ile | Ala | Leu | Gly | Leu | Lys | Gln | Ala | Met | Arg |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Asn | Ile | Ala | Ser | Ser | Phe | His | Ile | Ser | Thr | Arg | Ile | Asp | Pro | Val |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Tyr | Tyr | Val | Asn | Lys | Thr | Ala | Leu | Arg | Phe | Gly | Met | Val | Thr | Ser |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Gly | Leu | Gly | Ser | Val | Cys | Gly | Cys | Gly | Phe | Leu | Met | Leu | Ala | Leu | Ile |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |
| Asn | Val | Val | Gln | Ile | Lys | Leu | Gly | Thr | Leu | Gly | Cys | Gly | Ala | Ser | Gly |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |     |
| His | Thr | Tyr | Ala | Ala | Val | Val | Pro | Leu | Cys | Asp | Ser | Gly | Ser | Phe | Cys |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Thr | Phe | His | Leu | Cys | Phe | Ser | Tyr | Val | Ile | Cys | Phe | Tyr | Ser | Leu | Glu |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Thr | Trp | Phe | Leu | Ile | Pro | Trp | Leu | Met | Gln | Leu | Gly | Leu | Cys | Leu | Tyr |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 195 |     | 200 |     | 205 |     |     |     |     |     |     |     |     |     |
| Asp | Asp | Met | Met | Glu | Met | Arg | Met | Ile | Leu | Xaa | Phe | Asp | Met | Val |
| 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..209

(D) OTHER INFORMATION: / Ceres Seq. ID 1481921

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Thr | Ser | Ile | His | Ile | Thr | Ala | Leu | Asp | Gly | Ile | Val | Asn | Val |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Ser | Leu | Phe | Thr | Leu | Ala | Val | Phe | Ile | Gly | Leu | Ala | Trp | Asn | Pro |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Asp | Pro | Asp | Asn | Ser | Leu | Val | Thr | Asp | Pro | Asn | Cys | Val | Pro | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Arg | Met | Ala | Glu | Asn | Leu | Val | Ala | Phe | His | Val | Tyr | Ser | Phe | Ala |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Phe | Leu | Phe | Ser | Ser | Leu | Ile | Ala | Leu | Gly | Leu | Lys | Gln | Ala | Met |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Leu | Asn | Ile | Ala | Ser | Ser | Phe | His | Ile | Ser | Thr | Arg | Ile | Asp | Pro |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Val | Tyr | Tyr | Val | Asn | Lys | Thr | Ala | Leu | Arg | Phe | Gly | Met | Val | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Gly | Leu | Gly | Ser | Val | Cys | Gly | Cys | Gly | Phe | Leu | Met | Leu | Ala | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Asn | Val | Val | Gln | Ile | Lys | Leu | Gly | Thr | Leu | Gly | Cys | Gly | Ala | Ser |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | His | Thr | Tyr | Ala | Ala | Val | Val | Pro | Leu | Cys | Asp | Ser | Gly | Ser | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Cys | Thr | Phe | His | Leu | Cys | Phe | Ser | Tyr | Val | Ile | Cys | Phe | Tyr | Ser | Leu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Thr | Trp | Phe | Leu | Ile | Pro | Trp | Leu | Met | Gln | Leu | Gly | Leu | Cys | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Tyr | Asp | Asp | Asp | Met | Met | Glu | Met | Arg | Met | Ile | Leu | Xaa | Phe | Asp | Met |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |
| Val |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1481922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Glu | Asn | Leu | Val | Ala | Phe | His | Val | Tyr | Ser | Phe | Ala | Ser | Phe |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |

Leu Phe Ser Ser Leu Ile Ala Leu Gly Leu Lys Gln Ala Met Arg Leu  
20 25 30  
Asn Ile Ala Ser Ser Phe His Ile Ser Thr Arg Ile Asp Pro Val Val  
35 40 45  
Tyr Tyr Val Asn Lys Thr Ala Leu Arg Phe Gly Met Val Thr Ser Gly  
50 55 60  
Leu Gly Ser Val Cys Gly Cys Gly Phe Leu Met Leu Ala Leu Ile Asn  
65 70 75 80  
Val Val Gln Ile Lys Leu Gly Thr Leu Gly Cys Gly Ala Ser Gly His  
85 90 95  
Thr Tyr Ala Ala Val Val Pro Leu Cys Asp Ser Gly Ser Phe Cys Thr  
100 105 110  
Phe His Leu Cys Phe Ser Tyr Val Ile Cys Phe Tyr Ser Leu Glu Thr  
115 120 125  
Trp Phe Leu Ile Pro Trp Leu Met Gln Leu Gly Leu Cys Leu Tyr Asp  
130 135 140  
Asp Asp Met Met Glu Met Arg Met Ile Leu Xaa Phe Asp Met Val  
145 150 155

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..724
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aaaaagaagg atcaagaacc caaaatagag agcccaattt ctcttaaact tgccaaagta  | 60  |
| gctatcaggt ggttcttgat acggaacttc cagatcccaa gcagcagcag aggcctcatc  | 120 |
| accgtcgcct ccaccgagga aatctccggc agcgattctt gacttgatga aacggagctt  | 180 |
| gtgagtggcg agaccgagtg agcttatggc agcgacgctg gtacttgaag ccgttgatgc  | 240 |
| aacggagagt ttgagcgacg gagacgtaga agaagaggtg agagaaggat aggaggcaga  | 300 |
| tgggtgcccc gcaatggcgg cagtgaagac gacctgaggg ttgagagagg gagaagaaga  | 360 |
| ttacggcgag gaagatgaag aagagctgaa atagcttggt ggagcttctt cttctgggtg  | 420 |
| tcaatggctc gtttcttctc taagggtttt tcgaagtggg gctggattat tgagtttagt  | 480 |
| gcttgtagag cagtttcttt ggggatgaaa ggttggttat tctgggtcaat ttcgtcgtcg | 540 |
| tagtccgcca ttgaaggact gagaagagag aaaaagtgtt attgggttaga gagatgggtt | 600 |
| ggggattgtg tgtagygaac atgtgggtgt ggtytcgtat ctctagacaa gtattatcca  | 660 |
| tctcaacggt cttgttctga ttttgatgt tttgtccgta ctcaataaat attttactgg   | 720 |

gagt

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Lys Lys Lys Asp Gln Glu Pro Lys Ile Glu Ser Pro Ile Ser Leu Lys |  |
| 1 5 10 15                                                       |  |
| Leu Ala Lys Val Ala Ile Arg Trp Phe Leu Ile Arg Asn Phe Gln Ile |  |
| 20 25 30                                                        |  |



Pro Ser Ser Ser Arg Gly Leu Ile Thr Val Ala Ser Thr Glu Glu Ile  
35 40 45  
Ser Gly Ser Asp Ser  
50

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

Met Ala Arg Phe Phe Ser Lys Val Phe Ser Lys Trp Ser Trp Ile Ile  
1 5 10 15  
Glu Phe Ser Ala Cys Arg Ala Val Ser Leu Gly Met Lys Gly Trp Leu  
20 25 30  
Phe Trp Ser Ile Ser Ser Ser  
35

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..453
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| gcacgcac    | gacccccc   | tctgcgcacc | cgcaagcyta | ttcgccgcac | ctcctcaggt | 60  |
| gaccgggaag  | atgatgccgt | tgagccaaac | cgacttctcg | ccgtcgcagt | tcacctcctc | 120 |
| ccagaatgcc  | gccgccgact | ccaccacgcc | ttccaagatg | cgcggcgcgt | ccagcaccat | 180 |
| gcctctcacc  | gtgaagcagg | tcgtcgacgc | gcacgagtct | ggcacgggcg | acaagggcgc | 240 |
| tccgttcac   | gtcaatggcg | tcgagatggc | taacgtaccg | ataatcctct | tgttcgtcct | 300 |
| ttggctccgtt | gatatgcaga | tggtctcggc | gttaattcat | ctgccgcggt | tcccttttca | 360 |
| gattcgactt  | gtggggatgg | tcaatgccaa | ggtggagcgg | acgaccgatg | tgaccttcac | 420 |
| gctcgacgat  | ggcaccggcc | gcctcgattt | cat        |            |            |     |

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

His Arg Ile Asp Pro Pro Ile Cys Ala Pro Ala Ser Xaa Phe Ala Ala  
1 5 10 15  
Pro Pro Gln Val Thr Gly Lys Met Met Pro Leu Ser Gln Thr Asp Phe  
20 25 30  
Ser Pro Ser Gln Phe Thr Ser Ser Gln Asn Ala Ala Ala Asp Ser Thr

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 35                                                              | 40  | 45  |
| Thr Pro Ser Lys Met Arg Gly Ala Ser Ser Thr Met Pro Leu Thr Val |     |     |
| 50                                                              | 55  | 60  |
| Lys Gln Val Val Asp Ala His Glu Ser Gly Thr Gly Asp Lys Gly Ala |     |     |
| 65                                                              | 70  | 75  |
| Pro Phe Ile Val Asn Gly Val Glu Met Ala Asn Val Pro Ile Ile Leu |     |     |
| 85                                                              | 90  | 95  |
| Leu Phe Val Leu Trp Ser Val Asp Met Gln Met Phe Ser Ala Leu Ile |     |     |
| 100                                                             | 105 | 110 |
| His Leu Pro Arg Phe Pro Phe Gln Ile Arg Leu Val Gly Met Val Asn |     |     |
| 115                                                             | 120 | 125 |
| Ala Lys Val Glu Arg Thr Thr Asp Val Thr Phe Thr Leu Asp Asp Gly |     |     |
| 130                                                             | 135 | 140 |
| Thr Gly Arg Leu Asp Phe                                         |     |     |
| 145                                                             | 150 |     |

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Met Pro Leu Ser Gln Thr Asp Phe Ser Pro Ser Gln Phe Thr Ser |     |     |
| 1                                                               | 5   | 10  |
| Ser Gln Asn Ala Ala Ala Asp Ser Thr Thr Pro Ser Lys Met Arg Gly |     |     |
| 20                                                              | 25  | 30  |
| Ala Ser Ser Thr Met Pro Leu Thr Val Lys Gln Val Val Asp Ala His |     |     |
| 35                                                              | 40  | 45  |
| Glu Ser Gly Thr Gly Asp Lys Gly Ala Pro Phe Ile Val Asn Gly Val |     |     |
| 50                                                              | 55  | 60  |
| Glu Met Ala Asn Val Pro Ile Ile Leu Leu Phe Val Leu Trp Ser Val |     |     |
| 65                                                              | 70  | 75  |
| Asp Met Gln Met Phe Ser Ala Leu Ile His Leu Pro Arg Phe Pro Phe |     |     |
| 85                                                              | 90  | 95  |
| Gln Ile Arg Leu Val Gly Met Val Asn Ala Lys Val Glu Arg Thr Thr |     |     |
| 100                                                             | 105 | 110 |
| Asp Val Thr Phe Thr Leu Asp Asp Gly Thr Gly Arg Leu Asp Phe     |     |     |
| 115                                                             | 120 | 125 |

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| Met Pro Leu Ser Gln Thr Asp Phe Ser Pro Ser Gln Phe Thr Ser Ser |    |    |
| 1                                                               | 5  | 10 |
| Gln Asn Ala Ala Ala Asp Ser Thr Thr Pro Ser Lys Met Arg Gly Ala |    |    |
| 20                                                              | 25 | 30 |

Ser Ser Thr Met Pro Leu Thr Val Lys Gln Val Val Asp Ala His Glu  
35 40 45  
Ser Gly Thr Gly Asp Lys Gly Ala Pro Phe Ile Val Asn Gly Val Glu  
50 55 60  
Met Ala Asn Val Pro Ile Ile Leu Leu Phe Val Leu Trp Ser Val Asp  
65 70 75 80  
Met Gln Met Phe Ser Ala Leu Ile His Leu Pro Arg Phe Pro Phe Gln  
85 90 95  
Ile Arg Leu Val Gly Met Val Asn Ala Lys Val Glu Arg Thr Thr Asp  
100 105 110  
Val Thr Phe Thr Leu Asp Asp Gly Thr Gly Arg Leu Asp Phe  
115 120 125

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 677 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..677
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

|            |            |             |            |             |             |     |
|------------|------------|-------------|------------|-------------|-------------|-----|
| acattctagt | acaatatagt | ggttggtgctc | ctctattcta | tttccttggt  | gctactagtc  | 60  |
| tgagttgtga | gattagtgtt | gctaacaatt  | tggaagacgc | ggastccttt  | tcacctctag  | 120 |
| caaggttctc | caaatcgctc | gctaaatttt  | acaggcgctc | ccagagccgc  | taattgtcgt  | 180 |
| ggatcttcag | acgtccgcta | cacgccgatt  | cactccctct | cccgcgctag  | ggcggaacct  | 240 |
| tctcccttgc | gtcttcccat | cgcaaggtct  | tgtccatgcc | gacagctagt  | tcccgcacga  | 300 |
| cttcctcgga | ggcggtcagc | accgacgacg  | aggaggctgc | gcggggaagc  | aagggcggac  | 360 |
| gaccctcgcc | gccgcgctgc | tcgtcgtgca  | ggtagtcggc | tacttcttac  | acggtcgccg  | 420 |
| ccggtgttgg | gctctccgac | agtgcgtgca  | tcgatgggtg | agactctctg  | cacagccacg  | 480 |
| ccgatgagct | ctcctctgtt | gtcgtggaca  | tgcttcacgg | ttcctcsctc  | gcggccacaa  | 540 |
| caagcgatgg | tggtggctgg | tcgcgtctag  | gtgctcgatg | aaagggtgtg  | ttgtagttcg  | 600 |
| gcacttttta | ccacaggaaa | gagagagaag  | taaacaatat | gcattgcgaag | tcaataaaaag | 660 |
| tgaaatcgaa | attctttt   |             |            |             |             |     |

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Ile Leu Val Gln Tyr Ser Gly Cys Ala Pro Leu Phe Tyr Phe Leu Val  
1 5 10 15  
Ala Thr Ser Leu Ser Cys Glu Ile Ser Val Ala Asn Asn Leu Glu Asp  
20 25 30  
Ala Xaa Ser Phe Ser Pro Leu Ala Arg Phe Ser Lys Ser Ser Ala Lys  
35 40 45  
Phe Tyr Arg Arg Arg Gln Ser Arg  
50 55

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..39
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1481951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Met Pro Thr Ala Ser Ser Arg Arg Thr Ser Ser Glu Ala Val Ser Thr  
1                   5                   10                   15  
Asp Asp Glu Glu Ala Ala Arg Gly Ser Lys Gly Gly Arg Pro Ser Pro  
                  20                   25                   30  
Pro Arg Cys Ser Ser Cys Arg  
                  35

(2) INFORMATION FOR SEQ ID NO:263:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..38
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1481952

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

Met Val Gln Thr Leu Cys Thr Ala Thr Pro Met Ser Ser Pro Leu Leu  
1                   5                   10                   15  
Ser Trp Thr Cys Phe Thr Val Pro Xaa Ser Arg Pro Gln Gln Ala Met  
                  20                   25                   30  
Val Val Ala Gly Ala Leu  
                  35

(2) INFORMATION FOR SEQ ID NO:264:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 588 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..588
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1481965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| caacttcttg ccattgattc agcagctgca gtgcagctac ttcggagggtc tctgattggt | 60  |
| gatgaattaa caggaaaaga aaagaaagcc ctgcgcagaa ccatgactga cctggcggtca | 120 |
| gttattccca tcggtattct aatgcttctt cctgttacag cggttggtca cgctgccatg  | 180 |
| ctggctggaa ttcagagata tgtaccaggc ctgattcctt ccacatacgg gtccgaaagg  | 240 |
| ttgaacctat tgagacagct tgagaaaatc aaggaactgc aaacaaatga aaccgagagc  | 300 |
| gaagaaggcg tagaggaaat agcattatga gtagaaggaa gcaatataga cttgtacctc  | 360 |
| tattcacttt gttcggtaat tcattgccaa aagctgcgca tagagaatct cgttccatgt  | 420 |
| gtccggtact ccgggtaagc accagtgact gcagtcctga ggagcatctt caggagttcc  | 480 |
| cggttctcga taccgcgaag gatgagcatc ttctctgaac tcggtcagat atgtaattgt  | 540 |
| cagaaactta accttactat gttcatatct catttcttgg attgcttg               |     |

(2) INFORMATION FOR SEQ ID NO:265:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 109 amino acids
  - (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..109  
(D) OTHER INFORMATION: / Ceres Seq. ID 1481966  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:  
Gln Leu Leu Ala Ile Asp Ser Ala Ala Val Gln Leu Leu Arg Arg  
1 5 10 15  
Ser Leu Ile Gly Asp Glu Leu Thr Gly Lys Glu Lys Lys Ala Leu Arg  
20 25 30  
Arg Thr Met Thr Asp Leu Ala Ser Val Ile Pro Ile Gly Ile Leu Met  
35 40 45  
Leu Leu Pro Val Thr Ala Val Gly His Ala Ala Met Leu Ala Gly Ile  
50 55 60  
Gln Arg Tyr Val Pro Gly Leu Ile Pro Ser Thr Tyr Gly Ser Glu Arg  
65 70 75 80  
Leu Asn Leu Leu Arg Gln Leu Glu Lys Ile Lys Glu Leu Gln Thr Asn  
85 90 95  
Glu Thr Glu Ser Glu Glu Gly Val Glu Glu Ile Ala Leu  
100 105

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 75 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..75  
(D) OTHER INFORMATION: / Ceres Seq. ID 1481967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Met Thr Asp Leu Ala Ser Val Ile Pro Ile Gly Ile Leu Met Leu Leu  
1 5 10 15  
Pro Val Thr Ala Val Gly His Ala Ala Met Leu Ala Gly Ile Gln Arg  
20 25 30  
Tyr Val Pro Gly Leu Ile Pro Ser Thr Tyr Gly Ser Glu Arg Leu Asn  
35 40 45  
Leu Leu Arg Gln Leu Glu Lys Ile Lys Glu Leu Gln Thr Asn Glu Thr  
50 55 60  
Glu Ser Glu Glu Gly Val Glu Glu Ile Ala Leu  
65 70 75

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..63  
(D) OTHER INFORMATION: / Ceres Seq. ID 1481968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

Met Ser Arg Arg Lys Gln Tyr Arg Leu Val Pro Leu Phe Thr Leu Phe  
1 5 10 15  
Gly Asn Ser Leu Pro Lys Ala Ala His Arg Glu Ser Arg Ser Met Cys

20 25 30  
Pro Val Leu Arg Val Ser Thr Ser Asp Cys Ser Leu Glu Glu His Leu  
35 40 45  
Gln Glu Phe Pro Val Leu Asp Thr Ala Lys Asp Glu His Leu Ser  
50 55 60

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..498

(D) OTHER INFORMATION: / Ceres Seq. ID 1481973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| accatcacga atcgcgattt ttttttgaga ttacggaagc ttcgcttgat ttgggatttt | 60  |
| tagggttttt ttttccgaa gacgactccg agagaccaac agtgatttga caatgacgct  | 120 |
| acctccaggt ctttactccg gcaccagctc ttttgctctg gtggctcgtg cttcggcttt | 180 |
| tgggttgggt ctgctctatg ggaacatgaa gctcaagatc aaatcgatgt cacagaagaa | 240 |
| ggttgaagcc accgctcatc attaaaccac tcgttctttc tttacaataa gatgccaaaa | 300 |
| gctgggggtg atgtctcccc ggtagtttg atttcttctt tcatgattca tccttttagca | 360 |
| taagaaggaa caaatgtgtt ttgaaaagc atattatacg gttttaagac ctttttggag  | 420 |
| ccataattgc cattggctta aaaccgcagt caagaacatc tttccatttg ttgtcatcca | 480 |
| ataacaccgt tcacattc                                               |     |

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..35

(D) OTHER INFORMATION: / Ceres Seq. ID 1481974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| His His Glu Ser Arg Phe Phe Phe Glu Ile Thr Glu Ala Ser Leu Asp |  |
| 1 5 10 15                                                       |  |
| Leu Gly Phe Leu Gly Phe Ser Phe Ser Glu Asp Asp Ser Glu Arg Pro |  |
| 20 25 30                                                        |  |
| Thr Val Ile                                                     |  |
| 35                                                              |  |

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 1481975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Thr Leu Pro Pro Gly Leu Tyr Ser Gly Thr Ser Ser Leu Ala Leu |  |
| 1 5 10 15                                                       |  |
| Val Ala Arg Ala Ser Ala Phe Gly Leu Gly Leu Val Tyr Gly Asn Met |  |

20 25 30  
Lys Leu Lys Ile Lys Ser Met Ser Gln Lys Lys Val Glu Ala Thr Ala  
35 40 45

His His  
50

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..800
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

|             |             |             |            |            |            |     |
|-------------|-------------|-------------|------------|------------|------------|-----|
| atctatgcct  | acaccaacaa  | gcaacgggtca | tgcctctcgc | gtgcagattc | aagaaccaag | 60  |
| aataatgtct  | cctcttcctc  | cttcttcttc  | tccaatcgcc | ttcaaggaac | aacaaggtag | 120 |
| accacctcca  | acaacacaa   | aaaccatagc  | aggaaaactc | tttagaactc | ttttcaagg  | 180 |
| tcttctcttc  | tcacaactaa  | ccttaatctc  | acttttggtg | atcgttctca | ccattcgcg  | 240 |
| tctcatctca  | gcaagtacac  | accatttcca  | cctcaagaaa | tggtaccctc | ctttactagc | 300 |
| atctgttgct  | gtctcaggaa  | ttgcatcttt  | agcatggcaa | tgcattctta | tctacaatcc | 360 |
| atcaagagca  | gtcaaagcaa  | cgttctggct  | tagtccaata | ctcacctgct | cggtaggaat | 420 |
| cttgcttggt  | ttgattggct  | cagcggtaga  | tgcaggtata | ggtgcagtgt | ttgtcctttt | 480 |
| cgccattact  | cagtcctctc  | atggttgctg  | gattactccg | aggcttgagt | acaccgataa | 540 |
| aattattatca | cttgccacag  | catttccacc  | tgcaagaacc | agagaagtag | tctgcttata | 600 |
| aatcatagtc  | agtgtcggtt  | actctgggtt  | cttggtgact | ggaattggag | gagcaacttc | 660 |
| cactagaaca  | aattcttgata | tcttggttcat | atccgtaatc | ataataagct | tagcatggac | 720 |
| gatgcaagtt  | atcaagaatg  | ttcaacaagt  | tgcgatttca | cgggcgagat | atgtaaactt | 780 |
| tgcatatgga  | gaagatatgg  |             |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ser Met Pro Thr Pro Thr Ser Asn Gly His Ala Ser Arg Val Gln Ile |  |
| 1 5 10 15                                                       |  |
| Gln Glu Pro Arg Ile Met Ser Pro Leu Pro Pro Ser Ser Ser Pro Ile |  |
| 20 25 30                                                        |  |
| Ala Phe Lys Glu Gln Gln Gly Arg Pro Pro Pro Thr Thr Gln Gln Thr |  |
| 35 40 45                                                        |  |
| Ile Ala Gly Lys Leu Phe Arg Thr Leu Phe Lys Gly Leu Leu Phe Ser |  |
| 50 55 60                                                        |  |
| Gln Leu Thr Leu Ile Ser Leu Leu Val Ile Val Leu Thr Ile Arg Gly |  |
| 65 70 75 80                                                     |  |
| Leu Ile Ser Ala Ser Thr His His Phe His Leu Lys Lys Trp Tyr Pro |  |
| 85 90 95                                                        |  |
| Pro Leu Leu Ala Ser Val Ala Val Ser Gly Ile Ala Ser Leu Ala Trp |  |
| 100 105 110                                                     |  |
| Gln Cys Ile Phe Ile Tyr Asn Pro Ser Arg Ala Val Lys Ala Thr Phe |  |
| 115 120 125                                                     |  |

Trp Leu Ser Pro Ile Leu Thr Cys Ser Val Gly Ile Leu Leu Val Leu  
130 135 140  
Ile Gly Ser Ala Val Asp Ala Gly Ile Gly Ala Val Phe Val Leu Phe  
145 150 155 160  
Ala Ile Thr Gln Ser Leu Tyr Gly Cys Trp Ile Thr Pro Arg Leu Glu  
165 170 175  
Tyr Thr Asp Lys Ile Leu Ser Leu Ala Thr Ala Phe Pro Pro Ala Arg  
180 185 190  
Thr Arg Glu Val Val Cys Leu Ser Ile Ile Val Ser Val Val Tyr Ser  
195 200 205  
Gly Phe Leu Val Thr Gly Ile Gly Gly Ala Thr Ser Thr Arg Thr Asn  
210 215 220  
Leu Asp Ile Leu Phe Ile Ser Val Ile Ile Ile Ser Leu Ala Trp Thr  
225 230 235 240  
Met Gln Val Ile Lys Asn Val Gln Gln Val Ala Ile Ser Arg Ala Arg  
245 250 255  
Tyr Val Asn Phe Ala His Gly Glu Asp Met  
260 265

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..265
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Met Pro Thr Pro Thr Ser Asn Gly His Ala Ser Arg Val Gln Ile Gln  
1 5 10 15  
Glu Pro Arg Ile Met Ser Pro Leu Pro Pro Ser Ser Ser Pro Ile Ala  
20 25 30  
Phe Lys Glu Gln Gln Gly Arg Pro Pro Thr Thr Gln Gln Thr Ile  
35 40 45  
Ala Gly Lys Leu Phe Arg Thr Leu Phe Lys Gly Leu Leu Phe Ser Gln  
50 55 60  
Leu Thr Leu Ile Ser Leu Leu Val Ile Val Leu Thr Ile Arg Gly Leu  
65 70 75 80  
Ile Ser Ala Ser Thr His His Phe His Leu Lys Lys Trp Tyr Pro Pro  
85 90 95  
Leu Leu Ala Ser Val Ala Val Ser Gly Ile Ala Ser Leu Ala Trp Gln  
100 105 110  
Cys Ile Phe Ile Tyr Asn Pro Ser Arg Ala Val Lys Ala Thr Phe Trp  
115 120 125  
Leu Ser Pro Ile Leu Thr Cys Ser Val Gly Ile Leu Leu Val Leu Ile  
130 135 140  
Gly Ser Ala Val Asp Ala Gly Ile Gly Ala Val Phe Val Leu Phe Ala  
145 150 155 160  
Ile Thr Gln Ser Leu Tyr Gly Cys Trp Ile Thr Pro Arg Leu Glu Tyr  
165 170 175  
Thr Asp Lys Ile Leu Ser Leu Ala Thr Ala Phe Pro Pro Ala Arg Thr  
180 185 190  
Arg Glu Val Val Cys Leu Ser Ile Ile Val Ser Val Val Tyr Ser Gly  
195 200 205  
Phe Leu Val Thr Gly Ile Gly Gly Ala Thr Ser Thr Arg Thr Asn Leu  
210 215 220  
Asp Ile Leu Phe Ile Ser Val Ile Ile Ile Ser Leu Ala Trp Thr Met



(2) INFORMATION FOR SEO ID NO:274:

(A) LENGTH: 245 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..245

(D) OTHER INFORMATION: / Ceres Seq. ID 1481979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

(2) INFORMATION FOR SEQ ID NO:275:

(A) LENGTH: 711 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..711



65

70

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..750
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

|             |            |             |             |             |            |     |
|-------------|------------|-------------|-------------|-------------|------------|-----|
| aacattacac  | acagttcaag | aaagagatcg  | atgtcgacct  | tggaatctcc  | attagaggct | 60  |
| ctggcggtttg | aatacgctag | cttcgggtgtt | ttcgccgctcg | tcaacaacgt  | ctggacatgg | 120 |
| atcgccgctcg | tgactgccgc | cgtcagcttc  | tggaggatca  | gagtcacaac  | catcggagtc | 180 |
| ggagacggcc  | atgcatgtgt | cttgatagaa  | gaattaaccg  | gttctaaatc  | tgaaaacgaa | 240 |
| tccggtcgtc  | tcgaaccaaa | atcaataacc  | ggtccggtca  | aagaaacggt  | tgacacgagt | 300 |
| aaggaaacgg  | ttacgaaaac | ggagccgtta  | atatgcatg   | acggagtgac  | aaagaggaag | 360 |
| ctgacgatgt  | actacgaggt | agacgttgac  | ggtgacggtg  | ggaggtgtgt  | taacggagat | 420 |
| ttaacggcag  | ttagctacgg | aggaggtttg  | ggtaattgtg  | gcggggattg  | gstgggagaa | 480 |
| atgggatgga  | gtggtgagga | tgagaaatgg  | tgatgacagt  | tggtaccgtt  | acgtggattt | 540 |
| aacggtgatt  | aatggaaatg | tggtaaaggt  | atgggacgac  | aacaaaacac  | tagtaacggc | 600 |
| ggcatgtgtc  | taaattagac | aagtttcata  | tttcggaaa   | tttttaaatac | tagagaaact | 660 |
| ttcttgcttt  | aaagtttttt | tttttttggt  | tgattaagat  | ctgtaatttg  | taaataattt | 720 |
| tcacvrcaag  | agaccaagaa | ggaacgcttg  |             |             |            |     |

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Ile | Thr | His | Ser | Ser | Arg | Lys | Arg | Ser | Met | Ser | Thr | Leu | Glu | Ser |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Pro | Leu | Glu | Ala | Leu | Ala | Phe | Glu | Tyr | Ala | Ser | Phe | Gly | Val | Phe | Ala |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Val | Asn | Asn | Val | Trp | Thr | Trp | Ile | Ala | Val | Val | Thr | Ala | Ala | Val |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Phe | Trp | Arg | Ile | Arg | Val | Thr | Thr | Ile | Gly | Val | Gly | Asp | Gly | His |  |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Ala | Cys | Val | Leu | Ile | Glu | Glu | Leu | Thr | Gly | Ser | Lys | Ser | Glu | Asn | Glu |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Ser | Gly | Arg | Leu | Glu | Pro | Lys | Ser | Ile | Thr | Gly | Pro | Val | Lys | Glu | Thr |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Val | Ala | Arg | Val | Lys | Glu | Thr | Val | Thr | Lys | Thr | Glu | Pro | Leu | Ile | Cys |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Asp | Asp | Gly | Val | Thr | Lys | Arg | Lys | Leu | Thr | Met | Tyr | Tyr | Glu | Val | Asp |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Val | Asp | Val | Asp | Gly | Gly | Arg | Cys | Val | Asn | Gly | Asp | Leu | Thr | Ala | Val |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |  |
| Ser | Tyr | Gly | Gly | Gly | Leu | Gly | Asn | Cys | Gly | Gly | Asp | Trp | Xaa | Gly | Glu |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Met | Gly | Trp | Ser | Gly | Glu | Asp | Glu | Lys | Trp |     |     |     |     |     |     |  |

165170

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1481985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Thr | Leu | Glu | Ser | Pro | Leu | Glu | Ala | Leu | Ala | Phe | Glu | Tyr | Ala |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ser | Phe | Gly | Val | Phe | Ala | Val | Val | Asn | Asn | Val | Trp | Thr | Trp | Ile | Ala |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Val | Thr | Ala | Ala | Val | Ser | Phe | Trp | Arg | Ile | Arg | Val | Thr | Thr | Ile |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Gly | Val | Gly | Asp | Gly | His | Ala | Cys | Val | Leu | Ile | Glu | Glu | Leu | Thr | Gly |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ser | Lys | Ser | Glu | Asn | Glu | Ser | Gly | Arg | Leu | Glu | Pro | Lys | Ser | Ile | Thr |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Gly | Pro | Val | Lys | Glu | Thr | Val | Ala | Arg | Val | Lys | Glu | Thr | Val | Thr | Lys |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Thr | Glu | Pro | Leu | Ile | Cys | Asp | Asp | Gly | Val | Thr | Lys | Arg | Lys | Leu | Thr |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Met | Tyr | Tyr | Glu | Val | Asp | Val | Asp | Val | Asp | Gly | Gly | Arg | Cys | Val | Asn |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Gly | Asp | Leu | Thr | Ala | Val | Ser | Tyr | Gly | Gly | Gly | Leu | Gly | Asn | Cys | Gly |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |  |
| Gly | Asp | Trp | Xaa | Gly | Glu | Met | Gly | Trp | Ser | Gly | Glu | Asp | Glu | Lys | Trp |  |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |  |

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 598 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..598

(D) OTHER INFORMATION: / Ceres Seq. ID 1481986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| gaaaaggagc | ccttcttcaa | aattgggtca | tgtactcatg | cttcttcttc  | ttcttagctt | 60  |
| cctattgcac | cataccgaat | ctactttgcc | tcctgatcat | gaacaaactct | caataaatgg | 120 |
| gaggagaatt | atggcgtatt | acaagcacga | tggtgccata | gcagcaccac  | catcaagaag | 180 |
| tggacgaggt | ggtggtcacg | ggaagaggat | gatgccctac | cataagccaa  | atgctcctat | 240 |
| acaaacacca | ccatcaagaa | gtagacgacg | tgagggtggg | cacaacggga  | gtagacagat | 300 |
| gggtatatat | aggccaaatg | gagacatata | tacaggacca | tcaaatagtg  | gacatgggtg | 360 |
| tggtcacatt | catcaaaatt | catctcctta | gttttggggc | aatttacaaa  | attggaaact | 420 |
| tatctaaaaa | ttcgccaaaa | agattataga | tttgaatgta | atttgtgttt  | catgtgattc | 480 |
| caagtatgga | gtggatatgg | tggtgggcac | attcatcaac | atttcgatct  | ccttagtttt | 540 |
| ataygatatg | aatgtaattg | tattttatgt | tattccaagt | aaggatatat  | aaagtcgc   |     |

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..129
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1481987
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Lys Arg Ser Pro Ser Ser Lys Leu Gly His Val Leu Met Leu Leu Leu  
1 5 10 15  
Leu Leu Ser Phe Leu Leu His His Thr Glu Ser Thr Leu Pro Pro Asp  
20 25 30  
His Glu Gln Leu Ser Ile Asn Gly Arg Arg Ile Met Ala Tyr Tyr Lys  
35 40 45  
His Asp Gly Ala Ile Ala Ala Pro Pro Ser Arg Ser Gly Arg Gly Gly  
50 55 60  
Gly His Gly Lys Arg Met Met Pro Tyr His Lys Pro Asn Ala Pro Ile  
65 70 75 80  
Gln Thr Pro Pro Ser Arg Ser Arg Arg Arg Glu Gly Gly His Asn Gly  
85 90 95  
Ser Arg Gln Met Gly Ile Tyr Arg Pro Asn Gly Asp Ile Tyr Thr Gly  
100 105 110  
Pro Ser Asn Ser Gly His Gly Gly Gly His Ile His Gln Asn Ser Ser  
115 120 125  
Pro

- (2) INFORMATION FOR SEQ ID NO:283:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 117 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..117
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1481988
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Met Leu Leu Leu Leu Leu Ser Phe Leu Leu His His Thr Glu Ser Thr  
1 5 10 15  
Leu Pro Pro Asp His Glu Gln Leu Ser Ile Asn Gly Arg Arg Ile Met  
20 25 30  
Ala Tyr Tyr Lys His Asp Gly Ala Ile Ala Ala Pro Pro Ser Arg Ser  
35 40 45  
Gly Arg Gly Gly Gly His Gly Lys Arg Met Met Pro Tyr His Lys Pro  
50 55 60  
Asn Ala Pro Ile Gln Thr Pro Pro Ser Arg Ser Arg Arg Arg Glu Gly  
65 70 75 80  
Gly His Asn Gly Ser Arg Gln Met Gly Ile Tyr Arg Pro Asn Gly Asp  
85 90 95  
Ile Tyr Thr Gly Pro Ser Asn Ser Gly His Gly Gly Gly His Ile His  
100 105 110  
Gln Asn Ser Ser Pro  
115

- (2) INFORMATION FOR SEQ ID NO:284:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 86 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..86
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1481989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Tyr | Tyr | Lys | His | Asp | Gly | Ala | Ile | Ala | Ala | Pro | Pro | Ser | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Gly | Arg | Gly | Gly | Gly | His | Gly | Lys | Arg | Met | Met | Pro | Tyr | His | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Asn | Ala | Pro | Ile | Gln | Thr | Pro | Pro | Ser | Arg | Ser | Arg | Arg | Arg | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Gly | His | Asn | Gly | Ser | Arg | Gln | Met | Gly | Ile | Tyr | Arg | Pro | Asn | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Ile | Tyr | Thr | Gly | Pro | Ser | Asn | Ser | Gly | His | Gly | Gly | Gly | His | Ile |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| His | Gln | Asn | Ser | Ser | Pro |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:285:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 688 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..688
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1481990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

|             |            |             |            |             |            |     |
|-------------|------------|-------------|------------|-------------|------------|-----|
| gtgggtattac | cgaacttaaa | cctcgctcgtc | gagcttcgaa | actcttttttc | tcagttcacc | 60  |
| tggaaaacga  | tgcgtcgtca | caagcagacg  | ccatgagagc | ttgcaggagt  | ctctggagaa | 120 |
| atttgagat   | ttagatgaac | tccaatctat  | ctgctgatga | taatgataag  | gatttggaat | 180 |
| aactataagg  | gtaaatacag | attcttcctc  | tcaaattgcc | gctcttttctc | gtcaatcaaa | 240 |
| cgaccccaaa  | tcccagaaag | cgaagagact  | agcctctcga | tcacacaacg  | aagattcgac | 300 |
| ccagatttag  | ctcctatcaa | gactagagtt  | tacgtctctc | tcttccatac  | tctctttcgg | 360 |
| ctctatttaa  | gctgtgagag | actctacgga  | gcagcaagga | cgctctctgc  | gatgtgcaat | 420 |
| ttcgggggtg  | ttccggattc | gcgtctatgg  | aacagtctga | ttcatcaatt  | caatgtcaat | 480 |
| ggtttggtac  | acgatcaggt | atcgctgatt  | tacagcaaga | tgatagcttg  | tggagtttct | 540 |
| cccgatgttt  | ttgctctcaa | tgtattgatt  | cattcttttt | gcaaagtggg  | tcggttgagt | 600 |
| tttgcaatta  | gtttacttag | aaatagagta  | atcagcatcg | atactgttac  | ttataacact | 660 |
| gtgatttcgg  | gtttatgtga | acatggct    |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:286:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 177 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..177
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1481991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Met | Ile | Arg | Ile | Trp | Asn | Asn | Tyr | Lys | Gly | Lys | Tyr | Arg | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Phe Leu Ser Asn Cys Arg Ser Phe Ser Ser Ile Lys Arg Pro Gln Ile  
20 25 30  
Pro Glu Ser Glu Glu Thr Ser Leu Ser Ile Thr Gln Arg Arg Phe Asp  
35 40 45  
Pro Asp Leu Ala Pro Ile Lys Thr Arg Val Tyr Val Ser Leu Phe His  
50 55 60  
Thr Leu Phe Arg Leu Tyr Leu Ser Cys Glu Arg Leu Tyr Gly Ala Ala  
65 70 75 80  
Arg Thr Leu Ser Ala Met Cys Thr Phe Gly Val Val Pro Asp Ser Arg  
85 90 95  
Leu Trp Asn Ser Leu Ile His Gln Phe Asn Val Asn Gly Leu Val His  
100 105 110  
Asp Gln Val Ser Leu Ile Tyr Ser Lys Met Ile Ala Cys Gly Val Ser  
115 120 125  
Pro Asp Val Phe Ala Leu Asn Val Leu Ile His Ser Phe Cys Lys Val  
130 135 140  
Gly Arg Leu Ser Phe Ala Ile Ser Leu Leu Arg Asn Arg Val Ile Ser  
145 150 155 160  
Ile Asp Thr Val Thr Tyr Asn Thr Val Ile Ser Gly Leu Cys Glu His  
165 170 175  
Gly

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

Met Ile Arg Ile Trp Asn Asn Tyr Lys Gly Lys Tyr Arg Phe Phe Leu  
1 5 10 15  
Ser Asn Cys Arg Ser Phe Ser Ser Ile Lys Arg Pro Gln Ile Pro Glu  
20 25 30  
Ser Glu Glu Thr Ser Leu Ser Ile Thr Gln Arg Arg Phe Asp Pro Asp  
35 40 45  
Leu Ala Pro Ile Lys Thr Arg Val Tyr Val Ser Leu Phe His Thr Leu  
50 55 60  
Phe Arg Leu Tyr Leu Ser Cys Glu Arg Leu Tyr Gly Ala Ala Arg Thr  
65 70 75 80  
Leu Ser Ala Met Cys Thr Phe Gly Val Val Pro Asp Ser Arg Leu Trp  
85 90 95  
Asn Ser Leu Ile His Gln Phe Asn Val Asn Gly Leu Val His Asp Gln  
100 105 110  
Val Ser Leu Ile Tyr Ser Lys Met Ile Ala Cys Gly Val Ser Pro Asp  
115 120 125  
Val Phe Ala Leu Asn Val Leu Ile His Ser Phe Cys Lys Val Gly Arg  
130 135 140  
Leu Ser Phe Ala Ile Ser Leu Leu Arg Asn Arg Val Ile Ser Ile Asp  
145 150 155 160  
Thr Val Thr Tyr Asn Thr Val Ile Ser Gly Leu Cys Glu His Gly  
165 170 175

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..92  
(D) OTHER INFORMATION: / Ceres Seq. ID 1481993  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:  
Met Cys Thr Phe Gly Val Val Pro Asp Ser Arg Leu Trp Asn Ser Leu  
1 5 10 15  
Ile His Gln Phe Asn Val Asn Gly Leu Val His Asp Gln Val Ser Leu  
20 25 30  
Ile Tyr Ser Lys Met Ile Ala Cys Gly Val Ser Pro Asp Val Phe Ala  
35 40 45  
Leu Asn Val Leu Ile His Ser Phe Cys Lys Val Gly Arg Leu Ser Phe  
50 55 60  
Ala Ile Ser Leu Leu Arg Asn Arg Val Ile Ser Ile Asp Thr Val Thr  
65 70 75 80  
Tyr Asn Thr Val Ile Ser Gly Leu Cys Glu His Gly  
85 90

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..499  
(D) OTHER INFORMATION: / Ceres Seq. ID 1481994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

attgtaactt gtaaccagtgc tcggctaatt tcgacttttg tagatctttt tctgctcttt 60  
ctctctctct ctgctctctc tctctctctc tctctcttgc attatttcta tctccccgcg 120  
cgctgaaaga gaaacgctcga tcggagaacc tttgaaatgt cgactggatt agatatgtct 180  
ctcgacgaca tgatcgccaa gaaccgtaag tctcgtgggtg gagccggccc cgctcgtgga 240  
accgcatccg gatccggacc gggctccgact cgccgcaaca accctaatacg gaaatcaacc 300  
cgatctgctc cataccaatc agccaaggcg ccggagtcca cctgggggtca cgacatgttc 360  
tccgatagat ctgaagatca ccgatcggga cgttcctccg ccggaatcga aactggaacc 420  
aagctctaca tttccaattt ggayttacgg tgatcatgaac gaagacatca aggaactggt 480  
tgctgaagtt ggagaactt

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..161  
(D) OTHER INFORMATION: / Ceres Seq. ID 1481995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

Ile Val Thr Cys Asn Gln Cys Arg Leu Ile Ser Thr Phe Val Asp Leu  
1 5 10 15  
Phe Leu Leu Phe Leu Ser Leu Ser Ala Leu Ser Leu Ser Leu Ser Leu  
20 25 30  
Leu Tyr Tyr Phe Tyr Leu Pro Arg Arg Arg Lys Arg Asn Val Asp Arg



|                         |                         |                 |
|-------------------------|-------------------------|-----------------|
| 35                      | 40                      | 45              |
| Arg Thr Phe Glu Met Ser | Thr Gly Leu Asp Met Ser | Leu Asp Asp Met |
| 50                      | 55                      | 60              |
| Ile Ala Lys Asn Arg Lys | Ser Arg Gly Gly Ala Gly | Pro Ala Arg Gly |
| 65                      | 70                      | 75              |
| Thr Gly Ser Gly Ser Gly | Pro Gly Pro Thr Arg Arg | Asn Asn Pro Asn |
| 85                      | 90                      | 95              |
| Arg Lys Ser Thr Arg Ser | Ala Pro Tyr Gln Ser Ala | Lys Ala Pro Glu |
| 100                     | 105                     | 110             |
| Ser Thr Trp Gly His Asp | Met Phe Ser Asp Arg Ser | Glu Asp His Arg |
| 115                     | 120                     | 125             |
| Ser Gly Arg Ser Ser Ala | Gly Ile Glu Thr Gly Thr | Lys Leu Tyr Ile |
| 130                     | 135                     | 140             |
| Ser Asn Leu Xaa Leu Arg | Cys His Glu Arg Arg His | Gln Gly Thr Val |
| 145                     | 150                     | 155             |
| Cys                     |                         | 160             |

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

|                                                                 |                 |
|-----------------------------------------------------------------|-----------------|
| Met Ser Thr Gly Leu Asp Met Ser Leu Asp Asp Met                 | Ile Ala Lys Asn |
| 1                                                               | 5 10 15         |
| Arg Lys Ser Arg Gly Gly Ala Gly Pro Ala Arg Gly Thr Gly Ser Gly |                 |
| 20                                                              | 25 30           |
| Ser Gly Pro Gly Pro Thr Arg Arg Asn Asn Pro Asn Arg Lys Ser Thr |                 |
| 35                                                              | 40 45           |
| Arg Ser Ala Pro Tyr Gln Ser Ala Lys Ala Pro Glu Ser Thr Trp Gly |                 |
| 50                                                              | 55 60           |
| His Asp Met Phe Ser Asp Arg Ser Glu Asp His Arg Ser Gly Arg Ser |                 |
| 65                                                              | 70 75 80        |
| Ser Ala Gly Ile Glu Thr Gly Thr Lys Leu Tyr Ile Ser Asn Leu Xaa |                 |
| 85                                                              | 90 95           |
| Leu Arg Cys His Glu Arg Arg His Gln Gly Thr Val Cys             |                 |
| 100                                                             | 105             |

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1481997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

|                                                                 |         |
|-----------------------------------------------------------------|---------|
| Met Ser Leu Asp Asp Met Ile Ala Lys Asn Arg Lys Ser Arg Gly Gly |         |
| 1                                                               | 5 10 15 |
| Ala Gly Pro Ala Arg Gly Thr Gly Ser Gly Ser Gly Pro Gly Pro Thr |         |
| 20                                                              | 25 30   |

Arg Arg Asn Asn Pro Asn Arg Lys Ser Thr Arg Ser Ala Pro Tyr Gln  
35 40 45  
Ser Ala Lys Ala Pro Glu Ser Thr Trp Gly His Asp Met Phe Ser Asp  
50 55 60  
Arg Ser Glu Asp His Arg Ser Gly Arg Ser Ser Ala Gly Ile Glu Thr  
65 70 75 80  
Gly Thr Lys Leu Tyr Ile Ser Asn Leu Xaa Leu Arg Cys His Glu Arg  
85 90 95  
Arg His Gln Gly Thr Val Cys  
100

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..851
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| agagagaatc | gcattaacaa | aaaaacaaac | gaatcttttg | agtttaaaac | cctttttcac | 60  |
| ttaccggaga | aatggagaga | tcgacgcccg | aacatgtctc | ctccgcacac | aagcgcataa | 120 |
| gcgtgagctt | cctcgtgtct | ctcatggtag | tttgtgctag | acacgcaagc | agagtttcca | 180 |
| agaagcttaa | acccaagaag | actcggaaag | aaactcatct | tgaagactat | ctcgaaagcc | 240 |
| ctaagtctaa | cggaaacggt | agcgaagacg | gtagaggagg | aggaagggtt | ggatggagtc | 300 |
| cggcaaggac | tttttctcct | atgagggtgc | gtcctaagga | gctctacacg | accttgagca | 360 |
| acaaggcgat | gactatgggt | ggccggaaaa | acaaagctta | cgacgggtgg | ccgacgaaga | 420 |
| agacggcggt | ggagatgggt | atggaggagg | atgaggaaga | gtacggcggt | tggcagaggg | 480 |
| agattttgat | gggaggaaaa | tgtgagccgt | tggattactc | aggcgtgatc | tactacgatt | 540 |
| gtagtgga   | tcagctaaaa | caagtgcctc | caaggtctcc | acgtgccagt | ttggttcccg | 600 |
| agcggccgac | tcgttcttat | gtcgggtcat | tgttaaacc  | gacgggaaag | gaaattttaa | 660 |
| ttttagtttg | agaatttgaa | attttagtag | gagtatttga | ttgttggttg | aggtgtcatc | 720 |
| acgtaagtgg | taaattctct | aggagctttg | ttggtccctt | gtcattagta | gatgcatgac | 780 |
| atgtttttat | gcatattggt | gtgtagttta | tgtatttaag | acgtttggca | attttaaaac | 840 |
| tttagtagtt | t          |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..195
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Arg | Ser | Thr | Pro | Glu | His | Val | Ser | Ser | Ala | His | Lys | Arg | Ile |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Ser | Val | Ser | Phe | Leu | Val | Ser | Leu | Met | Val | Leu | Cys | Ala | Arg | His | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Arg | Val | Ser | Lys | Lys | Leu | Lys | Pro | Lys | Lys | Thr | Arg | Lys | Gln | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| His | Leu | Glu | Asp | Tyr | Leu | Glu | Ser | Pro | Lys | Ser | Asn | Gly | Asn | Gly | Ser |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Glu | Asp | Gly | Arg | Gly | Gly | Gly | Arg | Phe | Gly | Trp | Ser | Pro | Ala | Arg | Thr |
| 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ser | Pro | Met | Arg | Val | Arg | Pro | Lys | Glu | Leu | Tyr | Thr | Thr | Leu | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Lys | Ala | Met | Thr | Met | Val | Gly | Arg | Lys | Asn | Lys | Ala | Tyr | Asp | Gly |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Pro | Thr | Lys | Lys | Thr | Ala | Val | Glu | Met | Val | Met | Glu | Glu | Asp | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Glu | Tyr | Gly | Val | Trp | Gln | Arg | Glu | Ile | Leu | Met | Gly | Gly | Lys | Cys |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Glu | Pro | Leu | Asp | Tyr | Ser | Gly | Val | Ile | Tyr | Tyr | Asp | Cys | Ser | Gly | His |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Leu | Lys | Gln | Val | Pro | Pro | Arg | Ser | Pro | Arg | Ala | Ser | Leu | Val | Pro |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Arg | Pro | Thr | Arg | Ser | Tyr | Val | Gly | Ser | Leu | Leu | Asn | Pro | Thr | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Glu | Ile |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 195 |     |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:295:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1482011

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Leu | Cys | Ala | Arg | His | Ala | Ser | Arg | Val | Ser | Lys | Lys | Leu | Lys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Lys | Lys | Thr | Arg | Lys | Gln | Thr | His | Leu | Glu | Asp | Tyr | Leu | Glu | Ser |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Pro | Lys | Ser | Asn | Gly | Asn | Gly | Ser | Glu | Asp | Gly | Arg | Gly | Gly | Gly | Arg |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Phe | Gly | Trp | Ser | Pro | Ala | Arg | Thr | Phe | Ser | Pro | Met | Arg | Val | Arg | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Lys | Glu | Leu | Tyr | Thr | Thr | Leu | Ser | Asn | Lys | Ala | Met | Thr | Met | Val | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Lys | Asn | Lys | Ala | Tyr | Asp | Gly | Gly | Pro | Thr | Lys | Lys | Thr | Ala | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Met | Val | Met | Glu | Glu | Asp | Glu | Glu | Glu | Tyr | Gly | Val | Trp | Gln | Arg |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Glu | Ile | Leu | Met | Gly | Gly | Lys | Cys | Glu | Pro | Leu | Asp | Tyr | Ser | Gly | Val |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Ile | Tyr | Tyr | Asp | Cys | Ser | Gly | His | Gln | Leu | Lys | Gln | Val | Pro | Pro | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Pro | Arg | Ala | Ser | Leu | Val | Pro | Glu | Arg | Pro | Thr | Arg | Ser | Tyr | Val |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Gly | Ser | Leu | Leu | Asn | Pro | Thr | Gly | Lys | Glu | Ile |     |     |     |     |     |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:296:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1482012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Val | Arg | Pro | Lys | Glu | Leu | Tyr | Thr | Thr | Leu | Ser | Asn | Lys | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Thr | Met | Val | Gly | Arg | Lys | Asn | Lys | Ala | Tyr | Asp | Gly | Gly | Pro | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Lys | Thr | Ala | Val | Glu | Met | Val | Met | Glu | Glu | Asp | Glu | Glu | Glu | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Val | Trp | Gln | Arg | Glu | Ile | Leu | Met | Gly | Gly | Lys | Cys | Glu | Pro | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Tyr | Ser | Gly | Val | Ile | Tyr | Tyr | Asp | Cys | Ser | Gly | His | Gln | Leu | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gln | Val | Pro | Pro | Arg | Ser | Pro | Arg | Ala | Ser | Leu | Val | Pro | Glu | Arg | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Arg | Ser | Tyr | Val | Gly | Ser | Leu | Leu | Asn | Pro | Thr | Gly | Lys | Glu | Ile |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..576

(D) OTHER INFORMATION: / Ceres Seq. ID 1482013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

|          |      |          |     |            |            |            |             |     |
|----------|------|----------|-----|------------|------------|------------|-------------|-----|
| agatttgc | at   | tcgcaggg | ga  | taaggatcaa | aaatggagga | agcaaaggga | cctgtgaagc  | 60  |
| acgtattg | ct   | tgctagt  | ttc | aaagatggg  | g          | ttagtcctga | gaaaatcgaa  | 120 |
| aaggttac | gc   | caatctc  | g   | aatctcatc  | g          | aacctatgaa | agctttccac  | 180 |
| atgtgagc | at   | tgagaat  | ctg | catcaagg   | tt         | acacacacat | ctttgaatcc  | 240 |
| gtaaaga  | aagc | tggtgcag | ag  | tacattg    | ctc        | atcctgctca | cgttaaattc  | 300 |
| tccttggc | ag   | cttggata | aaa | gttttggt   | tta        | ttgactacaa | gcctacctct  | 360 |
| aattatct | tg   | tagcagca | tt  | ttcatcatt  | g          | atctttttct | cgggtatgca  | 420 |
| tgaataaa | agt  | atattcc  | ttt | tgagtttt   | cc         | tgcattgttc | tcatgtttct  | 480 |
| ctctcttt | ttt  | tgttgtt  | tg  | ttgtttc    | ct         | tctgttgat  | tataacttgat | 540 |
| atcatgag | tt   | tattaaga | gt  | gtttgatt   | tc         | agactc     |             |     |

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1482014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Glu | Ala | Lys | Gly | Pro | Val | Lys | His | Val | Leu | Leu | Ala | Ser | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Asp | Gly | Val | Ser | Pro | Glu | Lys | Ile | Glu | Glu | Leu | Ile | Lys | Gly | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Asn | Leu | Val | Asn | Leu | Ile | Glu | Pro | Met | Lys | Ala | Phe | His | Trp | Gly |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |

Lys Asp Val Ser Ile Glu Asn Leu His Gln Gly Tyr Thr His Ile Phe  
50 55 60  
Glu Ser Thr Phe Glu Ser Lys Glu Ala Val Ala Glu Tyr Ile Ala His  
65 70 75 80  
Pro Ala His Val Lys Phe Ala Thr Ile Phe Leu Gly Ser Leu Asp Lys  
85 90 95  
Val Leu Val Ile Asp Tyr Lys Pro Thr Ser Val Ser Leu  
100 105

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

Met Lys Ala Phe His Trp Gly Lys Asp Val Ser Ile Glu Asn Leu His  
1 5 10 15  
Gln Gly Tyr Thr His Ile Phe Glu Ser Thr Phe Glu Ser Lys Glu Ala  
20 25 30  
Val Ala Glu Tyr Ile Ala His Pro Ala His Val Lys Phe Ala Thr Ile  
35 40 45  
Phe Leu Gly Ser Leu Asp Lys Val Leu Val Ile Asp Tyr Lys Pro Thr  
50 55 60  
Ser Val Ser Leu  
65

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..664
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

gattaatttt tgagagagct gtctctcttg acagagattt tggaaggtaa gagagacgat 60  
gacgtatcac gtttttagac gagactatgg cgatggagag tgaattttgc ctttttggaa 120  
ttcccacgac tctctgtatc tttcttttagg cgagactatg gcgataaaga ttgaattttg 180  
cttcgacaat tgaggggtgaa attaacggca aattcaaaat tgcggtttct gacaagtcgt 240  
tccgctggat tcgtcagctt tctcaccatc ggcgaagcga ggttcaccta atcgagatt 300  
tgcgactccc agttggagag taatcgttga ggagaggcaa cgagtgcac gagcatatca 360  
cttctctcgc cattcttcgt acccatcgca agctaggtct cgtcactaag ctcagtgtg 420  
ccgctcaggc tgctatggaa cagcttaaag gtatgataaa cgacatggat cgtgtccaac 480  
tggaatgagg actcttgtgt gttacaccta tcgtcaatgc ccaactgata tgttgtgtct 540  
tataaccata aatttacttt gatccaaaca cttttgagaa gctgtcttca agtgggtcaaa 600  
aggtagcaac tcttttttct tgtgttaattg taatcatctg tgttatgaag tattgccatt 660  
ttcg

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 958 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..958  
(D) OTHER INFORMATION: / Ceres Seq. ID 1482021

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| aaagccctaa | aaatcagaga | ttccattttc | tcttatctct | ctctctctct  | ctttctcttt | 60  |
| ttccgattct | gattctatct | tttcttcacc | aaccacacaa | aacaattcta  | cgtttgatct | 120 |
| cttcttcttt | ctccgtccaa | attaatctct | acgtttaatt | tctcttggtc  | aatcatggga | 180 |
| cacgaaacaa | tgacgccggc | aacaacaacg | ctcgtgttca | cgtaacggaac | tctaaagaga | 240 |
| ggattctcaa | atcatgtcct | gatgcaagat | ctgatccgat | ctgggtgacgc | ttctttcaaa | 300 |
| ggtgtttacc | aaactctaga | caaatatcct | ctcgtctgtg | gaccttaccg  | agtccctttc | 360 |
| ctcctcaaca | aacctggatc | gggctatcac | gtcaccggcg | agctttacgc  | ggtttctcct | 420 |
| cgcggtctct | ctcgtctcga | tgagcttgaa | ggaatcagtc | gcggtcatta  | catccggcaa | 480 |
| ccgatacggt | ctcgcggcgg | cggaggaaga | agaagaagaa | ggagatctgg  | aaacagaggc | 540 |
| gccgtcgtcg | tgcggtggtg | aggcgtatta | cgctcataag | agttatgagg  | aagagctgtg | 600 |
| gaagaggaat | agaggaagat | cattcggcgc | gtacacggaa | aacgaagcgc  | gtggatatgt | 660 |
| gaaacgcaat | gataggcctc | agcatcttag | cttcttggtg | catatccgta  | ttttcgtatc | 720 |
| ttctccatgt | gattgatttt | tatttctttc | gtgggtctct | ccgctcgtcg  | cttttctatg | 780 |
| tttgtttggt | tttttctcgg | gacaaaagaa | acaaaaaaaa | aacacaaaca  | caaactagtt | 840 |
| ttacaacttg | taagggtccc | accagtcctg | ccgtccgtcg | tctccgtatc  | gatttgatta | 900 |
| gagagattgt | tgggtgtaaa | acttatgatt | cccattctaa | ataagtttta  | ggttggtt   |     |

(2) INFORMATION FOR SEQ ID NO:302:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 134 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..134  
(D) OTHER INFORMATION: / Ceres Seq. ID 1482022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | His | Glu | Thr | Met | Thr | Pro | Ala | Thr | Thr | Leu | Val | Phe | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| Tyr | Gly | Thr | Leu | Lys | Arg | Gly | Phe | Ser | Asn | His | Val | Leu | Met | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     | Asp |
| Leu | Ile | Arg | Ser | Gly | Asp | Ala | Ser | Phe | Lys | Gly | Val | Tyr | Gln | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     | Leu |
| Asp | Lys | Tyr | Pro | Leu | Val | Cys | Gly | Pro | Tyr | Arg | Val | Pro | Phe | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     | Leu |
| Asn | Lys | Pro | Gly | Ser | Gly | Tyr | His | Val | Thr | Gly | Glu | Leu | Tyr | Ala |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Ser | Pro | Arg | Gly | Leu | Ser | Arg | Leu | Asp | Glu | Leu | Glu | Gly | Ile | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  | Arg |
| Gly | His | Tyr | Ile | Arg | Gln | Pro | Ile | Arg | Ser | Arg | Gly | Gly | Gly | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Arg | Arg | Arg | Arg | Ser | Gly | Asn | Arg | Gly | Ala | Val | Val | Val | Arg | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Gly | Gly | Val | Leu | Arg | Ser |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:303:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 129 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1482023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

Met Thr Pro Ala Thr Thr Thr Leu Val Phe Thr Tyr Gly Thr Leu Lys  
1 5 10 15  
Arg Gly Phe Ser Asn His Val Leu Met Gln Asp Leu Ile Arg Ser Gly  
20 25 30  
Asp Ala Ser Phe Lys Gly Val Tyr Gln Thr Leu Asp Lys Tyr Pro Leu  
35 40 45  
Val Cys Gly Pro Tyr Arg Val Pro Phe Leu Leu Asn Lys Pro Gly Ser  
50 55 60  
Gly Tyr His Val Thr Gly Glu Leu Tyr Ala Val Ser Pro Arg Gly Leu  
65 70 75 80  
Ser Arg Leu Asp Glu Leu Glu Gly Ile Ser Arg Gly His Tyr Ile Arg  
85 90 95  
Gln Pro Ile Arg Ser Arg Gly Gly Gly Arg Arg Arg Arg Arg Arg  
100 105 110  
Ser Gly Asn Arg Gly Ala Val Val Val Arg Gly Gly Gly Val Leu Arg  
115 120 125  
Ser

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1482024

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Met Gln Asp Leu Ile Arg Ser Gly Asp Ala Ser Phe Lys Gly Val Tyr  
1 5 10 15  
Gln Thr Leu Asp Lys Tyr Pro Leu Val Cys Gly Pro Tyr Arg Val Pro  
20 25 30  
Phe Leu Leu Asn Lys Pro Gly Ser Gly Tyr His Val Thr Gly Glu Leu  
35 40 45  
Tyr Ala Val Ser Pro Arg Gly Leu Ser Arg Leu Asp Glu Leu Glu Gly  
50 55 60  
Ile Ser Arg Gly His Tyr Ile Arg Gln Pro Ile Arg Ser Arg Gly Gly  
65 70 75 80  
Gly Gly Arg Arg Arg Arg Arg Arg Ser Gly Asn Arg Gly Ala Val Val  
85 90 95  
Val Arg Gly Gly Gly Val Leu Arg Ser  
100 105

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 535 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..535

(D) OTHER INFORMATION: / Ceres Seq. ID 1482029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

|                                                                       |     |
|-----------------------------------------------------------------------|-----|
| atcatactct ctcaacttca tctctctctc tctctcaatc tcttaagatc ccacaagtca     | 60  |
| cttttcttct tcttaatcac ctttaatggc gaatttgatc cttaagcaat ctctaatacat    | 120 |
| actcctaatac atatatattcaa caccaatctt gagtttctcaa gctcgaatcc tccgtacata | 180 |
| tgcgccacaca accatgggagc atatggatag tcaggttctc ctacgtgaac tcgggattga   | 240 |
| tctctctaag ttcaaaggtc aagacgagag acgggttttta gtggattccg aaagggtttc    | 300 |
| tccgggggggt cctgatccac aacaccattg actgatcttt accgatatat atatacttta    | 360 |
| ccgaagatcg aagcacacat ataactgtga ctgatccatg caagtcaatt taaatatcgt     | 420 |
| catttacatg cttttcttdt ctttttcata aatcttccct acacttttgt tgtatcaaga     | 480 |
| ttttggtatt ctttwtgacc ttccttatct ttaaacaatca aggttttact chtt          |     |

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..81

(D) OTHER INFORMATION: / Ceres Seq. ID 1482030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asn | Leu | Ile | Leu | Lys | Gln | Ser | Leu | Ile | Ile | Leu | Leu | Ile | Ile |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Tyr | Ser | Thr | Pro | Ile | Leu | Ser | Ser | Gln | Ala | Arg | Ile | Leu | Arg | Thr | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Arg | Pro | Thr | Thr | Met | Gly | Asp | Met | Asp | Ser | Gln | Val | Leu | Leu | Arg | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Leu | Gly | Ile | Asp | Leu | Ser | Lys | Phe | Lys | Gly | Gln | Asp | Glu | Arg | Arg | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Leu | Val | Asp | Ser | Glu | Arg | Val | Ser | Pro | Gly | Gly | Pro | Asp | Pro | Gln | His |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| His |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..45

(D) OTHER INFORMATION: / Ceres Seq. ID 1482031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Asp | Met | Asp | Ser | Gln | Val | Leu | Leu | Arg | Glu | Leu | Gly | Ile | Asp |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Leu | Ser | Lys | Phe | Lys | Gly | Gln | Asp | Glu | Arg | Arg | Phe | Leu | Val | Asp | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Glu | Arg | Val | Ser | Pro | Gly | Gly | Pro | Asp | Pro | Gln | His | His |     |     |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:



- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..42  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1482032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

```
Met Asp Ser Gln Val Leu Leu Arg Glu Leu Gly Ile Asp Leu Ser Lys
1 5 10 15
Phe Lys Gly Gln Asp Glu Arg Arg Phe Leu Val Asp Ser Glu Arg Val
20 25 30
Ser Pro Gly Gly Pro Asp Pro Gln His His
35 40
```

(2) INFORMATION FOR SEQ ID NO:309:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 903 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..903  
(D) OTHER INFORMATION: / Ceres Seq. ID 1482033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

```
aatgtcgcgt gcgccacta gatttttccct gacgcggtgt ctgctccac tccccctcct 60
ctccccccagg tggcggcagc ggcggcgggg tagcatttgt gctacgaggg cttttgcaat 120
ggcggcttcg gggttcggcg gcggcgaggg gttccggctc tcggccgcac caggggcccgg 180
cttactgaag ctgcacaagg gcgacatcac cctctggtcc gtcgactgcg ccaccgacgc 240
catcgttaat gctgctaata agcgaatgtt aggtggcgga ggtgttgatg gagctataca 300
tcaagctgct ggaccagagc tagtgcaagc atgccggaaa gttccagagg tcaaaccagg 360
agttcgttgt cctactggag aagctaggat tactcctgct tttgagcttc ctgcctctcg 420
ggtgattcac actgttggcc ctatatatga tttggacaag catcctgagg tgtcattaaa 480
gaaggcctat gaaaatagct tgaagcttgc taaagataat ggcattcagt acatcgcat 540
ccctgctata tcttgtggtg tttatcgta tccctccaaag gaagcatcaa aaatagctgt 600
ttctaccgca cagaaatttt cagagggtat caaagaggtg cattttgttc tgttctcgga 660
tgacctttac aatatatggc gcgagactgc ccagcagttg ctatcacagt ttgagaaatg 720
aatggtccat aggcaagttt ctagcactag cagttgccca gcagtcgttg tctagtgttg 780
agatgtgagc gccataggca gtttgccctg tgtaataaaa atgggtgtat cagacaacgt 840
ttaaattctt atgaaaccgt gtattgcacc tgtggtataa tgctgaatga gtaaagtttg 900
gcc
```

(2) INFORMATION FOR SEQ ID NO:310:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 239 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..239  
(D) OTHER INFORMATION: / Ceres Seq. ID 1482034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

```
Met Ser Arg Ala Thr Arg Phe Phe Leu Thr Arg Cys Leu Leu Pro
1 5 10 15
Leu Pro Leu Leu Ser Pro Arg Trp Arg Gln Arg Arg Arg Gly Ser Ile
20 25 30
Cys Ala Thr Arg Ala Phe Ala Met Ala Ala Ser Gly Phe Gly Gly Gly
35 40 45
```

Glu Ala Phe Arg Leu Ser Ala Ala Pro Gly Ala Gly Leu Leu Lys Leu  
50 55 60  
His Lys Gly Asp Ile Thr Leu Trp Ser Val Asp Cys Ala Thr Asp Ala  
65 70 75 80  
Ile Val Asn Ala Ala Asn Glu Arg Met Leu Gly Gly Gly Gly Val Asp  
85 90 95  
Gly Ala Ile His Gln Ala Ala Gly Pro Glu Leu Val Gln Ala Cys Arg  
100 105 110  
Lys Val Pro Glu Val Lys Pro Gly Val Arg Cys Pro Thr Gly Glu Ala  
115 120 125  
Arg Ile Thr Pro Ala Phe Glu Leu Pro Ala Ser Arg Val Ile His Thr  
130 135 140  
Val Gly Pro Ile Tyr Asp Leu Asp Lys His Pro Glu Val Ser Leu Lys  
145 150 155 160  
Lys Ala Tyr Glu Asn Ser Leu Lys Leu Ala Lys Asp Asn Gly Ile Gln  
165 170 175  
Tyr Ile Ala Phe Pro Ala Ile Ser Cys Gly Val Tyr Arg Tyr Pro Pro  
180 185 190  
Lys Glu Ala Ser Lys Ile Ala Val Ser Thr Ala Gln Lys Phe Ser Glu  
195 200 205  
Gly Ile Lys Glu Val His Phe Val Leu Phe Ser Asp Asp Leu Tyr Asn  
210 215 220  
Ile Trp Arg Glu Thr Ala Gln Gln Leu Leu Ser Gln Phe Glu Lys  
225 230 235

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1482035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

Met Ser Arg Ala Ala Thr Arg Phe Phe Leu Thr Arg Cys Leu Leu Pro  
1 5 10 15  
Leu Pro Leu Leu Ser Pro Arg Trp Arg Gln Arg Arg Arg Gly Ser Ile  
20 25 30  
Cys Ala Thr Arg Ala Phe Ala Met Ala Ala Ser Gly Phe Gly Gly Gly  
35 40 45  
Glu Ala Phe Arg Leu Ser Ala Ala Pro Gly Ala Gly Leu Leu Lys Leu  
50 55 60  
His Lys Gly Asp Ile Thr Leu Trp Ser Val Asp Cys Ala Thr Asp Ala  
65 70 75 80  
Ile Val Asn Ala Ala Asn Glu Arg Met Leu Gly Gly Gly Gly Val Asp  
85 90 95  
Gly Ala Ile His Gln Ala Ala Gly Pro Glu Leu Val Gln Ala Cys Arg  
100 105 110  
Lys Val Pro Glu Val Lys Pro Gly Val Arg Cys Pro Thr Gly Glu Ala  
115 120 125  
Arg Ile Thr Pro Ala Phe Glu Leu Pro Ala Ser Arg Val Ile His Thr  
130 135 140  
Val Gly Pro Ile Tyr Asp Leu Asp Lys His Pro Glu Val Ser Leu Lys  
145 150 155 160  
Lys Ala Tyr Glu Asn Ser Leu Lys Leu Ala Lys Asp Asn Gly Ile Gln  
165 170 175  
Tyr Ile Ala Phe Pro Ala Ile Ser Cys Gly Val Tyr Arg Tyr Pro Pro

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 180 |     | 185 |     | 190 |     |     |     |     |     |     |     |     |     |     |
| Lys | Glu | Ala | Ser | Lys | Ile | Ala | Val | Ser | Thr | Ala | Gln | Lys | Phe | Ser | Glu |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Ile | Lys | Glu | Val | His | Phe | Val | Leu | Phe | Ser | Asp | Asp | Leu | Tyr | Asn |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Trp | Arg | Glu | Thr | Ala | Gln | Gln | Leu | Leu | Ser | Gln | Phe | Glu | Lys |     |
| 225 |     |     | 230 |     |     |     |     |     |     | 235 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..200
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Ser | Gly | Phe | Gly | Gly | Gly | Glu | Ala | Phe | Arg | Leu | Ser | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Pro | Gly | Ala | Gly | Leu | Leu | Lys | Leu | His | Lys | Gly | Asp | Ile | Thr | Leu |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Trp | Ser | Val | Asp | Cys | Ala | Thr | Asp | Ala | Ile | Val | Asn | Ala | Ala | Asn | Glu |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Arg | Met | Leu | Gly | Gly | Gly | Gly | Val | Asp | Gly | Ala | Ile | His | Gln | Ala | Ala |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Gly | Pro | Glu | Leu | Val | Gln | Ala | Cys | Arg | Lys | Val | Pro | Glu | Val | Lys | Pro |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Val | Arg | Cys | Pro | Thr | Gly | Glu | Ala | Arg | Ile | Thr | Pro | Ala | Phe | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Pro | Ala | Ser | Arg | Val | Ile | His | Thr | Val | Gly | Pro | Ile | Tyr | Asp | Leu |
|     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Asp | Lys | His | Pro | Glu | Val | Ser | Leu | Lys | Lys | Ala | Tyr | Glu | Asn | Ser | Leu |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Lys | Leu | Ala | Lys | Asp | Asn | Gly | Ile | Gln | Tyr | Ile | Ala | Phe | Pro | Ala | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Ser | Cys | Gly | Val | Tyr | Arg | Tyr | Pro | Pro | Lys | Glu | Ala | Ser | Lys | Ile | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Val | Ser | Thr | Ala | Gln | Lys | Phe | Ser | Glu | Gly | Ile | Lys | Glu | Val | His | Phe |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Val | Leu | Phe | Ser | Asp | Asp | Leu | Tyr | Asn | Ile | Trp | Arg | Glu | Thr | Ala | Gln |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Gln | Leu | Leu | Ser | Gln | Phe | Glu | Lys |     |     |     |     |     |     |     |     |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..806
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

|            |            |            |              |            |             |     |
|------------|------------|------------|--------------|------------|-------------|-----|
| aatttgcagc | ttgttcccca | cgagcttcct | ctgttcacatca | tcgtcctcga | gcttctctctg | 60  |
| ttcatcaagc | tcctctgttc | ttgaacatcg | acgaaatcag   | aggctgtggc | agatgcgaac  | 120 |

```
aaagcaattg agttggatca ttcattaatc aaagcttacc taagaaaagg gttacaactc 180
aagtgttttg agaaagaaga tggctaaaga tgtaagtgtt ttggttttta ttttagagtt 240
ttgggtcaatc agtttgctaa tgagtggcta ggttgagcat aaacgtgctt aacctttgat 300
ataacctcag tcaagcatga agaggagcta gctgaggtaa atatgaatgt ctttgtggta 360
ggctaaatat agccattgga tgtattcatt ttgtgtttgt aatatttagg ttgggttaacc 420
aaattgggtg cttctaacat gggttatattg aatatgcagc ctcaagaaat tgtggcagtg 480
aaagattgac atgttttggt tgtcttatgt gctatttatg cagctcggag atagatttat 540
ctatgaagtt gtggatgaag tgaataactt ccttcacttc tatggtccta tcaaaacctt 600
cgttcctctt cctttggatt atgttggtcaa agttgagaag ttaacattca tcaattgcaa 660
tttcacctgc agcttttttg acttgatgat tcagtggttt atgtgtaatt gcaatgtcac 720
tcttttaata atgtaattaa gagagatttg ttttctattc acaaaacagt gtatttatac 780
tattattaca atgcaagatt aagatc
```

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

```
Ile Cys Ser Leu Phe Pro Thr Ser Phe Leu Cys Ser Ser Ser Ser Ser
1 5 10 15
Ser Phe Leu Cys Ser Ser Ser Ser Ser Val Leu Glu His Arg Arg Asn
 20 25 30
Gln Arg Leu Trp Gln Met Arg Thr Lys Gln Leu Ser Trp Ile Ile His
 35 40 45
```

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..81
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

```
Met Phe Cys Leu Ser Tyr Val Leu Phe Met Gln Leu Gly Asp Arg Phe
1 5 10 15
Ile Tyr Glu Val Val Asp Glu Val Asn Asn Phe Pro His Phe Tyr Gly
 20 25 30
Pro Ile Lys Thr Phe Val Pro Leu Pro Leu Asp Tyr Val Val Lys Val
 35 40 45
Glu Lys Leu Thr Phe Ile Asn Cys Asn Phe Thr Cys Ser Phe Phe Asp
 50 55 60
Leu Met Ile Gln Trp Phe Met Cys Asn Cys Asn Val Thr Leu Leu Ile
 65 70 75 80
Met
```

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..72
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1482044
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

```
Met Gln Leu Gly Asp Arg Phe Ile Tyr Glu Val Val Asp Glu Val Asn
1 5 10 15
Asn Phe Pro His Phe Tyr Gly Pro Ile Lys Thr Phe Val Pro Leu Pro
20 25 30
Leu Asp Tyr Val Val Lys Val Glu Lys Leu Thr Phe Ile Asn Cys Asn
35 40 45
Phe Thr Cys Ser Phe Phe Asp Leu Met Ile Gln Trp Phe Met Cys Asn
50 55 60
Cys Asn Val Thr Leu Leu Ile Met
65 70
```

(2) INFORMATION FOR SEQ ID NO:317:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 576 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..576
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1482045
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

```
gtcggactca gtggagaaga aggaagatcc aaatcgatcc gttgaaaagg aatttcgaat 60
ttgctgtgcg atgtcgagtg cgggtggacgc tacgggaaac ccgatcccta cttcggcggt 120
ttaacggcg tcagcgaagc atatatggtat gaggtgtatg ccggagaatg ttgcgttcct 180
caaatgcaag aagaatgatc caaacccaga gaagtgtctc gacaaaggtc gtgacgtcac 240
tcgctgcgtg cttggcttga aaaggagatg ggattatgtt ggggtgtatgt attactacac 300
aaacgagttt gatctgtgta ggaaagagca agaagccttc gagaaagtgt gtcaccttgaa 360
atgagaatca caagtctctg tcatgttttg atttgtatct cataataaag caaaatgttc 420
atTTTTgaat gagctttact ctctccatct cttgtttgtt gtcatcccat ttatttcctc 480
tcagatgctt tcgtagttag ttccaaagac aactaaatga ctcagtttta ttgttcgatg 540
gttcactaat cagcacagaa tggaacaatt gttttt
```

(2) INFORMATION FOR SEQ ID NO:318:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 120 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..120
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1482046
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

```
Ser Asp Ser Val Glu Lys Lys Glu Asp Pro Asn Arg Ser Val Glu Lys
1 5 10 15
Glu Phe Arg Ile Cys Cys Ala Met Ser Ser Ala Val Asp Ala Thr Gly
20 25 30
Asn Pro Ile Pro Thr Ser Ala Val Leu Thr Ala Ser Ala Lys His Ile
35 40 45
```

Gly Met Arg Cys Met Pro Glu Asn Val Ala Phe Leu Lys Cys Lys Lys  
50 55 60  
Asn Asp Pro Asn Pro Glu Lys Cys Leu Asp Lys Gly Arg Asp Val Thr  
65 70 75 80  
Arg Cys Val Leu Gly Leu Lys Arg Arg Trp Asp Tyr Val Gly Cys Met  
85 90 95  
Tyr Tyr Tyr Thr Asn Glu Phe Asp Leu Cys Arg Lys Glu Gln Glu Ala  
100 105 110  
Phe Glu Lys Val Cys Pro Leu Lys  
115 120

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

Met Ser Ser Ala Val Asp Ala Thr Gly Asn Pro Ile Pro Thr Ser Ala  
1 5 10 15  
Val Leu Thr Ala Ser Ala Lys His Ile Gly Met Arg Cys Met Pro Glu  
20 25 30  
Asn Val Ala Phe Leu Lys Cys Lys Lys Asn Asp Pro Asn Pro Glu Lys  
35 40 45  
Cys Leu Asp Lys Gly Arg Asp Val Thr Arg Cys Val Leu Gly Leu Lys  
50 55 60  
Arg Arg Trp Asp Tyr Val Gly Cys Met Tyr Tyr Tyr Thr Asn Glu Phe  
65 70 75 80  
Asp Leu Cys Arg Lys Glu Gln Glu Ala Phe Glu Lys Val Cys Pro Leu  
85 90 95  
Lys

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

Met Arg Cys Met Pro Glu Asn Val Ala Phe Leu Lys Cys Lys Lys Asn  
1 5 10 15  
Asp Pro Asn Pro Glu Lys Cys Leu Asp Lys Gly Arg Asp Val Thr Arg  
20 25 30  
Cys Val Leu Gly Leu Lys Arg Arg Trp Asp Tyr Val Gly Cys Met Tyr  
35 40 45  
Tyr Tyr Thr Asn Glu Phe Asp Leu Cys Arg Lys Glu Gln Glu Ala Phe  
50 55 60  
Glu Lys Val Cys Pro Leu Lys  
65 70

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 645 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..645  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1482049  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| aacaaagtct | cttcctttat | tcatcaatga | ctacagcaat  | atcgatgaat | ccatctttgt | 60  |
| ttcgagtaat | ctgtatactc | cattcgataa | ttgcgcttac  | tagtggaacc | ttaatgatgt | 120 |
| tctacacaga | gaaagcttca | atctttggac | caggaagtga  | gattgctagc | aaactaaaag | 180 |
| gatcaacacc | acacgatgaa | ctactcatac | agattttctca | gtcattctct | ggtttgcttc | 240 |
| tgtttgcaat | tggtttggta | ctgttcattg | tttcgtttgt  | gaaagacaaa | gagtttcata | 300 |
| gcttcctcgc | tagtgggtcc | gtgattctgt | atgtgttaat  | ggctatgtgg | agggttttgt | 360 |
| tcgagtggaa | aattgaagat | cttgcttatg | aatggcctaa  | acaagctctt | ggagacattg | 420 |
| ctttggctat | ttcttgggtt | ttctttcttg | tttattcttg  | gagagagaag | tatgattgat | 480 |
| gtttttgatt | ttctcttttc | tttaaaaaaa | aaacttggtg  | gctaagcaaa | accagatgat | 540 |
| gtattatgat | atagtttttg | atcttcagat | ttgataaaa   | aggaaatgtg | aaaaagcttt | 600 |
| agattcagac | aagatcagaa | caaacaaaat | catagtttgg  | gattc      |            |     |

(2) INFORMATION FOR SEQ ID NO:322:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 158 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..158  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1482050  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ser | Leu | Phe | Tyr | Ser | Ser | Met | Thr | Thr | Ala | Ile | Ser | Met | Asn |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Ser | Leu | Phe | Arg | Val | Ile | Cys | Ile | Leu | His | Ser | Ile | Ile | Ala |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  | Leu |
| Thr | Ser | Gly | Thr | Leu | Met | Met | Phe | Tyr | Thr | Glu | Lys | Ala | Ser | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  | Phe |
| Gly | Pro | Gly | Ser | Glu | Ile | Ala | Ser | Lys | Leu | Lys | Gly | Ser | Thr | Pro |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  | His |
| Asp | Glu | Leu | Leu | Ile | Gln | Ile | Ser | Gln | Ser | Phe | Ser | Gly | Leu | Leu |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Phe | Ala | Ile | Gly | Leu | Val | Leu | Phe | Met | Val | Ser | Phe | Val | Lys | Asp |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | Lys |
|     |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |
| Glu | Phe | His | Ser | Phe | Phe | Ala | Ser | Gly | Ser | Val | Ile | Leu | Tyr | Val |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | Leu |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |
| Met | Ala | Met | Trp | Arg | Val | Leu | Phe | Glu | Trp | Lys | Ile | Glu | Asp | Leu |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | Ala |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |
| Tyr | Glu | Trp | Pro | Lys | Gln | Ala | Leu | Gly | Asp | Ile | Ala | Leu | Ala | Ile |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | Ser |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |
| Trp | Val | Phe | Phe | Leu | Val | Tyr | Ser | Trp | Arg | Glu | Lys | Tyr | Asp |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:323:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 150 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..150  
(D) OTHER INFORMATION: / Ceres Seq. ID 1482051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

Met Thr Thr Ala Ile Ser Met Asn Pro Ser Leu Phe Arg Val Ile Cys  
1 5 10 15  
Ile Leu His Ser Ile Ile Ala Leu Thr Ser Gly Thr Leu Met Met Phe  
20 25 30  
Tyr Thr Glu Lys Ala Ser Ile Phe Gly Pro Gly Ser Glu Ile Ala Ser  
35 40 45  
Lys Leu Lys Gly Ser Thr Pro His Asp Glu Leu Leu Ile Gln Ile Ser  
50 55 60  
Gln Ser Phe Ser Gly Leu Leu Phe Ala Ile Gly Leu Val Leu Phe  
65 70 75 80  
Met Val Ser Phe Val Lys Asp Lys Glu Phe His Ser Phe Phe Ala Ser  
85 90 95  
Gly Ser Val Ile Leu Tyr Val Leu Met Ala Met Trp Arg Val Leu Phe  
100 105 110  
Glu Trp Lys Ile Glu Asp Leu Ala Tyr Glu Trp Pro Lys Gln Ala Leu  
115 120 125  
Gly Asp Ile Ala Leu Ala Ile Ser Trp Val Phe Phe Leu Val Tyr Ser  
130 135 140  
Trp Arg Glu Lys Tyr Asp  
145 150

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 144 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..144  
(D) OTHER INFORMATION: / Ceres Seq. ID 1482052

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Met Asn Pro Ser Leu Phe Arg Val Ile Cys Ile Leu His Ser Ile Ile  
1 5 10 15  
Ala Leu Thr Ser Gly Thr Leu Met Met Phe Tyr Thr Glu Lys Ala Ser  
20 25 30  
Ile Phe Gly Pro Gly Ser Glu Ile Ala Ser Lys Leu Lys Gly Ser Thr  
35 40 45  
Pro His Asp Glu Leu Leu Ile Gln Ile Ser Gln Ser Phe Ser Gly Leu  
50 55 60  
Leu Leu Phe Ala Ile Gly Leu Val Leu Phe Met Val Ser Phe Val Lys  
65 70 75 80  
Asp Lys Glu Phe His Ser Phe Phe Ala Ser Gly Ser Val Ile Leu Tyr  
85 90 95  
Val Leu Met Ala Met Trp Arg Val Leu Phe Glu Trp Lys Ile Glu Asp  
100 105 110  
Leu Ala Tyr Glu Trp Pro Lys Gln Ala Leu Gly Asp Ile Ala Leu Ala  
115 120 125  
Ile Ser Trp Val Phe Phe Leu Val Tyr Ser Trp Arg Glu Lys Tyr Asp  
130 135 140



(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..623
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| aagaagagat | gggggaaatg  | ggaaaggcga | taggattgct | gataagcggg | accttgtgta  | 60  |
| tcaccattgc | gctaatacgca | acgcgactct | tctctcgctc | atctccgacg | ttctcatcgt  | 120 |
| tctcttatct | tcaactcgcca | ttctcggcct | tctttttcgt | cacctcaatg | tctcgggtacc | 180 |
| tgtggatcca | ttagagtggc  | aaatatcaca | agacacagcc | tgtaacattg | tggcgcgctt  | 240 |
| agctaatact | gttggagcag  | ctgaatccgt | tctgcgggtt | gcagcaacag | gacatgacaa  | 300 |
| gaggctcttt | gttaagggtg  | tgatctgtct | ttacttcttg | gcagctctag | gacgaatcat  | 360 |
| atcggtgac  | cattgcctat  | gcaggactat | gtttgttctg | tctctccatg | ctttttcgga  | 420 |
| gttcaattag | aaactccgta  | ttgaaccgaa | gaaacggaga | gattttggat | tgcgaaacac  | 480 |
| cttcagagtt | gtaatacaca  | atttgcctaa | acgtgttata | ttctttgtcc | tctttccacc  | 540 |
| tttacatgtt | catagctttg  | gatagtgtga | ataatgcttt | cagttcctaa | atgtagaaat  | 600 |
| attaatcata | gttaatcttt  | tct        |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | Arg | Asp | Gly | Gly | Asn | Gly | Lys | Gly | Asp | Arg | Ile | Ala | Asp | Lys | Arg |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Asp | Leu | Val | Tyr | His | His | Cys | Ala | Asn | Arg | Asn | Ala | Thr | Leu | Leu | Ser |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu | Ile | Ser | Asp | Val | Leu | Ile | Val | Leu | Leu | Ser | Ser | Leu | Ala | Ile | Leu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Gly | Leu | Leu | Phe | Arg | His | Leu | Asn | Val | Ser | Val | Pro | Val | Asp | Pro | Leu |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Glu | Trp | Gln | Ile | Ser | Gln | Asp | Thr | Ala | Cys | Asn | Ile | Val | Ala | Arg | Leu |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Ala | Asn | Thr | Val | Gly | Ala | Ala | Glu | Ser | Val | Leu | Arg | Val | Ala | Ala | Thr |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Gly | His | Asp | Lys | Arg | Leu | Phe | Val | Lys | Val | Val | Ile | Cys | Leu | Tyr | Phe |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Leu | Ala | Ala | Leu | Gly | Arg | Ile | Ile | Ser | Gly | Asp | His | Cys | Leu | Cys | Arg |  |
|     |     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |  |
| Thr | Met | Phe | Val | Leu | Ser | Leu | His | Ala | Phe | Ser | Glu | Phe | Asn |     |     |  |
|     | 130 |     |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |  |

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..505

(D) OTHER INFORMATION: / Ceres Seq. ID 1482066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

|             |             |            |             |             |             |     |
|-------------|-------------|------------|-------------|-------------|-------------|-----|
| gttccttagc  | gcagaagcgt  | ttcctggcat | ctccctatct  | ccttcacggc  | atcagaaacc  | 60  |
| agcacattct  | tcctcctcct  | ctttgattcc | gcgcaggagc  | aagggagctc  | ccatggccac  | 120 |
| cttcgtggcg  | ccctctcgcc  | cctgctctct | cctaggccgt  | cggctctgcc  | ttcccagtg   | 180 |
| cctgctcggtg | gtctcccca   | ccgacgccc  | agctccctca  | actgcccattg | gcgccacaaa  | 240 |
| tctccagccg  | gcttccccctg | cgtcttctc  | cctgcgctcc  | tgcaggcctc  | cctggcgccac | 300 |
| ctcgccagca  | gcagggatct  | ttccctctcc | ccatggcggtg | caagcmctga  | gctccccac   | 360 |
| acgtgttccc  | ttccccaggc  | gcgtgastcc | ctccggcgctc | ggccaatagg  | caagtttgag  | 420 |
| caccgagctc  | atccatggmg  | cmtccmctmc | mctcggctcc  | agcmccctcg  | agctccattt  | 480 |
| ctgcgtmcga  | gctcgagcag  | cttgc      |             |             |             |     |

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1482067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Phe | Leu | Ser | Ala | Glu | Ala | Phe | Pro | Gly | Ile | Ser | Leu | Ser | Pro | Ser | Arg |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| His | Gln | Lys | Pro | Ala | His | Ser | Ser | Ser | Ser | Ser | Leu | Ile | Pro | Arg | Arg |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | Lys | Gly | Ala | Pro | Met | Ala | Thr | Phe | Val | Ala | Pro | Ser | Arg | Pro | Cys |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Leu | Leu | Gly | Arg | Arg | Leu | Cys | Leu | Pro | Ser | Ala | Leu | Leu | Val | Val |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Ser | Pro | Thr | Asp | Ala | Arg | Ala | Pro | Ser | Thr | Ala | His | Gly | Ala | Thr | Asn |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Leu | Gln | Pro | Ala | Ser | Pro | Ala | Ser | Ser | Ser | Leu | Arg | Ser | Cys | Arg | Pro |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Pro | Trp | Arg | Thr | Ser | Pro | Ala | Ala | Gly | Ile | Phe | Pro | Ser | Pro | His | Gly |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |
| Val | Gln | Xaa | Leu | Ser | Ser | Pro | Thr | Arg | Val | Pro | Phe | Pro | Arg | Arg | Val |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |
| Xaa | Pro | Ser | Gly | Val | Gly | Gln |     |     |     |     |     |     |     |     |     |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1482068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Thr | Phe | Val | Ala | Pro | Ser | Arg | Pro | Cys | Ser | Leu | Leu | Gly | Arg |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |

Arg Leu Cys Leu Pro Ser Ala Leu Leu Val Val Ser Pro Thr Asp Ala  
20 25 30  
Arg Ala Pro Ser Thr Ala His Gly Ala Thr Asn Leu Gln Pro Ala Ser  
35 40 45  
Pro Ala Ser Ser Ser Leu Arg Ser Cys Arg Pro Pro Trp Arg Thr Ser  
50 55 60  
Pro Ala Ala Gly Ile Phe Pro Ser Pro His Gly Val Gln Xaa Leu Ser  
65 70 75 80  
Ser Pro Thr Arg Val Pro Phe Pro Arg Arg Val Xaa Pro Ser Gly Val  
85 90 95  
Gly Gln

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..542
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

aaaaaagaaa aggtctaatt actcgctct cttgctcgcc aacgccagtg nccagaggcc 60  
agagcttcgt caaagacacg ccgaaaagag ggggaggcga ctcggccgag gtccgggttcc 120  
gaactccggt cctccgattt gcgcgtccgg atctaccagc catggcatca tcttcggacc 180  
cgtggatgaa ggagtacaat gaagcatcca gacttgctga tgacatcagt tccatgattg 240  
ctgatagagg gtcccttcca caatcaggcc cagaaattat gcggcatact tcagccatcc 300  
ggagaaaaat aactattctt gggactagac tggatagctt ggagtcgttg cttggcagaa 360  
ttcctccaaa gtcaatcact gacaaggaga tgcataagcg ccaagacatg ttttccagtt 420  
tgaagtctaa agcaaagcag atggcgacaa gtttcaacat gtcaaacttt gctaacaggg 480  
aggatctgct tggtcagagt aaaaaggcag atgacatgag cagagttgct ggggttagata 540  
ac

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..180
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482070

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

Lys Arg Lys Gly Leu Ile Thr Arg Leu Ser Cys Ser Pro Thr Pro Val  
1 5 10 15  
Xaa Arg Gly Gln Ser Phe Val Lys Asp Thr Pro Lys Arg Gly Gly Gly  
20 25 30  
Asp Ser Ala Glu Val Arg Phe Arg Thr Pro Val Leu Arg Phe Ala Arg  
35 40 45  
Pro Asp Leu Pro Ala Met Ala Ser Ser Ser Asp Pro Trp Met Lys Glu  
50 55 60  
Tyr Asn Glu Ala Ser Arg Leu Ala Asp Asp Ile Ser Ser Met Ile Ala  
65 70 75 80  
Asp Arg Gly Ser Leu Pro Gln Ser Gly Pro Glu Ile Met Arg His Thr  
85 90 95  
Ser Ala Ile Arg Arg Lys Ile Thr Ile Leu Gly Thr Arg Leu Asp Ser

100 105 110  
Leu Glu Ser Leu Leu Gly Arg Ile Pro Pro Lys Ser Ile Thr Asp Lys  
115 120 125  
Glu Met His Lys Arg Gln Asp Met Phe Ser Ser Leu Lys Ser Lys Ala  
130 135 140  
Lys Gln Met Ala Thr Ser Phe Asn Met Ser Asn Phe Ala Asn Arg Glu  
145 150 155 160  
Asp Leu Leu Gly Gln Ser Lys Lys Ala Asp Asp Met Ser Arg Val Ala  
165 170 175  
Gly Leu Asp Asn  
180

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Met Ala Ser Ser Ser Asp Pro Trp Met Lys Glu Tyr Asn Glu Ala Ser  
1 5 10 15  
Arg Leu Ala Asp Asp Ile Ser Ser Met Ile Ala Asp Arg Gly Ser Leu  
20 25 30  
Pro Gln Ser Gly Pro Glu Ile Met Arg His Thr Ser Ala Ile Arg Arg  
35 40 45  
Lys Ile Thr Ile Leu Gly Thr Arg Leu Asp Ser Leu Glu Ser Leu Leu  
50 55 60  
Gly Arg Ile Pro Pro Lys Ser Ile Thr Asp Lys Glu Met His Lys Arg  
65 70 75 80  
Gln Asp Met Phe Ser Ser Leu Lys Ser Lys Ala Lys Gln Met Ala Thr  
85 90 95  
Ser Phe Asn Met Ser Asn Phe Ala Asn Arg Glu Asp Leu Leu Gly Gln  
100 105 110  
Ser Lys Lys Ala Asp Asp Met Ser Arg Val Ala Gly Leu Asp Asn  
115 120 125

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Met Lys Glu Tyr Asn Glu Ala Ser Arg Leu Ala Asp Asp Ile Ser Ser  
1 5 10 15  
Met Ile Ala Asp Arg Gly Ser Leu Pro Gln Ser Gly Pro Glu Ile Met  
20 25 30  
Arg His Thr Ser Ala Ile Arg Arg Lys Ile Thr Ile Leu Gly Thr Arg  
35 40 45  
Leu Asp Ser Leu Glu Ser Leu Leu Gly Arg Ile Pro Pro Lys Ser Ile  
50 55 60

Thr Asp Lys Glu Met His Lys Arg Gln Asp Met Phe Ser Ser Leu Lys  
65 70 75 80  
Ser Lys Ala Lys Gln Met Ala Thr Ser Phe Asn Met Ser Asn Phe Ala  
85 90 95  
Asn Arg Glu Asp Leu Leu Gly Gln Ser Lys Lys Ala Asp Asp Met Ser  
100 105 110  
Arg Val Ala Gly Leu Asp Asn  
115

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 652 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..652
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

gaaaaacgca accaagtcaa ccaacgtcgg cttgaaattc ggccatcacc gttcggatct 60  
ttccccacc cggttgtata aaagcgggcg cctgggattc ccctctcatc cctccttcac 120  
catcagcaaa tcggtctgcc ctggtttccc ccgtcgtgaa gcagaaacct ctctgctgcc 180  
attaccgtgc tgcgcgccgt cgcggtgagg cttggccaca accgtggaac ctgtctccat 240  
atggcgtagg cggcgtagcg agcttcgcct gatggatttg cagtccagtg ggcccataat 300  
ttctcgccgg accgcgagca gcaacaacct ctccctcgccg gccatgacct ctacgcactc 360  
caagctctcc tccgaggacc gtcattctcg tgcattgtag cgagtaaggc cagcaggatc 420  
tgaagaatca ccctgggtatc tggaatctca agtgctagga gaagagcagg tggttcagga 480  
ggagccgcct aacactgagg agttcgatct gatctagggt gcgtttccca gtcgacattg 540  
gcgcccagca tccttagttc gttttatgtt tattctttta ttttgtaata agtcttccgc 600  
tatgtaataa gtactctgat gttttatgac atttatctct atacactctg tg

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

Lys Asn Ala Thr Lys Ser Thr Asn Val Gly Leu Lys Phe Gly His His  
1 5 10 15  
Arg Ser Asp Leu Ser Pro Thr Arg Leu Tyr Lys Ser Gly Arg Leu Gly  
20 25 30  
Phe Pro Ser His Pro Ser Phe Thr Ile Ser Lys Ser Val Cys Pro Gly  
35 40 45  
Phe Pro Arg Arg Glu Ala Glu Thr Ser Leu Leu Pro Leu Pro Cys Cys  
50 55 60  
Ala Pro Ser Arg  
65

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..81
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1482075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

```
Met Asp Leu Gln Ser Ser Gly Pro Ile Ser Arg Arg Thr Ala Ser
1 5 10 15
Ser Asn Asn Leu Ser Ser Pro Ala Met Thr Ser Thr His Ser Lys Leu
20 25 30
Ser Ser Glu Asp Arg His Leu Arg Ala Cys Ser Arg Val Arg Ser Arg
35 40 45
Gly Ser Glu Glu Ser Pro Trp Tyr Leu Glu Ser Gln Val Leu Gly Glu
50 55 60
Glu Gln Val Val Gln Glu Glu Pro Pro Asn Thr Glu Glu Phe Asp Leu
65 70 75 80
Ile
```

(2) INFORMATION FOR SEQ ID NO:337:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 57 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..57
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1482076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

```
Met Thr Ser Thr His Ser Lys Leu Ser Ser Glu Asp Arg His Leu Arg
1 5 10 15
Ala Cys Ser Arg Val Arg Ser Arg Gly Ser Glu Glu Ser Pro Trp Tyr
20 25 30
Leu Glu Ser Gln Val Leu Gly Glu Gln Val Val Gln Glu Glu Pro
35 40 45
Pro Asn Thr Glu Glu Phe Asp Leu Ile
50 55
```

(2) INFORMATION FOR SEQ ID NO:338:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 814 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..814
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1482081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

```
attctacatg cgcacacttc gtcgaggaca tgagccagct acttactcgg cttcgcgga 60
gtacagatcc ggccgacact tcactcgtcaa gctctcgcca ttacaactc cttgctccgc 120
cgacctcgac gcaaactgca acttctcgct cgcgcctgtc caggatctgc tctcgccatg 180
gacaggaag ccaagaaaga agcgttcagg aagtatcttg aatccagtgg cgtgctcgat 240
accctcacga aagctcttgt ggcgctgtac gaggagaacg ataagccttc atctgcagtc 300
gaatttggtc agcagaagtt ggggtggccg tcaatctctg actatgaaaa gctcaaggca 360
gagaagctgg acttgcaatt gaagtatgat aagcttttag aaaccacaa ggaaacatgc 420
agacagctgg aggaacttaa gaatatgaag tacggtgcac cctggaactg aaataacgtg 480
tgttgacact gtaaattgat catgaagcat gtacttttta cacctctctg aagcattgct 540
```

aagctcttttg tacaatggaa acatctcatg tatctgattt tagccatctg gatccctttt 600  
ggattatgaa gacacccaac tcactgtagg tcccaggtat cagatatcac caatgcagga 660  
taaaggatgt gacaactatc atagttgaac catgagcaat tgtttaacca gtaatccagt 720  
atcgacaaaag agtgtggtct attgacttga gacttctctt ggcattggctt gtaagcagat 780  
tttagtagat ttcagtggaa gagatatggc gtgc

## (2) INFORMATION FOR SEQ ID NO:339:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1482082

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

Phe Tyr Met Pro Thr Leu Arg Arg Gly His Glu Pro Ala Thr Tyr Ser  
1 5 10 15  
Ala Ser Arg Gln Tyr Arg Ser Gly Arg His Phe Ile Val Lys Leu Ser  
20 25 30  
Pro Phe Thr Thr Pro Cys Ser Ala Asp Leu Asp Ala Asn Cys Asn Phe  
35 40 45  
Ser Leu Ala Pro Val Gln Asp Leu Leu Ser Pro Trp Thr Gly Lys Pro  
50 55 60  
Arg Lys Lys Arg Ser Gly Ser Ile Leu Asn Pro Val Ala Cys Ser Ile  
65 70 75 80  
Pro Ser Arg Lys Leu Leu Trp Arg Cys Thr Arg Arg Thr Ile Ser Leu  
85 90 95  
His Leu Gln Ser Asn Leu Phe Ser Arg Ser Trp Val Ala Arg Gln Ser  
100 105 110  
Leu Thr Met Lys Ser Ser Arg Gln Arg Ser Trp Thr Cys Asn  
115 120 125

## (2) INFORMATION FOR SEQ ID NO:340:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1482083

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

Met Pro Thr Leu Arg Arg Gly His Glu Pro Ala Thr Tyr Ser Ala Ser  
1 5 10 15  
Arg Gln Tyr Arg Ser Gly Arg His Phe Ile Val Lys Leu Ser Pro Phe  
20 25 30  
Thr Thr Pro Cys Ser Ala Asp Leu Asp Ala Asn Cys Asn Phe Ser Leu  
35 40 45  
Ala Pro Val Gln Asp Leu Leu Ser Pro Trp Thr Gly Lys Pro Arg Lys  
50 55 60  
Lys Arg Ser Gly Ser Ile Leu Asn Pro Val Ala Cys Ser Ile Pro Ser  
65 70 75 80  
Arg Lys Leu Leu Trp Arg Cys Thr Arg Arg Thr Ile Ser Leu His Leu  
85 90 95  
Gln Ser Asn Leu Phe Ser Arg Ser Trp Val Ala Arg Gln Ser Leu Thr  
100 105 110

Met Lys Ser Ser Arg Gln Arg Ser Trp Thr Cys Asn  
115 120

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482084

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Met Asp Arg Glu Ala Lys Lys Glu Ala Phe Arg Lys Tyr Leu Glu Ser  
1 5 10 15  
Ser Gly Val Leu Asp Thr Leu Thr Lys Ala Leu Val Ala Leu Tyr Glu  
20 25 30  
Glu Asn Asp Lys Pro Ser Ser Ala Val Glu Phe Val Gln Gln Lys Leu  
35 40 45  
Gly Gly Pro Ser Ile Ser Asp Tyr Glu Lys Leu Lys Ala Glu Lys Leu  
50 55 60  
Asp Leu Gln Leu Lys Tyr Asp Lys Leu Leu Glu Thr His Lys Glu Thr  
65 70 75 80  
Cys Arg Gln Leu Glu Leu Lys Asn Met Lys Tyr Gly Ala Pro Trp  
85 90 95  
Asn

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..592
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

gaagaatagc cttgtctagc aagaagaaga tagagggatg atgtgattat acgcaaaata 60  
ctaaaacctt ggggtgtagt acaagcagta gttatgagca ggcctcttct ctttctttcc 120  
tggtccggtt tttttctttt tccctgcgga attccccttc ttccctagtgc cctcgattcg 180  
atatttcgat tggattggat taccaaggga cagagggagg gaatcccaca cacacctctg 240  
gccctgcgga ggccaaggga agggaagcac tcagcaccca gcagcagaag gaccgccgta 300  
aatggcgctg ccggtggcga actggggacc ctggcgctgc ggacgctgtc caagcccatc 360  
gccagccgcc tcaagagcca ggccgctgtc caccccaagt tccgcaactt catcatcgcc 420  
atcggccagg caaaccacca gatcaccaca aagatacaga ggcgcattha tgagcatgcc 480  
acagatgtgg cgatcaggcc ttgggatgag cagaaagctg ttcaagctgc tacagatctc 540  
atcggggaag cctttatctt ctgggtcgct gtttgctgct ctaatttttg ag

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide



(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1482086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

Met Ala Leu Pro Val Ala Asn Trp Gly Pro Trp Arg Cys Gly Arg Cys  
1 5 10 15  
Pro Ser Pro Ser Pro Ala Ala Ser Arg Ala Arg Pro Leu Ser Thr Pro  
20 25 30  
Ser Ser Ala Thr Ser Ser Ser Pro Ser Pro Arg Gln Thr Thr Arg Ser  
35 40 45  
Pro Gln Arg Tyr Arg Gly Ala Phe Met Ser Met Pro Gln Met Trp Arg  
50 55 60  
Ser Gly Leu Trp Met Ser Arg Lys Leu Phe Lys Leu Leu Gln Ile Ser  
65 70 75 80  
Ser Gly Lys Pro Leu Ser Ser Arg Ser Leu Phe Ala Ala Leu Ile Phe  
85 90 95  
Glu

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 624 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..624

(D) OTHER INFORMATION: / Ceres Seq. ID 1482091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

gattaaactc acagcccaac tcctcttctc gccctcgtct gacttcgttt cggacctccc 60  
cagtttttcc cctccggccg ccgcacggag aagcagaagc catgcaggcc gccgccgcgc 120  
gcgcccgcgc cctcctcgcc ttaccggcgg cctcggggat ccccggaata ctctccggac 180  
cgatcccagg gcgcgcacatc tacgccgagg gcgttctctt ttaccgtctc aatggcgctc 240  
ccgcttcgcc gtcttctccg cagcatacca ggggcttctc ctctcctgc ttgcctccc 300  
gatcacactg taacctccca tcgcctacca tagcttctca atggttgaat gagaaatcag 360  
tacactatca catgacgaca gcacacttct caacggaagc aagtdacatg gaccacccta 420  
cagaagctgt agaggagatg taccagaaaa tgttgaaatc tgttgaagct gagaccatgc 480  
ctccaaatgc ctgggtgtgg tcaatgattg atagctgctc caataaggag gacatcaaac 540  
ttctttttca aattttgcag aaactcagag tatttagact atcaaattct cgcacatcagt 600  
caacttcaat gagcatctct gcag

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1482092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

Ile Lys Leu Thr Ala Gln Leu Leu Phe Ser Pro Ser Ser Asp Phe Val  
1 5 10 15  
Ser Asp Leu Pro Ser Phe Ser Pro Pro Ala Ala Ala Arg Arg Ser Arg  
20 25 30  
Ser His Ala Gly Arg Arg Arg Ala Arg Pro Pro Pro Pro Arg Leu Thr  
35 40 45  
Gly Gly Leu Gly Asp Pro Arg Asn Thr Leu Arg Thr Asp Pro Arg Ala

50 55 60  
Arg Ile Ile Arg Arg Gly Arg Ser Pro Leu Pro Ser Gln Trp Arg Ser  
65 70 75 80  
Arg Phe Ala Val Phe Ser Ala Ala Tyr Gln Gly Leu Leu Leu Leu Leu  
85 90 95  
Leu Arg Leu Pro Ile Thr Leu  
100

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..207
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Leu Asn Ser Gln Pro Asn Ser Ser Ser Arg Pro Arg Leu Thr Ser Phe  
1 5 10 15  
Arg Thr Ser Pro Val Phe Pro Leu Arg Pro Pro His Gly Glu Ala Glu  
20 25 30  
Ala Met Gln Ala Ala Ala Ala Arg Ala Arg Arg Leu Leu Ala Leu Pro  
35 40 45  
Ala Ala Ser Gly Ile Pro Gly Ile Leu Ser Gly Pro Ile Pro Gly Arg  
50 55 60  
Ala Ser Tyr Ala Glu Gly Val Leu Leu Tyr Arg Leu Asn Gly Ala Pro  
65 70 75 80  
Ala Ser Pro Ser Ser Pro Gln His Thr Arg Gly Phe Ser Ser Ser Cys  
85 90 95  
Phe Ala Ser Arg Ser His Cys Asn Leu Pro Ser Pro Thr Ile Ala Ser  
100 105 110  
Gln Trp Leu Asn Glu Lys Ser Val His Tyr His Met Thr Thr Ala His  
115 120 125  
Phe Ser Thr Glu Ala Ser Xaa Met Asp His Pro Thr Glu Ala Val Glu  
130 135 140  
Glu Met Tyr Gln Lys Met Leu Lys Ser Val Glu Ala Glu Thr Met Pro  
145 150 155 160  
Pro Asn Ala Trp Leu Trp Ser Met Ile Asp Ser Cys Ser Asn Lys Glu  
165 170 175  
Asp Ile Lys Leu Leu Phe Gln Ile Leu Gln Lys Leu Arg Val Phe Arg  
180 185 190  
Leu Ser Asn Leu Arg Ile Ser Ala Thr Ser Met Ser Ile Ser Ala  
195 200 205

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Met Gln Ala Ala Ala Ala Arg Ala Arg Arg Leu Leu Ala Leu Pro Ala  
1 5 10 15

Ala Ser Gly Ile Pro Gly Ile Leu Ser Gly Pro Ile Pro Gly Arg Ala  
20 25 30  
Ser Tyr Ala Glu Gly Val Leu Leu Tyr Arg Leu Asn Gly Ala Pro Ala  
35 40 45  
Ser Pro Ser Ser Pro Gln His Thr Arg Gly Phe Ser Ser Ser Cys Phe  
50 55 60  
Ala Ser Arg Ser His Cys Asn Leu Pro Ser Pro Thr Ile Ala Ser Gln  
65 70 75 80  
Trp Leu Asn Glu Lys Ser Val His Tyr His Met Thr Thr Ala His Phe  
85 90 95  
Ser Thr Glu Ala Ser Xaa Met Asp His Pro Thr Glu Ala Val Glu Glu  
100 105 110  
Met Tyr Gln Lys Met Leu Lys Ser Val Glu Ala Glu Thr Met Pro Pro  
115 120 125  
Asn Ala Trp Leu Trp Ser Met Ile Asp Ser Cys Ser Asn Lys Glu Asp  
130 135 140  
Ile Lys Leu Leu Phe Gln Ile Leu Gln Lys Leu Arg Val Phe Arg Leu  
145 150 155 160  
Ser Asn Leu Arg Ile Ser Ala Thr Ser Met Ser Ile Ser Ala  
165 170

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..558
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| atgtataacg cgacccccct cccagtcctc cccagcggca aggcggcaac cgttctcccg | 60  |
| cgccccgcac tccccccct tttccttttg ctcccttcctt cctcggaag cctagggctt  | 120 |
| aggctttaag cgccgcgant gtacggcggc ggccggcgcg gcgggcacta cgacggaggc | 180 |
| agcgggtggc cggggaacgc taacgcgctc ttcggcgggc ggggcttcat gccctcacag | 240 |
| tccacgggtg tccccggaga cagcggcctc tctaagggtc ggagcgcgca gacgctgctc | 300 |
| ccgctcaccg tgaacacagc catggacgcg gcgcaaacca gcggtgacag gtctaatttc | 360 |
| gccatcaacg gcgttgaggt gtctacgatt aggcttggtg gacgcatgct aggtaagggt | 420 |
| gagcgtgtca cagatgttgt attcactctt gatgatggtg ctggcaagat agatgtgaat | 480 |
| cgctgggaaa atgaggcttc cgatgctaag gagatggctg atgctaataa cgagaactat | 540 |
| gtcatagtca ttggcggg                                               |     |

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

Met Pro Ser Gln Ser Thr Val Val Pro Glu Asn Ser Gly Leu Ser Lys  
1 5 10 15  
Gly Arg Ser Ala Gln Thr Leu Leu Pro Leu Thr Val Lys Gln Thr Met  
20 25 30  
Asp Ala Ala Gln Thr Ser Gly Asp Arg Ser Asn Phe Ala Ile Asn Gly

```

 35 40 45
Val Glu Val Ser Thr Ile Arg Leu Val Gly Arg Met Leu Gly Lys Val
 50 55 60
Glu Arg Val Thr Asp Val Val Phe Thr Leu Asp Asp Gly Thr Gly Lys
65 70 75 80
Ile Asp Val Asn Arg Trp Glu Asn Glu Ala Ser Asp Ala Lys Glu Met
 85 90 95
Ala Asp Ala Asn Asn Glu Asn Tyr Val Ile Val Ile Gly Gly
 100 105 110
```

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

```

Met Asp Ala Ala Gln Thr Ser Gly Asp Arg Ser Asn Phe Ala Ile Asn
1 5 10 15
Gly Val Glu Val Ser Thr Ile Arg Leu Val Gly Arg Met Leu Gly Lys
 20 25 30
Val Glu Arg Val Thr Asp Val Val Phe Thr Leu Asp Asp Gly Thr Gly
 35 40 45
Lys Ile Asp Val Asn Arg Trp Glu Asn Glu Ala Ser Asp Ala Lys Glu
 50 55 60
Met Ala Asp Ala Asn Asn Glu Asn Tyr Val Ile Val Ile Gly Gly
65 70 75
```

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..581
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

```

aaagatattt gtgtagataa cagtagatta aagtctaaaa taagagagga gatggtggat 60
gaaatagggg agttttgaca gcctaattgt aattggaagc ctttcttggc ctgccctcgg 120
cgcggaaccg tcccgcactc acgcatcagc gtcgcacact cgcacgtgcc tccgtcttcg 180
ctccctcggg ccctccgcag cgtcagatcg accgtcgctc gcggasccta gcgacgccgt 240
tctcaagtcc gagccggagt agcacgagag ccttgcggnat tatgagtcgc gccgcggcag 300
caagaacgat ggatgaggaa gccgagtagc tggagacggc tcggggccgac cgctccgtgt 360
ggctcatgaa gtgccccccg gtcgtttccc gcgcctggca ggccgcctcc gcctcttcc 420
ccgatgctgc caacgccaac ccgctcgttg ccaaggtcgt cctttccctt gacctgttgc 480
gccaagaaga acgcccggaa gagcctacgc tccagttcaa gatggaattg gctcaacta 540
acaccgggaa tacacctaag agctactctt tgaatatgtt c
```

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1482103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

Met Ser Arg Ala Ala Ala Arg Thr Met Asp Glu Glu Ala Glu Tyr  
1 5 10 15  
Leu Glu Thr Ala Arg Ala Asp Arg Ser Val Trp Leu Met Lys Cys Pro  
20 25 30  
Pro Val Val Ser Arg Ala Trp Gln Ala Ala Ser Ala Ser Ser Ser Asp  
35 40 45  
Ala Ala Asn Ala Asn Pro Val Val Ala Lys Val Val Leu Ser Leu Asp  
50 55 60  
Leu Leu Arg Gln Glu Glu Arg Pro Glu Glu Pro Thr Leu Gln Phe Lys  
65 70 75 80  
Met Glu Leu Ala Gln Thr Asn Thr Gly Asn Thr Pro Lys Ser Tyr Ser  
85 90 95  
Leu Asn Met Phe  
100

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1482104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

Met Asp Glu Glu Ala Glu Tyr Leu Glu Thr Ala Arg Ala Asp Arg Ser  
1 5 10 15  
Val Trp Leu Met Lys Cys Pro Pro Val Ser Arg Ala Trp Gln Ala  
20 25 30  
Ala Ser Ala Ser Ser Ser Asp Ala Ala Asn Ala Asn Pro Val Val Ala  
35 40 45  
Lys Val Val Leu Ser Leu Asp Leu Leu Arg Gln Glu Glu Arg Pro Glu  
50 55 60  
Glu Pro Thr Leu Gln Phe Lys Met Glu Leu Ala Gln Thr Asn Thr Gly  
65 70 75 80  
Asn Thr Pro Lys Ser Tyr Ser Leu Asn Met Phe  
85 90

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1482105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

Met Lys Cys Pro Pro Val Val Ser Arg Ala Trp Gln Ala Ala Ser Ala  
1 5 10 15  
Ser Ser Ser Asp Ala Ala Asn Ala Asn Pro Val Val Ala Lys Val Val

20 25 30  
Leu Ser Leu Asp Leu Leu Arg Gln Glu Glu Arg Pro Glu Glu Pro Thr  
35 40 45  
Leu Gln Phe Lys Met Glu Leu Ala Gln Thr Asn Thr Gly Asn Thr Pro  
50 55 60  
Lys Ser Tyr Ser Leu Asn Met Phe  
65 70

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..812  
(D) OTHER INFORMATION: / Ceres Seq. ID 1482106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

gatcgagttg gctcattaac aattcagttt cgtaaacaag cctggaggga aaaaggacac 60  
atcacccaaa ggcacaggga atcgaccat cgtgggaccc gtacagcgca ccgcccagcc 120  
gccggatctg cgccggcgac gcgcccggac gtcggatcta cgccgcccga ggarggggga 180  
ggcggcgctg tggccgttct ctgcccgta gcgcccggat ccgtcccgc gcaaggatta 240  
tgatccgaa agagaagcca aatgtatcga gcagtccacc aacaccacgg ctggactgca 300  
taaaatgctt tgatattgctc tggttctgtt actcaccatt ccaccagatg cagaattatt 360  
accggtatgg ggagttcgac acctgcttcg gcaagtgggg cgatcttatg ggctgcctcg 420  
ctctcaagac aaagcggaag gcagaggtgg aggagatcct catcgcgcg gagaaaggcca 480  
aaccacatat ctggacctac cggacggctg atgaggcatc ggagaattgg tggcggatgt 540  
acaagcatgc tgtgatgatg tcaccactgc caggttctgc tcagcttcct cccaggtccg 600  
atgaatcttg atagtcgagg ggatttgtgc aagtgttttg tttgcgctta tgtcacatta 660  
tggcattagc gatcatttct gttcaaaatc ttactgtaaa ctacaatacc aagagatgga 720  
accattgagg taggcagaac atgtactgct gaagattgag aatttgaaat cgccttgat 780  
tcagaagcaa ataaatgaac gaggtttcct tt

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..202  
(D) OTHER INFORMATION: / Ceres Seq. ID 1482107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

Ser Ser Trp Leu Ile Asn Asn Ser Val Ser Leu Thr Ser Leu Glu Gly  
1 5 10 15  
Lys Arg Thr His His Pro Lys Ala Gln Gly Ile Ala Pro Ser Trp Asp  
20 25 30  
Pro Tyr Ser Ala Pro Pro Ser Arg Arg Ile Cys Ala Gly Asp Ala Pro  
35 40 45  
Gly Arg Arg Ile Tyr Ala Ala Ala Gly Xaa Gly Arg Arg Cys Gly  
50 55 60  
Arg Ser Leu Pro Val Ser Ala Arg Ile Arg Pro Ala Ala Arg Ile Met  
65 70 75 80  
Asp Pro Lys Glu Lys Pro Asn Val Ser Ser Ser Pro Pro Thr Pro Arg  
85 90 95  
Leu Asp Cys Ile Lys Cys Phe Asp Met Leu Trp Phe Cys Tyr Ser Pro  
100 105 110

Phe His Gln Met Gln Asn Tyr Tyr Arg Tyr Gly Glu Phe Asp Thr Cys  
115 120 125  
Phe Gly Lys Trp Gly Asp Leu Met Gly Cys Leu Ala Leu Lys Thr Lys  
130 135 140  
Arg Lys Ala Glu Val Glu Ile Leu Ile Ala Arg Glu Lys Ala Lys  
145 150 155 160  
Pro His Ile Trp Thr Tyr Arg Thr Val Asp Glu Ala Ser Glu Asn Trp  
165 170 175  
Trp Arg Met Tyr Lys His Ala Val Met Met Ser Pro Leu Pro Gly Ser  
180 185 190  
Ala Gln Leu Pro Pro Arg Ser Asp Glu Ser  
195 200

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1482108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

Met Asp Pro Lys Glu Lys Pro Asn Val Ser Ser Pro Pro Thr Pro  
1 5 10 15  
Arg Leu Asp Cys Ile Lys Cys Phe Asp Met Leu Trp Phe Cys Tyr Ser  
20 25 30  
Pro Phe His Gln Met Gln Asn Tyr Tyr Arg Tyr Gly Glu Phe Asp Thr  
35 40 45  
Cys Phe Gly Lys Trp Gly Asp Leu Met Gly Cys Leu Ala Leu Lys Thr  
50 55 60  
Lys Arg Lys Ala Glu Val Glu Glu Ile Leu Ile Ala Arg Glu Lys Ala  
65 70 75 80  
Lys Pro His Ile Trp Thr Tyr Arg Thr Val Asp Glu Ala Ser Glu Asn  
85 90 95  
Trp Trp Arg Met Tyr Lys His Ala Val Met Met Ser Pro Leu Pro Gly  
100 105 110  
Ser Ala Gln Leu Pro Pro Arg Ser Asp Glu Ser  
115 120

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 675 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..675

(D) OTHER INFORMATION: / Ceres Seq. ID 1482113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

|            |             |            |            |             |             |     |
|------------|-------------|------------|------------|-------------|-------------|-----|
| ataaatcccg | agaccaaacc  | ctcgctcca  | ttcgctcccc | gccgcgcgcg  | ctcccagttct | 60  |
| ctacgcggaa | gcagcgccctc | gcaccgctcc | tacccaatgg | cgccgacgtc  | gaagctgtcg  | 120 |
| atgagcatca | agcgtgcgtc  | gcgctcgcac | gcgtaccacc | gccgtgggct  | ctggggccatc | 180 |
| aaggccaaga | acggcggcgt  | cttcccgaag | gccgagaaac | mngcmgcccgc | cgcggaaccc  | 240 |
| aagttctacc | ccgccgacga  | cgtcaagcct | cgcgttccca | gcacccgcaa  | gcctaataccc | 300 |
| accaagctca | ggtcgagcat  | cacgcctggg | acggtgctga | tcctcctcgc  | ggggcagaac  | 360 |
| ttgggttccg | cggcggcggc  | kcgcgccggg | tccgacggcg | cggccgcggc  | gcaggcggcg  | 420 |

gccttcgga aggccaacga gggcaaggcg tagctgcctg tgctgtgcat atgcatgtgt 480  
ggttaattag ctggagtgt cgggtcgctt aatctgttgg atttgatggt ttgttggttg 540  
tgtgcgcgtg tgtttcagtg atttgctcct ttttttttct ttctcgtgga tctatcgatg 600  
gatgaacatg aatgaatgaa ccgaactgca cagctccgtt gtgagctgat gcatgcatgc 660  
actagctagt agctg

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1482114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

Ile Asn Pro Glu Thr Lys Pro Ser Pro Pro Phe Val Pro Arg Arg Arg  
1 5 10 15  
Arg Ser Gln Ser Leu Arg Gly Ser Ser Ala Ser His Arg Ser Tyr Pro  
20 25 30  
Met Ala Pro Thr Ser Lys Leu Ser Met Ser Ile Lys Arg Ala Ser Arg  
35 40 45  
Ser His Ala Tyr His Arg Arg Gly Leu Trp Ala Ile Lys Ala Lys Asn  
50 55 60  
Gly Gly Val Phe Pro Lys Ala Glu Lys Xaa Xaa Ala Ala Ala Glu Pro  
65 70 75 80  
Lys Phe Tyr Pro Ala Asp Asp Val Lys Pro Arg Val Pro Ser Thr Arg  
85 90 95  
Lys Pro Asn Pro Thr Lys Leu Arg Ser Ser Ile Thr Pro Gly Thr Val  
100 105 110  
Leu Ile Leu Leu Ala Gly Gln Asn Leu Gly Ser Ala Ala Ala Xaa Ala  
115 120 125  
Ala Gly Ser Asp Gly Ala Ala Ala Ala Gln Ala Ala Ala Phe Arg Lys  
130 135 140  
Ala Asn Glu Gly Lys Ala  
145 150

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1482115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

Met Ala Pro Thr Ser Lys Leu Ser Met Ser Ile Lys Arg Ala Ser Arg  
1 5 10 15  
Ser His Ala Tyr His Arg Arg Gly Leu Trp Ala Ile Lys Ala Lys Asn  
20 25 30  
Gly Gly Val Phe Pro Lys Ala Glu Lys Xaa Xaa Ala Ala Ala Glu Pro  
35 40 45  
Lys Phe Tyr Pro Ala Asp Asp Val Lys Pro Arg Val Pro Ser Thr Arg  
50 55 60  
Lys Pro Asn Pro Thr Lys Leu Arg Ser Ser Ile Thr Pro Gly Thr Val  
65 70 75 80



Leu Ile Leu Leu Ala Gly Gln Asn Leu Gly Ser Ala Ala Ala Xaa Ala  
85 90 95  
Ala Gly Ser Asp Gly Ala Ala Ala Ala Gln Ala Ala Ala Phe Arg Lys  
100 105 110  
Ala Asn Glu Gly Lys Ala  
115

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

Met Ser Ile Lys Arg Ala Ser Arg Ser His Ala Tyr His Arg Arg Gly  
1 5 10 15  
Leu Trp Ala Ile Lys Ala Lys Asn Gly Gly Val Phe Pro Lys Ala Glu  
20 25 30  
Lys Xaa Xaa Ala Ala Ala Glu Pro Lys Phe Tyr Pro Ala Asp Asp Val  
35 40 45  
Lys Pro Arg Val Pro Ser Thr Arg Lys Pro Asn Pro Thr Lys Leu Arg  
50 55 60  
Ser Ser Ile Thr Pro Gly Thr Val Leu Ile Leu Ala Gly Gln Asn  
65 70 75 80  
Leu Gly Ser Ala Ala Ala Xaa Ala Ala Gly Ser Asp Gly Ala Ala Ala  
85 90 95  
Ala Gln Ala Ala Ala Phe Arg Lys Ala Asn Glu Gly Lys Ala  
100 105 110

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 871 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..871
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

|            |             |            |             |             |            |     |
|------------|-------------|------------|-------------|-------------|------------|-----|
| gagccaaaca | tgcccgtccg  | cccagtctcg | ctccaaacca  | aagccatcgg  | aggagcaact | 60  |
| ggacgaccat | ggcctcgccg  | ctgctcaagt | cacactctca  | gctcgccgcc  | gccgccgccc | 120 |
| tgcactccgt | gaggagagcc  | gaccgctgcc | ctgcgacact  | acacctgggc  | aagttccatg | 180 |
| accacgggct | caggtccggc  | cgttctaaga | gatccggttc  | agcgaggggtg | ggcgcccttc | 240 |
| cgtcgctgga | cgtaggtgccg | ctgatggtga | cgatggtgga  | gcacgtggac  | atgtcgcggg | 300 |
| actacgtcgt | gaccaagtcc  | atctggcatc | tcagcgacgt  | agccctcaag  | agcgtctata | 360 |
| ccttctacgc | catgttcacc  | gtctggggag | tctgcttctt  | cgcgctccatg | aaggatccct | 420 |
| tctacgacag | cgagacgtac  | aggagccagg | gtggcgacgg  | gaccgtgcac  | tggtactacg | 480 |
| acaggcaaga | ggacctggag  | gcgtctgcga | gggaggagct  | gctgcgggag  | gagctgctcg | 540 |
| aggagattga | gcagaggggtt | gggggcctca | gggagctgga  | ggaagcgagc  | aaggaggagc | 600 |
| agctcacaaa | gtgatcacgc  | gcgggcgaat | accgaatggg  | atggatacgg  | gctactcatc | 660 |
| agctctctat | ctgagcttcg  | ttagcaaata | agttcagact  | tctttactgc  | cctgctcaag | 720 |
| tctgtatatg | gccaaaaccc  | aaaacgattg | atcaactgcg  | ctactgcagt  | gcaatagcag | 780 |
| gatacgtata | gttttttttt  | caagggaaac | aggagggggag | tgcagtgcac  | ccctgcccac | 840 |
| actgcatgtt | attaataaaa  | gaaagttatt | t           |             |            |     |

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..203

(D) OTHER INFORMATION: / Ceres Seq. ID 1482118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

Ala Lys His Ala Arg Pro Pro Ser Leu Ala Pro Asn Gln Ser His Arg  
1 5 10 15  
Arg Ser Asn Trp Thr Thr Met Ala Ser Pro Leu Leu Lys Ser His Ser  
20 25 30  
Gln Leu Ala Ala Ala Ala Leu His Ser Val Arg Arg Ala Asp Arg  
35 40 45  
Cys Pro Ala Thr Leu His Leu Gly Lys Phe His Asp His Gly Leu Arg  
50 55 60  
Ser Gly Arg Ser Lys Arg Ser Gly Ser Ala Arg Val Gly Ala Phe Pro  
65 70 75 80  
Ser Leu Asp Val Val Pro Leu Met Val Thr Met Val Glu His Val Asp  
85 90 95  
Met Ser Arg Asp Tyr Val Val Thr Lys Ser Ile Trp His Leu Ser Asp  
100 105 110  
Val Ala Leu Lys Ser Val Tyr Thr Phe Tyr Ala Met Phe Thr Val Trp  
115 120 125  
Gly Val Cys Phe Phe Ala Ser Met Lys Asp Pro Phe Tyr Asp Ser Glu  
130 135 140  
Thr Tyr Arg Ser Gln Gly Gly Asp Gly Thr Val His Trp Tyr Tyr Asp  
145 150 155 160  
Arg Gln Glu Asp Leu Glu Ala Ser Ala Arg Glu Glu Leu Leu Arg Glu  
165 170 175  
Glu Leu Leu Glu Glu Ile Glu Gln Arg Val Gly Gly Leu Arg Glu Leu  
180 185 190  
Glu Glu Ala Ser Lys Glu Glu Gln Leu Thr Lys  
195 200

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..181

(D) OTHER INFORMATION: / Ceres Seq. ID 1482119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

Met Ala Ser Pro Leu Leu Lys Ser His Ser Gln Leu Ala Ala Ala  
1 5 10 15  
Ala Leu His Ser Val Arg Arg Ala Asp Arg Cys Pro Ala Thr Leu His  
20 25 30  
Leu Gly Lys Phe His Asp His Gly Leu Arg Ser Gly Arg Ser Lys Arg  
35 40 45  
Ser Gly Ser Ala Arg Val Gly Ala Phe Pro Ser Leu Asp Val Val Pro  
50 55 60  
Leu Met Val Thr Met Val Glu His Val Asp Met Ser Arg Asp Tyr Val

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Val | Thr | Lys | Ser | Ile | Trp | His | Leu | Ser | Asp | Val | Ala | Leu | Lys | Ser | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Thr | Phe | Tyr | Ala | Met | Phe | Thr | Val | Trp | Gly | Val | Cys | Phe | Phe | Ala |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Ser | Met | Lys | Asp | Pro | Phe | Tyr | Asp | Ser | Glu | Thr | Tyr | Arg | Ser | Gln | Gly |
|     |     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |
| Gly | Asp | Gly | Thr | Val | His | Trp | Tyr | Tyr | Asp | Arg | Gln | Glu | Asp | Leu | Glu |
|     |     |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |
| Ala | Ser | Ala | Arg | Glu | Glu | Leu | Leu | Arg | Glu | Glu | Leu | Leu | Glu | Glu | Ile |
|     |     |     |     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |
| Glu | Gln | Arg | Val | Gly | Gly | Leu | Arg | Glu | Leu | Glu | Glu | Ala | Ser | Lys | Glu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Gln | Leu | Thr | Lys |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 180 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1482120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Thr | Met | Val | Glu | His | Val | Asp | Met | Ser | Arg | Asp | Tyr | Val | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Lys | Ser | Ile | Trp | His | Leu | Ser | Asp | Val | Ala | Leu | Lys | Ser | Val | Tyr |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Thr | Phe | Tyr | Ala | Met | Phe | Thr | Val | Trp | Gly | Val | Cys | Phe | Phe | Ala | Ser |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |
| Met | Lys | Asp | Pro | Phe | Tyr | Asp | Ser | Glu | Thr | Tyr | Arg | Ser | Gln | Gly | Gly |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |
| Asp | Gly | Thr | Val | His | Trp | Tyr | Tyr | Asp | Arg | Gln | Glu | Asp | Leu | Glu | Ala |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |
| Ser | Ala | Arg | Glu | Glu | Leu | Leu | Arg | Glu | Glu | Leu | Leu | Glu | Glu | Ile | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Arg | Val | Gly | Gly | Leu | Arg | Glu | Leu | Glu | Glu | Ala | Ser | Lys | Glu | Glu |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Gln | Leu | Thr | Lys |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..531

(D) OTHER INFORMATION: / Ceres Seq. ID 1482121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tatggacttc | attaccgcca | cttaataacg | gatctacaga | gcatccgaaa | cctttaatat | 60  |
| tggctattgc | gtctcaagac | tctgcatcgt | tttttcggga | ccgtagtctt | ggttcagatt | 120 |
| ctcccatatc | tggattgatt | gctttgctca | ctgctgttga | tgctctttct | cacattcatg | 180 |
| gtctaagcaa | gcttaagaaa | cagcttggtg | tcgctgtttt | taatggtgag | gcctgggggt | 240 |

atcttggttag tcggaaattc ttacaggaat tagatgaagg cgctgcttct gtgaatggaa 300  
ttagtagctt aaagattgac caggtagctg agattgggtc tgttggaag gctatacttg 360  
aggaatatcc atcattttat gtgcatgctg aagggaaatcc atcagcttca aaggaaatat 420  
tagatgcact gcaaagtsca gcaagtctct tggttctgat aatgttaaag taaaacaagc 480  
agcttcatca aatcctggtg ttccaccatc ttcattaatg tcattcataa g

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

Trp Thr Ser Leu Pro Leu Asn Asn Gly Ser Thr Glu His Pro Lys  
1 5 10 15  
Pro Leu Ile Leu Ala Ile Ala Ser Gln Asp Ser Ala Ser Phe Phe Arg  
20 25 30  
Asp Arg Ser Leu Gly Ser Asp Ser Pro Ile Ser Gly Leu Ile Ala Leu  
35 40 45  
Leu Thr Ala Val Asp Ala Leu Ser His Ile His Gly Leu Ser Lys Leu  
50 55 60  
Lys Lys Gln Leu Val Phe Ala Val Phe Asn Gly Glu Ala Trp Gly Tyr  
65 70 75 80  
Leu Gly Ser Arg Lys Phe Leu Gln Glu Leu Asp Glu Gly Ala Ala Ser  
85 90 95  
Val Asn Gly Ile Ser Ser Leu Lys Ile Asp Gln Val Leu Glu Ile Gly  
100 105 110  
Ser Val Gly Lys Ala Ile Leu Glu Tyr Pro Ser Phe Tyr Val His  
115 120 125  
Ala Glu Gly Asn Pro Ser Ala Ser Lys Glu Ile Leu Asp Ala Leu Gln  
130 135 140  
Ser Xaa Ala Ser Leu Leu Val Leu Ile Met Leu Lys  
145 150 155

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..985
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

aaatttctcg atcaaacatg ctctattgcc ctgtatctat cctctatcga agccggagac 60  
cccagaaaaga gtccgtaaac aactcccggc catggcgacc gcagaccggg tcgccgccac 120  
cttcctctcc tctttcccca ctcaccatcc cgcccccttt tccctccgttt ccctcgtgac 180  
aaaccctgtc ctaccggtct cccttcgggc cgtgtgcaca ggtggccac ggctcgcctc 240  
ccgtctccgg gtccaccgcg tcggcgccgc cgctcgccag ctccccacca cgaatccgga 300  
ggtagcttct ggggagaaga agatcagatg gtcataaagg gctgtgcggt cttttgcgat 360  
ggcagagctg gaggcccgga agatgaggta ccctaccaca ggcaccgagg ggctcctcat 420  
gggcattctt gttgaaggaa ctagtggcgc asaaaacttt tgcgtgctaa tggaaccaca 480  
cttctcaaag tgcgtgagga ggcagcgaat gttcttggga aatcagaaat gttttacttt 540  
agtcccatgc atccaccatt gacagaagct gcacaacgag cccttgattg ggctgtcaat 600

gaaaaattga aatcaggtga ggatggagaa gtaaccgcca atcatttgct actygggata 660  
tggtcagata aagagtggc tggtcataaa atcctgtatt cgcctggatt tgacgatgag 720  
aaagccagtt tactggccaa aacggctggt gaagaggctg caatgagtct tagagagcaa 780  
ggagagcacc taatttattc gtcaacttaa gttgggtattg tgcactagct tttatgcact 840  
tcttggtgcc tcgagacgtt gacctggaga ggctgcctct acaaacttta gaacttatta 900  
tgagatatg ttaggtcaga tacgatattt gtactctcac gattgccgat gcctgtgaaa 960  
acgttgcgct ttgtttgtca cgggg

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

Asn Phe Ser Ile Lys His Ala Leu Leu Pro Cys Ile Tyr Pro Leu Ser  
1 5 10 15  
Lys Pro Glu Thr Pro Glu Arg Val Arg Lys Gln Leu Pro Ala Met Ala  
20 25 30  
Thr Ala Asp Arg Val Ala Ala Thr Phe Leu Ser Ser Phe Pro Thr His  
35 40 45  
His Pro Arg Pro Phe Ser Ser Val Ser Leu Val Thr Asn Pro Val Leu  
50 55 60  
Pro Val Ser Leu Arg Ala Ala Val Thr Gly Gly Pro Arg Leu Ala Ser  
65 70 75 80  
Arg Leu Arg Val His Arg Val Gly Ala Ala Val Ala Gln Leu Pro Thr  
85 90 95  
Thr Asn Pro Glu Val Ala Ser Gly Glu Lys Lys Ile Arg Trp Ser Ser  
100 105 110  
Arg Ala Val Arg Ser Phe Ala Met Ala Glu Leu Glu Ala Arg Lys Met  
115 120 125  
Arg Tyr Pro Thr Thr Gly Thr Glu Gly Leu Leu Met Gly Ile Leu Val  
130 135 140  
Glu Gly Thr Ser Gly Ala Xaa Asn Phe Cys Val Leu Met Glu Pro His  
145 150 155 160  
Phe Ser Lys Cys Val Arg Arg Gln Arg Met Phe Leu Gly Asn Gln Lys  
165 170 175  
Cys Phe Thr Leu Val Pro Cys Ile His His  
180 185

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

Met Ala Thr Ala Asp Arg Val Ala Ala Thr Phe Leu Ser Ser Phe Pro  
1 5 10 15  
Thr His His Pro Arg Pro Phe Ser Ser Val Ser Leu Val Thr Asn Pro  
20 25 30

Val Leu Pro Val Ser Leu Arg Ala Ala Val Thr Gly Gly Pro Arg Leu  
35 40 45  
Ala Ser Arg Leu Arg Val His Arg Val Gly Ala Ala Val Ala Gln Leu  
50 55 60  
Pro Thr Thr Asn Pro Glu Val Ala Ser Gly Glu Lys Lys Ile Arg Trp  
65 70 75 80  
Ser Ser Arg Ala Val Arg Ser Phe Ala Met Ala Glu Leu Glu Ala Arg  
85 90 95  
Lys Met Arg Tyr Pro Thr Thr Gly Thr Glu Gly Leu Leu Met Gly Ile  
100 105 110  
Leu Val Glu Gly Thr Ser Gly Ala Xaa Asn Phe Cys Val Leu Met Glu  
115 120 125  
Pro His Phe Ser Lys Cys Val Arg Arg Gln Arg Met Phe Leu Gly Asn  
130 135 140  
Gln Lys Cys Phe Thr Leu Val Pro Cys Ile His His  
145 150 155

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

Met Phe Tyr Phe Ser Pro Met His Pro Pro Leu Thr Glu Ala Ala Gln  
1 5 10 15  
Arg Ala Leu Asp Trp Ala Val Asn Glu Lys Leu Lys Ser Gly Glu Asp  
20 25 30  
Gly Glu Val Thr Ala Asn His Leu Leu Leu Gly Ile Trp Ser Asp Lys  
35 40 45  
Glu Ser Ala Gly His Lys Ile Leu Tyr Ser Leu Gly Phe Asp Asp Glu  
50 55 60  
Lys Ala Ser Leu Leu Ala Lys Thr Ala Gly Glu Glu Ala Ala Met Ser  
65 70 75 80  
Leu Arg Glu Gln Gly Glu His Leu Ile Tyr Ser Ser Thr  
85 90

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..852
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ataggtgggt cgaacttcga aggggttcga ggacttcagc tatggcatct gtgggacgtg | 60  |
| caggacgagg agggaaagga gatggaggga agggagaagg gtcgctggct cgcagggcgt | 120 |
| ggaggcagta cctgctccag ctccagcaac atcctctccg cacaaagatg atcacggcgg | 180 |
| ggtgcctcgc cggcgtcagt gactccgtgg cgcagaagct ctctgggttc cagaagattg | 240 |
| agaaacgcag actcctgctc aagatgctct ttggttttgc atatggtggc ccatttggac | 300 |
| atttcttgca caaaattttg gattacatct tccaagggaa gaaggatacc aaaaccatag | 360 |
| caaagaaggt gttattggag caagtgacat cttctccctg gaataacata ttgttcttgt | 420 |

|            |            |             |            |             |             |     |
|------------|------------|-------------|------------|-------------|-------------|-----|
| tctattatgg | atatgttggt | gagaggaggc  | ctttgaagga | ggtgacgacc  | agggtgaaga  | 480 |
| aacaataccc | ttctgtgcaa | ctcagcgctt  | ggatgttttg | gccgatagtt  | ggttggataa  | 540 |
| accaccagta | catgccttta | caattccgag  | tgatcttcca | cagctttgtc  | gcatgttggt  | 600 |
| gggggatttt | cctgaacctt | cgtgcaaggg  | ctatgtctct | gaagcaggcc  | tagatggttt  | 660 |
| agaaggaacg | tatagcagca | aagctcctgc  | ccggtgctaa | ctaaagcagc  | cgaagaagga  | 720 |
| ggatgctgga | agctgtatcc | tgcacgggta  | caaaaaccgt | tgttttatttc | ctggtagtag  | 780 |
| tcggtttatt | tgaatgtcaa | cgcattgcgaa | gacagattat | gctttttgta  | aaaaaaaaatt | 840 |
| gtgatgggag | cg         |             |            |             |             |     |

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..216

(D) OTHER INFORMATION: / Ceres Seq. ID 1482132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Trp | Val | Glu | Leu | Arg | Arg | Gly | Ser | Arg | Thr | Ser | Ala | Met | Ala | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Gly | Arg | Ala | Gly | Arg | Gly | Gly | Lys | Gly | Asp | Gly | Gly | Lys | Gly | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ser | Leu | Ala | Arg | Arg | Ala | Trp | Arg | Gln | Tyr | Leu | Leu | Gln | Leu | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | His | Pro | Leu | Arg | Thr | Lys | Met | Ile | Thr | Ala | Gly | Cys | Leu | Ala | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Ser | Asp | Ser | Val | Ala | Gln | Lys | Leu | Ser | Gly | Phe | Gln | Lys | Ile | Glu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Arg | Arg | Leu | Leu | Leu | Lys | Met | Leu | Phe | Gly | Phe | Ala | Tyr | Gly | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Pro | Phe | Gly | His | Phe | Leu | His | Lys | Ile | Leu | Asp | Tyr | Ile | Phe | Gln | Gly |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Lys | Lys | Asp | Thr | Lys | Thr | Ile | Ala | Lys | Lys | Val | Leu | Leu | Glu | Gln | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Ser | Ser | Pro | Trp | Asn | Asn | Ile | Leu | Phe | Leu | Phe | Tyr | Tyr | Gly | Tyr |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Val | Val | Glu | Arg | Arg | Pro | Leu | Lys | Glu | Val | Thr | Thr | Arg | Val | Lys | Lys |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Gln | Tyr | Pro | Ser | Val | Gln | Leu | Ser | Ala | Trp | Met | Phe | Trp | Pro | Ile | Val |
|     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Gly | Trp | Ile | Asn | His | Gln | Tyr | Met | Pro | Leu | Gln | Phe | Arg | Val | Ile | Phe |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| His | Ser | Phe | Val | Ala | Cys | Cys | Trp | Gly | Ile | Phe | Leu | Asn | Leu | Arg | Ala |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Arg | Ala | Met | Ser | Leu | Lys | Gln | Ala |     |     |     |     |     |     |     |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..203

(D) OTHER INFORMATION: / Ceres Seq. ID 1482133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Ala | Ser | Val | Gly | Arg | Ala | Gly | Arg | Gly | Gly | Lys | Gly | Asp | Gly | Gly |  |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |  |
| Lys | Gly | Glu | Gly | Ser | Leu | Ala | Arg | Arg | Ala | Trp | Arg | Gln | Tyr | Leu | Leu |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Gln | Leu | Gln | Gln | His | Pro | Leu | Arg | Thr | Lys | Met | Ile | Thr | Ala | Gly | Cys |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Leu | Ala | Gly | Val | Ser | Asp | Ser | Val | Ala | Gln | Lys | Leu | Ser | Gly | Phe | Gln |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Lys | Ile | Glu | Lys | Arg | Arg | Leu | Leu | Leu | Lys | Met | Leu | Phe | Gly | Phe | Ala |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |
| Tyr | Gly | Gly | Pro | Phe | Gly | His | Phe | Leu | His | Lys | Ile | Leu | Asp | Tyr | Ile |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Phe | Gln | Gly | Lys | Lys | Asp | Thr | Lys | Thr | Ile | Ala | Lys | Lys | Val | Leu | Leu |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Glu | Gln | Val | Thr | Ser | Ser | Pro | Trp | Asn | Asn | Ile | Leu | Phe | Leu | Phe | Tyr |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |  |
| Tyr | Gly | Tyr | Val | Val | Glu | Arg | Pro | Leu | Lys | Glu | Val | Thr | Thr | Arg |     |  |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Val | Lys | Lys | Gln | Tyr | Pro | Ser | Val | Gln | Leu | Ser | Ala | Trp | Met | Phe | Trp |  |  |
| 145 |     |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Pro | Ile | Val | Gly | Trp | Ile | Asn | His | Gln | Tyr | Met | Pro | Leu | Gln | Phe | Arg |  |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |  |
| Val | Ile | Phe | His | Ser | Phe | Val | Ala | Cys | Cys | Trp | Gly | Ile | Phe | Leu | Asn |  |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Leu | Arg | Ala | Arg | Ala | Met | Ser | Leu | Lys | Gln | Ala |     |     |     |     |     |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Ile | Thr | Ala | Gly | Cys | Leu | Ala | Gly | Val | Ser | Asp | Ser | Val | Ala | Gln |  |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |  |
| Lys | Leu | Ser | Gly | Phe | Gln | Lys | Ile | Glu | Lys | Arg | Arg | Leu | Leu | Lys |     |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Met | Leu | Phe | Gly | Phe | Ala | Tyr | Gly | Gly | Pro | Phe | Gly | His | Phe | Leu | His |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Lys | Ile | Leu | Asp | Tyr | Ile | Phe | Gln | Gly | Lys | Lys | Asp | Thr | Lys | Thr | Ile |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Ala | Lys | Lys | Val | Leu | Leu | Glu | Gln | Val | Thr | Ser | Ser | Pro | Trp | Asn | Asn |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |  |
| Ile | Leu | Phe | Leu | Phe | Tyr | Tyr | Gly | Tyr | Val | Val | Glu | Arg | Arg | Pro | Leu |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |  |
| Lys | Glu | Val | Thr | Arg | Val | Lys | Lys | Gln | Tyr | Pro | Ser | Val | Gln | Leu |     |  |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |  |
| Ser | Ala | Trp | Met | Phe | Trp | Pro | Ile | Val | Gly | Trp | Ile | Asn | His | Gln | Tyr |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Met | Pro | Leu | Gln | Phe | Arg | Val | Ile | Phe | His | Ser | Phe | Val | Ala | Cys | Cys |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Trp | Gly | Ile | Phe | Leu | Asn | Leu | Arg | Ala | Arg | Ala | Met | Ser | Leu | Lys | Gln |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |



Ala

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..533
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| cgaaaaatgg attcattcag acgtgatcct tggcccttga attgggagac cttctgcaga  | 60  |
| gacgcacaag cccaggggga aaaaagtttc agtcagtaag ggagaataag cattgcaaac  | 120 |
| cgaaacagag gtaatcaata aaggatggga aacatggata aggatcaatt agagcatcta  | 180 |
| accccgcat tccaaccaat gactcggtga atcgctgac taggaatact ctgatattac    | 240 |
| atctgctctg ccatcataa tctgttcacg ttctacaacg aakcctataa gttgaagcaa   | 300 |
| ccgcagatgc aattgtagga gtattttgtt tcttttctgt gatttggctt cagcacaac   | 360 |
| agcacaaggg catctccaaa gacagtcagc taccgtgacc gtgaggcatg acatcgttta  | 420 |
| ttcagtgaag gaaaaaaaaa tgcaacgagc agctaagggtc gcaagtaccc aagctagtca | 480 |
| tcgctaagct gtaastgaga gtatgtatca gtttctacag acgactgtgg aag         |     |

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

|                                                                                                              |  |
|--------------------------------------------------------------------------------------------------------------|--|
| Arg Lys Met Asp Ser Phe Arg Arg Asp Pro Trp Pro Leu Asn Trp Glu                                              |  |
| 1                  5                                          10                                          15 |  |
| Thr Phe Cys Arg Asp Ala Gln Ala Gln Gly Glu Lys Ser Phe Ser Gln                                              |  |
| 20                                          25                                          30                   |  |

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

|                                                                                                              |  |
|--------------------------------------------------------------------------------------------------------------|--|
| Met Asp Ser Phe Arg Arg Asp Pro Trp Pro Leu Asn Trp Glu Thr Phe                                              |  |
| 1                  5                                          10                                          15 |  |
| Cys Arg Asp Ala Gln Ala Gln Gly Glu Lys Ser Phe Ser Gln                                                      |  |
| 20                                          25                                          30                   |  |

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..450

(D) OTHER INFORMATION: / Ceres Seq. ID 1482142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| attcgaattt cgaacgccgc cggtcgctcc ctgttcccta gctctctcct ccgcgggtcc  | 60  |
| gcctccggcc tccacgggtt cgcaggcaga gatgaagaag gcgtccgcgg cgtcgcgcta  | 120 |
| cgcgccctac gactccccgt ccccttcgcc gcgcgcgcgc gscncttccg cggccgccgc  | 180 |
| gaccccgga gcagcgcacg gcagcagccg cgccttggtg gtcgcgggga gatccggccg   | 240 |
| cgatctactg ggcgccaagc cgcaagccca cggcaacctt ggctccgtgc tacggcggtc  | 300 |
| catctccatg gacaagaagc cgccttcctc caagaaccag ctcccggttc cccctgcmgc  | 360 |
| mgcmgccgca gcagcagcag cagcgaagaa caacgggtggc gggaagctgc mggggctgtm | 420 |
| gcggaagtgt ttccagaaa cctcgtccac                                    |     |

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1482143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ile Arg Ile Ser Asn Ala Ala Gly Arg Ser Leu Phe Pro Ser Ser Leu |  |
| 1 5 10 15                                                       |  |
| Leu Arg Gly Ser Ala Ser Gly Leu His Gly Phe Ala Gly Arg Asp Glu |  |
| 20 25 30                                                        |  |
| Glu Gly Val Arg Gly Val Ala Leu Arg Gly Leu Arg Leu Pro Val Pro |  |
| 35 40 45                                                        |  |
| Phe Ala Ala Pro Arg Xaa Xaa Phe Arg Gly Arg Arg Asp Pro Gly Ser |  |
| 50 55 60                                                        |  |
| Ser Ala Arg Gln Gln Pro Arg Pro Gly Gly Arg Gly Glu Ile Arg Pro |  |
| 65 70 75 80                                                     |  |
| Arg Ser Thr Gly Arg Gln Ala Ala Ser Pro Arg Gln Pro Arg Leu Arg |  |
| 85 90 95                                                        |  |
| Ala Thr Ala Ala His Leu His Gly Gln Glu Ala Ala Phe Leu Gln Glu |  |
| 100 105 110                                                     |  |
| Pro Ala Pro Gly Ser Pro Cys Xaa Xaa Xaa Arg Ser Ser Ser Ser Ser |  |
| 115 120 125                                                     |  |
| Glu Glu Gln Arg Trp Arg Glu Ala Xaa Gly Ala Xaa Ala Glu Val Val |  |
| 130 135 140                                                     |  |
| Pro Glu Ser Leu Val His                                         |  |
| 145 150                                                         |  |

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1482144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

Phe Glu Phe Arg Thr Pro Pro Val Ala Pro Cys Ser Leu Ala Leu Ser  
1 5 10 15  
Ser Ala Ala Pro Pro Ala Ser Thr Val Ser Gln Ala Glu Met Lys  
20 25 30  
Lys Ala Ser Ala Ala Ser Arg Tyr Ala Ala Tyr Asp Ser Pro Ser Pro  
35 40 45  
Ser Pro Arg Arg Ala Xaa Xaa Ser Ala Ala Ala Ala Thr Pro Gly Ala  
50 55 60  
Ala His Gly Ser Ser Arg Ala Leu Val Val Ala Gly Arg Ser Gly Arg  
65 70 75 80  
Asp Leu Leu Gly Ala Lys Pro Gln Ala His Gly Asn Leu Gly Ser Val  
85 90 95  
Leu Arg Arg Leu Ile Ser Met Asp Lys Lys Pro Pro Ser Ser Lys Asn  
100 105 110  
Gln Leu Pro Val Pro Pro Xaa Xaa Xaa Ala Ala Ala Ala Ala Ala Ala  
115 120 125  
Lys Asn Asn Gly Gly Gly Lys Leu Xaa Gly Leu Xaa Arg Lys Leu Phe  
130 135 140  
Gln Lys Ala Ser Ser  
145

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1482145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

Met Lys Lys Ala Ser Ala Ala Ser Arg Tyr Ala Ala Tyr Asp Ser Pro  
1 5 10 15  
Ser Pro Ser Pro Arg Arg Ala Xaa Xaa Ser Ala Ala Ala Ala Thr Pro  
20 25 30  
Gly Ala Ala His Gly Ser Ser Arg Ala Leu Val Val Ala Gly Arg Ser  
35 40 45  
Gly Arg Asp Leu Leu Gly Ala Lys Pro Gln Ala His Gly Asn Leu Gly  
50 55 60  
Ser Val Leu Arg Arg Leu Ile Ser Met Asp Lys Lys Pro Pro Ser Ser  
65 70 75 80  
Lys Asn Gln Leu Pro Val Pro Pro Xaa Xaa Xaa Ala Ala Ala Ala Ala  
85 90 95  
Ala Ala Lys Asn Asn Gly Gly Gly Lys Leu Xaa Gly Leu Xaa Arg Lys  
100 105 110  
Leu Phe Gln Lys Ala Ser Ser  
115

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 434 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..36

(D) OTHER INFORMATION: / Ceres Seq. ID 1482156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

Met Ala Ser Ser Gln Cys Cys Asp Asn Pro Pro Ala Leu Asn Pro Ala  
1 5 10 15  
Cys Gly Glu Gly Lys Val Val Asp Ser Phe Gly Gly Leu Lys Ala Tyr  
20 25 30  
Xaa Ala Gly Pro  
35

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 633 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..633

(D) OTHER INFORMATION: / Ceres Seq. ID 1482157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

agagttcagg ggggagccag cgaagacaag acaagccagg ccagcggcgg aggagagggg 60  
gagagagaga gagagagcac ggcacagtag gcaggagggc gaggaggagc ttgtagaggg 120  
ttaaggaagg cgaccgccat gggggactcc agcggctccg tgctcggtcga cgctcagcgg 180  
atcttcttcg gcggcaagga gcatcgagta agaacgaggc atggctctct ttcggtttct 240  
gtgtatggag acgaggacaa gccgcgcgtc gtaacttata cggatgtagc cttaaatcac 300  
atgtcttgct tccaaggatt gttcttctgt ccgagggtg cgtccctggt gcttcacagt 360  
ttctgcgtgt accacatcac acctcaagga cagcagttgg gagcagctcc gatttcagct 420  
gatgtgcctg tgccatctgt cgacgacctt gcagatcagg ttgctgatgt cctcgatttt 480  
ttcagtttag ggtctgtcat gtgcttgggt gtcactgctg gtgcctatgt tctcaccctc 540  
tttgcaacta agtatcgga gaggggtcct ggctcatgt tggtttcacc tgtatgcaaa 600  
gccccctcct ggagcgagtg gctgtataat aag

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1482158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

Met Gly Asp Ser Ser Gly Ser Val Ser Val Asp Val Glu Arg Ile Phe  
1 5 10 15  
Phe Gly Gly Lys Glu His Arg Val Arg Thr Arg His Gly Ser Leu Ser  
20 25 30  
Val Ser Val Tyr Gly Asp Glu Asp Lys Pro Ala Leu Val Thr Tyr Pro  
35 40 45  
Asp Val Ala Leu Asn His Met Ser Cys Phe Gln Gly Leu Phe Phe Cys  
50 55 60  
Pro Glu Ala Ala Ser Leu Leu Leu His Ser Phe Cys Val Tyr His Ile  
65 70 75 80  
Thr Pro Gln Gly His Glu Leu Gly Ala Ala Pro Ile Ser Ala Asp Val  
85 90 95  
Pro Val Pro Ser Val Asp Asp Leu Ala Asp Gln Val Ala Asp Val Leu  
100 105 110  
Asp Phe Phe Ser Leu Gly Ser Val Met Cys Leu Gly Val Thr Ala Gly

115 120 125  
Ala Tyr Val Leu Thr Leu Phe Ala Thr Lys Tyr Arg Glu Arg Val Leu  
130 135 140  
Gly Leu Met Leu Val Ser Pro Val Cys Lys Ala Pro Ser Trp Ser Glu  
145 150 155 160  
Trp Leu Tyr Asn Lys  
165

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

Met Ser Cys Phe Gln Gly Leu Phe Phe Cys Pro Glu Ala Ala Ser Leu  
1 5 10 15  
Leu Leu His Ser Phe Cys Val Tyr His Ile Thr Pro Gln Gly His Glu  
20 25 30  
Leu Gly Ala Ala Pro Ile Ser Ala Asp Val Pro Val Pro Ser Val Asp  
35 40 45  
Asp Leu Ala Asp Gln Val Ala Asp Val Leu Asp Phe Phe Ser Leu Gly  
50 55 60  
Ser Val Met Cys Leu Gly Val Thr Ala Gly Ala Tyr Val Leu Thr Leu  
65 70 75 80  
Phe Ala Thr Lys Tyr Arg Glu Arg Val Leu Gly Leu Met Leu Val Ser  
85 90 95  
Pro Val Cys Lys Ala Pro Ser Trp Ser Glu Trp Leu Tyr Asn Lys  
100 105 110

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..461
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

ctcgagtcga gcgaaccgaa gccgaacata cccacccatc gtctcgtcgt ctcgtcgcgc 60  
gtgggctgtg ctctctctcc cccacactcc tcttttaaga cgacgccatc gccagccggc 120  
cctccctcgc cgtccggcgc cgtcctcctt cgtccttccc tctcatcaca gtttccacct 180  
cgcgaggggc tcgcgcgcgc gcccatcccg gccgatcgac tcacgaattc gcgcgcgatc 240  
atattcgtgc aagggcaccc ccgcacggcc ggaagcacgg aatcacttcc ccgcccccca 300  
attcccgggc tctcggcgc mgatccctcg ccggtgttcg ctttcgggcg gtttcgcgcg 360  
cgtgtcgcgg gcaggcgcag gcggctcggc tcggttgttt cctcctcgtg ccatcatcca 420  
tggaggcgaa sagcgcmcgc ggcacggcgg ggagaggagg c

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1482165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

Leu Glu Ser Ser Glu Pro Lys Pro Asn Ile Pro Thr His Arg Leu Val  
1 5 10 15  
Val Ser Ser Arg Val Gly Val Ala Leu Ser Pro Pro Thr Ser Ser Phe  
20 25 30  
Lys Thr Thr Pro Ser Pro Ala Gly Pro Pro Ser Pro Ser Gly Ala Val  
35 40 45  
Leu Leu Arg Pro Ser Leu Ser Ser Gln Phe Pro Pro Arg Glu Gly Leu  
50 55 60  
Ala Arg Ala Pro Ile Pro Ala Asp Arg Leu Thr Asn Ser Arg Ala Ile  
65 70 75 80  
Ile Phe Val Gln Gly His Pro Arg Thr Ala Gly Ser Thr Glu Ser Leu  
85 90 95  
Pro Arg Pro Pro Ile Pro Gly Leu Leu Gly Xaa Asp Pro Ser Pro Val  
100 105 110  
Phe Ala Phe Arg Arg Phe Pro Arg Arg Val Ala Gly Arg Arg Arg Arg  
115 120 125  
Leu Gly Ser Val Val Ser Ser Ser Cys His His Pro Trp Arg Arg Xaa  
130 135 140  
Ala Xaa Ala Ala Arg Arg Gly Glu Glu  
145 150

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1482166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

Ser Ser Arg Ala Asn Arg Ser Arg Thr Tyr Pro Pro Ile Val Ser Ser  
1 5 10 15  
Ser Arg Arg Ala Trp Ala Trp Leu Ser Leu Pro Pro Pro Pro Leu Leu  
20 25 30  
Arg Arg Arg His Arg Gln Pro Ala Leu Pro Arg Arg Pro Ala Pro Ser  
35 40 45  
Ser Phe Val Leu Pro Ser His His Ser Phe His Leu Ala Arg Gly Ser  
50 55 60  
Arg Ala Arg Pro Ser Arg Pro Ile Asp Ser Arg Ile Arg Ala Arg Ser  
65 70 75 80  
Tyr Ser Cys Lys Gly Ile Pro Ala Arg Pro Glu Ala Arg Asn His Phe  
85 90 95  
Pro Ala Pro Gln Phe Pro Gly Ser Ser Ala Xaa Ile Pro Arg Arg Cys  
100 105 110  
Ser Leu Ser Gly Gly Phe Arg Gly Val Ser Arg Ala Gly Ala Gly Gly  
115 120 125  
Ser Ala Arg Leu Phe Pro Pro Arg Ala Ile Ile His Gly Gly Glu Xaa  
130 135 140  
Arg Xaa Arg His Gly Gly Glu Arg Arg  
145 150

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..615
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| aaaacccaaaa | agaagggttg | ctcccaacgc | aacgaactgc | ctttcccgtc | agcagcagca | 60  |
| gcagctgcys  | cntgctgctg | tccatctcca | tcctcccat  | cgcccactg  | gatttctccc | 120 |
| tcgaattcgc  | acctccggcc | tccccctca  | cttcgctgtg | tctcatcaac | gccggcatca | 180 |
| ccgcgaggac  | tgggccagcg | ctccctccct | ttctcctccc | tccgccttta | ttgctgacgg | 240 |
| cgacgactgg  | gcgagctctg | ccgcgcgtct | gcgctaggtg | cccaggtcct | cctcgggcac | 300 |
| ttcacccggc  | acgagcacc  | atcaggagcg | aaatggacga | ggctgttcct | gctttggcta | 360 |
| ctggccaagc  | ttcaaccgac | ggcgtgacag | agcagcctgt | gaatgtgtac | atatgggaca | 420 |
| tggatgagac  | actcattttg | ctcaagtcac | ttctggatgg | ctcatatgct | ggggcttttg | 480 |
| atggcctcaa  | ggatcatgag | aaaagtactg | aaataggaaa | gcgatgggag | aacctcattc | 540 |
| ttgaactctg  | tgatgagcac | ttcttttatg | aggagattga | gaactacaat | gaaccctatc | 600 |
| tcaatgcctt  | gaatg      |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..204
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Gln | Lys | Glu | Gly | Leu | Leu | Pro | Thr | Gln | Arg | Thr | Ala | Phe | Pro | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ser | Ser | Ser | Ser | Cys | Xaa | Xaa | Leu | Leu | Ser | Ile | Ser | Ile | Leu | Pro |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ile | Ala | Arg | Leu | Asp | Phe | Ser | Leu | Glu | Phe | Ala | Pro | Pro | Ala | Ser | Pro |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Leu | Thr | Ser | Leu | Cys | Leu | Ile | Asn | Ala | Gly | Ile | Thr | Ala | Arg | Thr | Gly |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Pro | Ala | Leu | Pro | Pro | Phe | Leu | Leu | Pro | Pro | Pro | Leu | Leu | Leu | Thr | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Thr | Gly | Arg | Ala | Leu | Pro | Pro | Leu | Cys | Ala | Arg | Cys | Pro | Gly | Leu |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Pro | Arg | Ala | Leu | His | Arg | Arg | Arg | Ala | Pro | Ile | Arg | Ser | Glu | Met | Asp |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Glu | Ala | Val | Pro | Ala | Leu | Ala | Thr | Gly | Gln | Ala | Ser | Thr | Asp | Gly | Val |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Thr | Glu | Gln | Pro | Val | Asn | Val | Tyr | Ile | Trp | Asp | Met | Asp | Glu | Thr | Leu |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |
| Ile | Leu | Leu | Lys | Ser | Leu | Leu | Asp | Gly | Ser | Tyr | Ala | Gly | Ala | Phe | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gly | Leu | Lys | Asp | His | Glu | Lys | Ser | Thr | Glu | Ile | Gly | Lys | Arg | Trp | Glu |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Asn | Leu | Ile | Leu | Glu | Leu | Cys | Asp | Glu | His | Phe | Phe | Tyr | Glu | Glu | Ile |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Glu | Asn | Tyr | Asn | Glu | Pro | Tyr | Leu | Asn | Ala | Leu | Asn |     |     |     |     |



195 200

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 508 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..508

(D) OTHER INFORMATION: / Ceres Seq. ID 1482169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| attcgataac | caagaacaaa | ccattgttgg | acgcgttccc | ctcctgcacg  | caacctcatc  | 60  |
| tcgtcctcca | gatccaggat | ggccgtcctc | cttgagacct | tgccctccccg | agtgtctctcg | 120 |
| gtgagctact | ttgtttcgat | ttatcaggaa | atccgtttgc | ttcatgttgt  | gcaggctcat  | 180 |
| atctgattgc | tggattcggc | aaaccgcgt  | tggatcctgt | atcggttagt  | ccttgccctgc | 240 |
| aaggttcttg | ttgtwttgtt | ttgttggtcg | agcatcgcat | gttctgcttc  | tggatccaga  | 300 |
| tctggagaaa | tcgcgaagtc | gtcgtcgttc | ggttcggagc | ggatctgagg  | cgacgataga  | 360 |
| tggaggcggc | gggatctctc | ggtctgcagt | cctgctccac | ctcgatggat  | gatgtctctg  | 420 |
| cgctgataat | tattggatca | atttcgataa | ttatwagtag | atctatgaga  | tatgcccgct  | 480 |
| ggaagaggcg | aggtaagctg | cagcatgt   |            |             |             |     |

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..40

(D) OTHER INFORMATION: / Ceres Seq. ID 1482170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Asp | Asn | Gln | Glu | Gln | Thr | Ile | Val | Gly | Arg | Val | Pro | Leu | Leu | His |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Thr | Ser | Ser | Arg | Pro | Pro | Asp | Pro | Gly | Trp | Pro | Ser | Ser | Leu | Arg |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Pro | Cys | Leu | Pro | Glu | Cys | Ser | Arg |     |     |     |     |     |     |     |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..35

(D) OTHER INFORMATION: / Ceres Seq. ID 1482171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Val | Leu | Glu | Thr | Leu | Pro | Pro | Arg | Val | Leu | Ser | Val | Ser |     |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |     |
| Tyr | Phe | Val | Ser | Ile | Tyr | Gln | Glu | Ile | Arg | Leu | Leu | His | Val | Val | Gln |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ala | His | Ile |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 35  |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 49 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..49  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1482172  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:  
Met Glu Ala Ala Gly Ser Leu Gly Leu Gln Ser Cys Ser Thr Ser Met  
1                    5                    10                    15  
Asp Asp Val Ser Ala Leu Ile Ile Ile Gly Ser Ile Ser Ile Ile Xaa  
                    20                    25                    30  
Ser Arg Ser Met Arg Tyr Ala Ala Trp Lys Arg Arg Gly Lys Leu Gln  
                    35                    40                    45  
His

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 597 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..597  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1482177  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:  
aatcctaccc cgcgggggga attctctctc agttctctcg gcgacgactg ggagaccgcc          60  
gccgccgcca tctactcca ggtgccctga gaactcgatc ggagtcttcg ctggcgacga          120  
acaccacca gctatcaggt gtacaacat gtacttcacc gtgtccgcc ctgcaatgct          180  
tctatgatcc tccagctacg gtagacgccc cgttcgctag ctgaggacct cctggttcct          240  
gtgagcaggc ggcgtgggta gctgctgcct tcaagcatgc agagacccaa cgcgccgctc          300  
gcttgcgcta ccatacctt cgcggaggct ctaaggaggg agatggagta ccgaagtgg          360  
gtggagagga cccaccaca tctgctcgtc ggaatctgcg gasccctgaa atgcagagag          420  
atttcagtgc aggaccagta cctgatgcga tcaagagaaa actagctgcc gagaccagtg          480  
tgccctccaca acaatcaagt ttcagctgtg taactggaca gaagcagccc caaaactggt          540  
acccacaaaa gaaaaagggtg aaagttccac atcttccgtc gcagattctg cagtgtc

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 61 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..61  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1482178  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:  
Ile Leu Pro Arg Gly Gly Asn Ser Leu Ser Val Leu Ser Ala Thr Thr  
1                    5                    10                    15  
Gly Arg Pro Pro Pro Pro Pro Ser Tyr Ser Arg Cys Pro Glu Asn Ser  
                    20                    25                    30  
Ile Gly Val Phe Ala Gly Asp Glu His Pro Pro Ala Ile Arg Cys Thr  
                    35                    40                    45

Thr Met Tyr Phe Thr Val Ser Ala Pro Ala Met Ser Leu  
50 55 60

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

Ser Tyr Pro Ala Gly Gly Ile Leu Ser Gln Phe Ser Arg Arg Arg Leu  
1 5 10 15  
Gly Asp Arg Arg Arg His Pro Thr Pro Gly Ala Leu Arg Thr Arg  
20 25 30  
Ser Glu Ser Ser Leu Ala Thr Asn Thr His Gln Leu Ser Gly Val Gln  
35 40 45  
Pro Cys Thr Ser Pro Cys Pro Pro Leu Gln Cys Leu Tyr Asp Pro Pro  
50 55 60  
Ala Thr Val Asp Ala Pro Phe Ala Ser  
65 70

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..62
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

Met Gln Arg Pro Asn Ala Pro Ser Ala Cys Ala Thr Ile Thr Phe Ala  
1 5 10 15  
Glu Ala Leu Arg Arg Glu Met Glu Tyr Arg Lys Trp Val Glu Arg Thr  
20 25 30  
His Pro His Leu Leu Val Gly Ile Cys Gly Xaa Leu Lys Cys Arg Glu  
35 40 45  
Ile Ser Val Gln Asp Gln Tyr Leu Met Arg Ser Arg Glu Asn  
50 55 60

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..576
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

aggattcaca agtgctcgta gcaaattctac aaaatcccca accgcctctc aacaaagtct 60  
ccccacggag gtacacagct acgcgcaaac cgcgtctcgc gcgaagaatc cgcatttccc 120  
cttccccgca ccgcaccgca cccaaccccc gtcggagaga gagatggcat cgggtggcgga 180

```
gatgcagccc ctgcgcgcgg cgggggtaccg cscgcgcggg agatgaagga gaaggtggag 240
gcgtcgggtg tggacctgga ggccggggacc ggggagacgc tgtaccgggg gatctcgcgc 300
ggggagagcg ccctccgatg gggcttcgtc cgcaaggtct acggcatcct cgctgcgcas 360
tgctcctcac caccgccgtc tccgcmctca ccgttctcca cccaccctc aacgccacgc 420
tctccgactc cccgggmctm gcgctmgtrc tgcgmgtmmt gcccttmatc ctgatgatcc 480
cattgtatca ttatcagcac aagcaccac acaattccgt tttcctgggt ctgttcacgt 540
tggtgcttga gcttcagcat cggcgtgggt tgtgct
```

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..191
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

```
Asp Ser Gln Val Leu Val Ala Asn Leu Gln Asn Pro Gln Pro Pro Leu
1 5 10 15
Asn Lys Val Ser Pro Arg Arg Tyr Thr Ala Thr Arg Lys Pro Arg Leu
20 25 30
Ala Arg Arg Ile Arg Ile Ser Pro His Arg Thr Ala Pro Asn
35 40 45
Pro Arg Arg Arg Glu Arg Trp His Arg Trp Arg Arg Cys Ser Pro Ser
50 55 60
Arg Arg Arg Gly Thr Xaa Arg Ala Gly Asp Glu Gly Glu Gly Gly Gly
65 70 75 80
Val Gly Gly Gly Pro Gly Gly Arg Asp Arg Gly Asp Ala Val Pro Gly
85 90 95
Asp Leu Ala Arg Gly Glu Arg Pro Pro Met Gly Leu Arg Pro Gln Gly
100 105 110
Leu Arg His Pro Arg Cys Ala Xaa Leu Leu Thr Thr Ala Val Ser Xaa
115 120 125
Leu Thr Val Leu His Pro Thr Leu Asn Ala Thr Leu Ser Asp Ser Pro
130 135 140
Xaa Xaa Ala Xaa Xaa Leu Xaa Xaa Xaa Pro Xaa Ile Leu Met Ile Pro
145 150 155 160
Leu Tyr His Tyr Gln His Lys His Pro His Asn Ser Val Phe Leu Gly
165 170 175
Leu Phe Thr Leu Val Leu Glu Leu Gln His Arg Arg Gly Leu Cys
180 185 190
```

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..412
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

```
actccactct actccacccg cgcacaacag atcgacgccc tcggttcctt ccaactcgacg 60
cttctcccg ccttaacccc tagtaccttc gctcgctctg ccgcctccgc cgacgacgcg 120
ccagatccgc gcrsagtggg gtccctccgc gcggatcgag ctcccgatcc gcgcagtggg 180
agtggcgggc agcgcaggag cgctcggccc ggggttccgc gaggctggag acggaggagg 240
```

aaggagcg tagttccg gtagtagatc cgccggctcct gtcgcccggag atggactcat 300  
ctgtcgagaa gcaggggagc gtggcgctgg atccggacga gcgcrcgccc gcgtccggcg 360  
aaaccaaggc ctgcaccgag tgccacacca ccaagacccc gctctggcgc gg

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Pro | Leu | Tyr | Ser | Thr | Arg | Ala | Gln | Gln | Ile | Ala | Arg | Leu | Gly | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | His | Ser | Thr | Leu | Leu | Pro | Leu | Leu | Thr | Pro | Ser | Thr | Phe | Ala | Arg |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ser | Ala | Ala | Ser | Ala | Asp | Asp | Ala | Pro | Asp | Pro | Arg | Xaa | Val | Val | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ala | Ala | Asp | Arg | Ala | Pro | Asp | Pro | Arg | Ser | Gly | Ser | Gly | Gly | Glu |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Arg | Arg | Ser | Ala | Arg | Pro | Gly | Val | Pro | Arg | Gly | Trp | Arg | Arg | Arg | Arg |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Lys | Gly | Ala | Val | Val | Pro | Arg | Trp |     |     |     |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..486
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| attcattacc | ggaagagaaa | aaagtaactc | ggaaaagaag | gagacgccga | aaattcgaaa  | 60  |
| ggggagggga | aagcaaagct | gatggcggag | gcccagggga | aagcaaagca | aatggcggag  | 120 |
| gccccgagca | agatcgaatc | catgaggaag | tgggtcgctc | agcacaagct | ccgagccgta  | 180 |
| gttgccctct | gctaggtggg | atcagcagtt | cgatcgccct | caactggctc | cggcccaata  | 240 |
| tgaagcctag | cgtaagatc  | atccacgcaa | ggttgcatgc | tcaagctcta | accctggctg  | 300 |
| cattagttgg | ttctgcatgc | gtggagtact | atgaccagaa | gtatggttct | tctgggccaa  | 360 |
| aggtggacaa | atacacaagc | caatacctgg | cccattcgca | taaagattaa | aggtcgccat  | 420 |
| gttggttcct | gcatgccgga | taaattttgg | gctcatctcg | ggttgctcat | gagtcattgac | 480 |
| ccgccc     |            |            |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

```
Ser Leu Pro Glu Glu Lys Lys Val Thr Arg Lys Arg Arg Arg Arg Arg
1 5 10 15
Lys Phe Glu Arg Gly Gly Glu Ser Lys Ala Asp Gly Gly Gly Pro Gly
20 25 30
Glu Ser Lys Ala Asn Gly Gly Gly Pro Glu Gln Asp Arg Ile His Glu
35 40 45
Glu Val Gly Arg Arg Ala Gln Ala Pro Ser Arg Ser Cys Leu Trp Leu
50 55 60
Gly Gly Ile Ser Ser Ser Ile Ala Tyr Asn Trp Ser Arg Pro Asn Met
65 70 75 80
Lys Pro Ser Val Lys Ile Ile His Ala Arg Leu His Ala Gln Ala Leu
85 90 95
Thr Leu Ala Ala Leu Val Gly Ser Ala Cys Val Glu Tyr Tyr Asp Gln
100 105 110
Lys Tyr Gly Ser Ser Gly Pro Lys Val Asp Lys Tyr Thr Ser Gln Tyr
115 120 125
Leu Ala His Ser His Lys Asp
130 135
```

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..778
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

```
ggcagaggca cggagcctca actccactgc cctgctgcaa ttttttctct gttagtcgat 60
cagccagcga gtgaaaccaa gaaattcatg gcggttgaa ggagacacgg gagggaggta 120
tgcattgtcc tggcgaggtg ctcccagcgg cgtagtccacc agtctgttga ctcattggga 180
catggtcata gtcggcgtcg gcttgctcga gtgccagcag caaccatggc cctattcgca 240
gccatagggg gtcagccttc ttgcgctctc atggcatcgg tggagctgat agaggggtctt 300
gggggggctcc ccgtcgacgg gtctccagcg gccactgcag caccacgaag cacaatgttg 360
ttgcccgggt ctgccagggg ggcgctgtcg aagggtcgac ccaagaagcg gatctcgatg 420
ttgagtggcg cagcgtgctc cactttgcat ctcccagatg tggtcctcca ccggcggcga 480
gcccgggtgg aggtggagct cttgtggctg gaaggcggag gggaggaatg gatcggtaga 540
tgggagggag aggaaggtct tscggtgggg aggaatacac ggatggcgaat tcgggagggg 600
acgacggcga tctactaggg tttagtttgg gcgtgagggg atgagggcgg atggcgatct 660
ggagacaatg acggcggttc agattagggt tgcgagcggc tcgatgggcg cgtacgtggg 720
gtggatccga gcggtccgcc gcgtcacaa tcaactat tttttatgta aaacggat
```

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

```
Met Phe Leu Ala Arg Cys Ser Gln Arg Arg Ser His Gln Ser Val Asp
1 5 10 15
Ser Trp Gly His Gly His Ser Arg Arg Arg Leu Ala Arg Val Pro Ala
```

|             |             |             |             |             |     |
|-------------|-------------|-------------|-------------|-------------|-----|
|             | 20          |             | 25          |             | 30  |
| Ala Thr Met | Ala Leu Phe | Ala Ala Ile | Gly Gly Gln | Pro Ser Cys | Ala |
| 35          |             | 40          |             | 45          |     |
| Leu Met Ala | Ser Val Glu | Leu Ile Glu | Gly Leu Gly | Gly Leu Pro | Val |
| 50          |             | 55          |             | 60          |     |
| Asp Gly Ser | Pro Ala Ala | Thr Ala Ala | Pro Arg Ser | Thr Met Leu | Leu |
| 65          |             | 70          |             | 75          | 80  |
| Pro Gly Ser | Ala Arg Gly | Ala Leu Ser | Lys Gly Arg | Pro Lys Lys | Arg |
|             | 85          |             | 90          |             | 95  |
| Ile Ser Met | Leu Ser Gly | Ala Ala Cys | Ser Thr Leu | His Leu Pro | Asp |
|             | 100         |             | 105         |             | 110 |
| Val Val Leu | His Arg Arg | Arg Ala Arg | Val Glu Val | Glu Leu Leu | Trp |
|             | 115         |             | 120         |             | 125 |
| Leu Glu Gly | Gly Gly Glu | Glu Trp Ile | Gly Arg Trp | Glu Gly Glu | Glu |
| 130         |             | 135         |             | 140         |     |
| Gly Leu Xaa | Val Gly Arg | Asn Thr Arg | Met Ala Ile | Arg Glu Gly | Thr |
| 145         |             | 150         |             | 155         | 160 |
| Thr Ala Ile | Tyr         |             |             |             |     |

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1482209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

|                 |             |             |             |             |
|-----------------|-------------|-------------|-------------|-------------|
| Met Ala Leu Phe | Ala Ala Ile | Gly Gly Gln | Pro Ser Cys | Ala Leu Met |
| 1               | 5           | 10          |             | 15          |
| Ala Ser Val     | Glu Leu Ile | Gly Leu Gly | Leu Pro Val | Asp Gly     |
|                 | 20          | 25          |             | 30          |
| Ser Pro Ala     | Ala Thr Ala | Ala Pro Arg | Ser Thr Met | Leu Leu Pro |
|                 | 35          | 40          |             | 45          |
| Ser Ala Arg     | Gly Ala Leu | Ser Lys Gly | Arg Pro Lys | Lys Arg Ile |
|                 | 50          | 55          |             | 60          |
| Met Leu Ser     | Gly Ala Ala | Cys Ser Thr | Leu His Leu | Pro Asp Val |
|                 | 65          | 70          |             | 75          |
| Leu His Arg     | Arg Arg Ala | Arg Val Glu | Val Glu Leu | Leu Trp Leu |
|                 | 85          | 90          |             | 95          |
| Gly Gly Gly     | Glu Glu Trp | Ile Gly Arg | Trp Glu Gly | Glu Glu Gly |
|                 | 100         | 105         |             | 110         |
| Xaa Val Gly     | Arg Asn Thr | Arg Met Ala | Ile Arg Glu | Gly Thr Thr |
|                 | 115         | 120         |             | 125         |
| Ile Tyr         |             |             |             |             |
| 130             |             |             |             |             |

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1482210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

Met Ala Ser Val Glu Leu Ile Glu Gly Leu Gly Gly Leu Pro Val Asp  
1 5 10 15  
Gly Ser Pro Ala Ala Thr Ala Ala Pro Arg Ser Thr Met Leu Leu Pro  
20 25 30  
Gly Ser Ala Arg Gly Ala Leu Ser Lys Gly Arg Pro Lys Lys Arg Ile  
35 40 45  
Ser Met Leu Ser Gly Ala Ala Cys Ser Thr Leu His Leu Pro Asp Val  
50 55 60  
Val Leu His Arg Arg Arg Ala Arg Val Glu Val Glu Leu Leu Trp Leu  
65 70 75 80  
Glu Gly Gly Gly Glu Glu Trp Ile Gly Arg Trp Glu Gly Glu Glu Gly  
85 90 95  
Leu Xaa Val Gly Arg Asn Thr Arg Met Ala Ile Arg Glu Gly Thr Thr  
100 105 110  
Ala Ile Tyr  
115

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..721

(D) OTHER INFORMATION: / Ceres Seq. ID 1482217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

atcggttgggc cggcgcaaac cctagtcgcc acatcactgc ctctcacac catctgcctg 60  
tggttcccat gtcacctcc cccgtttgag gtcttcctgc tccttcagat ccgtctatgt 120  
gtgtgtttgt cgtgcctgat actggctcgg aaggtattcc gatctgttc ttcggtgccg 180  
tatatttcgt tgcgattttg gttcggttct ttcttgctct tcgtgggtcg ttgctggata 240  
acacggatcg ttgatgctgt tcaagaagta ctgcgttatc ttctgatgc aagtgttagg 300  
ccctcgttac gaaggcttcc tgacgacaca aatatcttgc tgagatccaa gtgcgcaact 360  
tctctctttt ttctctttct tttccgtatt tctcgccgtc tgctttttct cctctggatt 420  
gaattttgcg tacagttagg tttttaccaa atgcaatcgt aacttacggg caggatgggt 480  
tcagcaacga agtaaaggag gagattatc cgtcaaccgt aaggtgccgc taagagcttt 540  
agaatatgaa aggcattagt ggtaacaaga tttgatttgg ttaggtgtta gtacaaaaaa 600  
atgagattcg attccaatgc tgttgggggt actgctagtg aatatggccg ggcattctatc 660  
acggtgttgt atgtgtacga aataatgtct gctttcgata cggtaagttt tgctttaagt 720  
t

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1482218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

Ile Val Gly Pro Ala Gln Thr Leu Val Ala Thr Ser Leu Pro Pro His  
1 5 10 15  
Thr Ile Cys Leu Trp Phe Pro Cys His Pro Pro Pro Phe Glu Val Phe  
20 25 30



Leu Leu Leu Gln Ile Arg Leu Cys Val Cys Leu Ser Cys Leu Ile Leu  
35 40 45  
Ala Arg Lys Val Phe Arg Ser Val Ser Ser Val Pro Tyr Ile Ser Leu  
50 55 60  
Arg Phe Trp Phe Gly Ser Phe Leu Leu Phe Val Gly Arg Cys Trp Ile  
65 70 75 80  
Thr Arg Ile Val Asp Ala Val Gln Glu Val Leu Arg Tyr Leu Pro Asp  
85 90 95  
Ala Ser Val Arg Pro Ser Leu Arg Arg Leu Pro Asp Asp Thr Asn Ile  
100 105 110  
Leu Leu Arg Ser Lys Cys Ala Thr Ser Leu Phe Phe Leu Phe Leu Phe  
115 120 125  
Arg Ile Ser Arg Arg Leu Leu Phe Leu Leu Trp Ile Glu Phe Cys Val  
130 135 140  
Gln Phe Ser Phe Tyr Gln Met Gln Ser  
145 150

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..883
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| acgtctgttg | ctctctaccg  | gagacggatc | agcgtgtcaa | ctgacagccc | tatgtccttc | 60  |
| gccgctttct | catggccgtt  | tcgcccgcgg | ggcggggctg | gcagcagtgg | cgcaasaagt | 120 |
| ccgccgccac | ggcagaggag  | gacgaggagc | tgggcgtgac | cccgcagctc | ctcgacttcc | 180 |
| tccggacgct | ctcgcccgcac | gccttcaagg | ccgccgcact | ccagctccaa | ggagggtcca | 240 |
| cggaggcggc | cgccggncga  | cctcaccagc | tggcaggagc | ggcacgccgt | gctcgtgcta | 300 |
| tccaaagcta | aggaactcgc  | caagattcgg | tatgatctgt | gccctcggca | cctgaaggat | 360 |
| aagcagttct | ggaggatata  | cttctgtctc | gccaagagtt | acatctcacc | gtatgaacta | 420 |
| cgtgccatac | agaaggaaaa  | actcagacgg | atggagacag | aaaactgcaa | gccccaaaca | 480 |
| gtgatctctg | ttgaggtgga  | gatgcaagaa | tcgaagcgca | ctagtctctc | acaagcatca | 540 |
| gaagtagatc | tagaatctca  | ggtttagttt | tgcagttata | gcttctaaca | gatctagctt | 600 |
| aggtaacgca | atcagtagcc  | cttttatgat | tcctccacac | accaaatagc | tccacgagtt | 660 |
| cttcagatct | tggatcgact  | ctcgctagac | taccagtccg | ctgtgtgctt | ttgtgtactg | 720 |
| aaaccaagta | ggtccttttc  | tgcattacgc | agcatatgtg | cttgttggct | gtgctccgat | 780 |
| ccactgacat | gtaaatctag  | ggtatcttgc | gcgtgaacaa | aaacgactgc | gtttcatgta | 840 |
| gctatagatt | atgtcaactt  | cgattctgct | gtgcatgtgt | tgg        |            |     |

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

Arg Leu Leu Leu Ser Thr Gly Asp Gly Ser Ala Cys Gln Leu Thr Ala  
1 5 10 15  
Leu Cys Pro Ser Pro Leu Ser His Gly Arg Phe Ala Ala Gly Ala Gly  
20 25 30

Leu Ala Ala Val Ala Gln Xaa Val Arg Arg His Gly Arg Gly Gly Arg  
35 40 45  
Gly Ala Gly Arg Asp Pro Ala Ala Pro Arg Leu Pro Pro Asp Ala Leu  
50 55 60  
Ala Arg Arg Leu Gln Gly Arg Arg Thr Pro Ala Pro Arg Arg Leu His  
65 70 75 80  
Gly Gly Gly Arg Arg Xaa Thr Ser Pro Ala Gly Arg Ser Gly Thr Pro  
85 90 95  
Cys Ser Cys Tyr Pro Lys Leu Arg Asn Ser Pro Arg Phe Gly Met Ile  
100 105 110  
Cys Ala Leu Gly Thr  
115

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1482221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

Met Ala Val Ser Pro Gly Arg Gly Trp Gln Gln Trp Arg Xaa Lys  
1 5 10 15  
Ser Ala Ala Thr Ala Glu Glu Asp Glu Glu Leu Gly Val Thr Pro Gln  
20 25 30  
Leu Leu Asp Phe Leu Arg Thr Leu Ser Pro Asp Ala Phe Lys Ala Ala  
35 40 45  
Ala Leu Gln Leu Gln Gly Gly Ser Thr Glu Ala Ala Ala Xaa Arg Pro  
50 55 60  
His Gln Leu Ala Gly Ala Ala Arg Arg Ala Arg Ala Ile Gln Ser  
65 70 75

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 732 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..732

(D) OTHER INFORMATION: / Ceres Seq. ID 1482230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

taaaggcatc gacaaaatct ataagcagct gacaaaaagc catacacatc cactcggagg 60  
aacagcatat ttaaattctag aaaatgaaga cgaaccgttt cttaatggaa tcaagtacac 120  
agctatgcc a cctaccaagc ggtttagaga tatggaacag ttatccggtg gggagaagac 180  
tggtgcagca ctggctttgc tttttgccat tcacagtttt aggccatcac cgttcttcat 240  
attggacgaa ttagatgctg ctctggacaa tttaatgtg gccaagggtg ccgggtttat 300  
cagatcaaaa tcatgtgaac gtgttggtga tgaacaaggc agcgatggcg agagtggttt 360  
tcagagcata gttatatctc tgaaggacag tttctatgac aaggccgagg cacttggttg 420  
tgtttatagg gactcagaac gaagttgctc gaggactctc accttcgacc tgagaaagta 480  
tagggaatcg tgaagcagct tttgttgaat gtttgacta tgtgtgtagt tgcctgctcc 540  
atcagcttgc tagatagctg tcgtgagcct tcgatgtttt aactatctgt atactcctag 600  
tcctacataa gtgctagctg aacaaggacc ctgaaatatt catttggtag gtggataact 660  
gatgtttcga acacgcataa acttttttac ctgttgtagt aagccatttc tccgaattac 720  
tataatctgt tt

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

Lys Gly Ile Asp Lys Ile Tyr Lys Gln Leu Thr Lys Ser His Thr His  
1 5 10 15  
Pro Leu Gly Gly Thr Ala Tyr Leu Asn Leu Glu Asn Glu Asp Glu Pro  
20 25 30  
Phe Leu Asn Gly Ile Lys Tyr Thr Ala Met Pro Pro Thr Lys Arg Phe  
35 40 45  
Arg Asp Met Glu Gln Leu Ser Gly Gly Glu Lys Thr Val Ala Ala Leu  
50 55 60  
Ala Leu Leu Phe Ala Ile His Ser Phe Arg Pro Ser Pro Phe Phe Ile  
65 70 75 80  
Leu Asp Glu Val Asp Ala Ala Leu Asp Asn Leu Asn Val Ala Lys Val  
85 90 95  
Ala Gly Phe Ile Arg Ser Lys Ser Cys Glu Arg Val Gly Asp Glu Gln  
100 105 110  
Gly Ser Asp Gly Glu Ser Gly Phe Gln Ser Ile Val Ile Ser Leu Lys  
115 120 125  
Asp Ser Phe Tyr Asp Lys Ala Glu Ala Leu Val Gly Val Tyr Arg Asp  
130 135 140  
Ser Glu Arg Ser Cys Ser Arg Thr Leu Thr Phe Asp Leu Arg Lys Tyr  
145 150 155 160  
Arg Glu Ser

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

Met Pro Pro Thr Lys Arg Phe Arg Asp Met Glu Gln Leu Ser Gly Gly  
1 5 10 15  
Glu Lys Thr Val Ala Ala Leu Ala Leu Phe Ala Ile His Ser Phe  
20 25 30  
Arg Pro Ser Pro Phe Phe Ile Leu Asp Glu Val Asp Ala Ala Leu Asp  
35 40 45  
Asn Leu Asn Val Ala Lys Val Ala Gly Phe Ile Arg Ser Lys Ser Cys  
50 55 60  
Glu Arg Val Gly Asp Glu Gln Gly Ser Asp Gly Glu Ser Gly Phe Gln  
65 70 75 80  
Ser Ile Val Ile Ser Leu Lys Asp Ser Phe Tyr Asp Lys Ala Glu Ala  
85 90 95  
Leu Val Gly Val Tyr Arg Asp Ser Glu Arg Ser Cys Ser Arg Thr Leu

100 105 110  
Thr Phe Asp Leu Arg Lys Tyr Arg Glu Ser  
115 120  
(2) INFORMATION FOR SEQ ID NO:421:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..113  
(D) OTHER INFORMATION: / Ceres Seq. ID 1482233  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:  
Met Glu Gln Leu Ser Gly Gly Glu Lys Thr Val Ala Ala Leu Ala Leu  
1 5 10 15  
Leu Phe Ala Ile His Ser Phe Arg Pro Ser Pro Phe Phe Ile Leu Asp  
20 25 30  
Glu Val Asp Ala Ala Leu Asp Asn Leu Asn Val Ala Lys Val Ala Gly  
35 40 45  
Phe Ile Arg Ser Lys Ser Cys Glu Arg Val Gly Asp Glu Gln Gly Ser  
50 55 60  
Asp Gly Glu Ser Gly Phe Gln Ser Ile Val Ile Ser Leu Lys Asp Ser  
65 70 75 80  
Phe Tyr Asp Lys Ala Glu Ala Leu Val Gly Val Tyr Arg Asp Ser Glu  
85 90 95  
Arg Ser Cys Ser Arg Thr Leu Thr Phe Asp Leu Arg Lys Tyr Arg Glu  
100 105 110  
Ser

(2) INFORMATION FOR SEQ ID NO:422:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 773 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..773  
(D) OTHER INFORMATION: / Ceres Seq. ID 1482234  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:  
ctccgcccgc aggacgacgg caaatvcgcc cagacagggg ggacgtcgac gccggcgcaat 60  
cctgctcgga ttgcacacat caccgccacc cgtcgtgcgc cgacatctgt aggtcgccag 120  
ccaacaacct tagactgagg caccctgaat ccatctgcta ttgttcagct tgggtgttcgg 180  
gcaatccttg ttctgcctc agcacaaata gatcgccaag atgaatagaa gttggttgaa 240  
tgggtacattg ttttcccctg aatatatcaa tgggtgtcaaa gaatttatga gctttattca 300  
aagaaaattc ggtgaggatg aagatatttt gtgtccatgt agtagatgtc tcaacaaaaa 360  
gtcctttcat caagcctttg tggagaagca tatattaatg aatgggatgg aaagtacata 420  
tactcgatgg attcatcatg gagagaactt tgaggaagat gccggtcatt cgatacatgg 480  
gacaggtgtg attgatgatg acagctatgg tgcgtattgt tttgatggga tgttacaaga 540  
cctatgcact gcataagagc aagataaaga gcatgggtgaa aatgaggatg gagacaatac 600  
taatgatgac aatgagtcatt tttatagtgt rgtgctgaaa gaggcgaaac gtcatatatta 660  
tcctggttgt accaaatttt caaggttrtc ctttgtwgta aagcttcttc atatgaagtc 720  
attatatagg atcactaact ctgcatktac tgcarkatww aagttgttgg ttg  
(2) INFORMATION FOR SEQ ID NO:423:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 73 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..73
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1482235
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

Pro Pro Pro Gly Arg Arg Gln Xaa Arg Pro Asp Arg Val Asp Val Asp  
1 5 10 15  
Ala Gly Glu Ser Cys Ser Asp Cys Thr His His Arg His Pro Ser Cys  
20 25 30  
Ala Asp Ile Cys Arg Ser Pro Ala Asn Asn Leu Arg Leu Arg His Pro  
35 40 45  
Glu Ser Ile Cys Tyr Cys Ser Ala Trp Cys Ser Gly Asn Pro Cys Ser  
50 55 60  
Arg Leu Ser Thr Asn Arg Ser Pro Arg  
65 70

(2) INFORMATION FOR SEQ ID NO:424:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 111 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..111
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1482236
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

Met Asn Arg Ser Trp Leu Asn Gly Thr Leu Phe Ser Pro Glu Tyr Ile  
1 5 10 15  
Asn Gly Val Lys Glu Phe Met Ser Phe Ile Gln Arg Lys Phe Gly Glu  
20 25 30  
Asp Glu Asp Ile Leu Cys Pro Cys Ser Arg Cys Leu Asn Gln Lys Ser  
35 40 45  
Phe His Gln Ala Phe Val Glu Lys His Ile Leu Met Asn Gly Met Glu  
50 55 60  
Ser Thr Tyr Thr Arg Trp Ile His His Gly Glu Asn Phe Glu Glu Asp  
65 70 75 80  
Ala Gly His Ser Ile His Gly Thr Gly Val Ile Asp Asp Asp Ser Tyr  
85 90 95  
Gly Asp Asp Cys Phe Asp Gly Met Leu Gln Asp Leu Cys Thr Ala  
100 105 110

(2) INFORMATION FOR SEQ ID NO:425:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 89 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..89
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1482237
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

Met Ser Phe Ile Gln Arg Lys Phe Gly Glu Asp Glu Asp Ile Leu Cys  
1 5 10 15

Pro Cys Ser Arg Cys Leu Asn Gln Lys Ser Phe His Gln Ala Phe Val  
                  20                  25                  30  
Glu Lys His Ile Leu Met Asn Gly Met Glu Ser Thr Tyr Thr Arg Trp  
          35                  40                  45  
Ile His His Gly Glu Asn Phe Glu Glu Asp Ala Gly His Ser Ile His  
      50                  55                  60  
Gly Thr Gly Val Ile Asp Asp Asp Ser Tyr Gly Asp Asp Cys Phe Asp  
65                  70                  75                  80  
Gly Met Leu Gln Asp Leu Cys Thr Ala  
                  85

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..501
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| cacggcgccc gtcctctgtc gttgaaggac agggagcggc ggctaggggtt tgcggtgct  | 60  |
| gtggcgcccg acgcccgtcc tctactatcc gtggcgacca tcgtcggtta tccgcggast  | 120 |
| gtggcgatcg gcctgtgtc ctatccgcgg ttgccgagga aagtactatg ttgttgatgc   | 180 |
| tggatatcca aatagggatg agtacttggc cccgtacaaa ggacaactgt atcatgttcc  | 240 |
| ggaatggaga aatgatcctc cacctaattg ctcactcgaa ggtgaagcat gggaaagtgar | 300 |
| tcacaggtcc aacgacctcc atgaaggtaa agcacatggc ttcaagtkag tcgcaagtcc  | 360 |
| aatcgagtcc atgaaggtga agcatgggag gtccaagtra atctggaaag aataacgggtg | 420 |
| gaagtaggtt gggccttata ataggggagg agtagtagaa attattttcc gcgtagtctg  | 480 |
| ggttttaatt atttagataa g                                            |     |

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

His Gly Ala Arg Pro Leu Ser Leu Lys Asp Arg Glu Arg Arg Leu Gly  
1                  5                  10                  15  
Phe Arg Gly Ala Val Ala Ala Asp Ala Arg Pro Leu Leu Ser Val Ala  
          20                  25                  30  
Thr Ile Val Gly Tyr Pro Arg Xaa Val Ala Ile Gly Leu Cys Ser Tyr  
          35                  40                  45  
Pro Arg Leu Pro Arg Lys Val Leu Cys Cys  
50                  55

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..98  
(D) OTHER INFORMATION: / Ceres Seq. ID 1482240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Arg | Pro | Ser | Ser | Val | Val | Glu | Gly | Gln | Gly | Ala | Ala | Ala | Arg | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Arg | Cys | Cys | Gly | Gly | Arg | Arg | Pro | Ser | Ser | Thr | Ile | Arg | Gly | Asp |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Arg | Arg | Leu | Ser | Ala | Xaa | Cys | Gly | Asp | Arg | Pro | Val | Leu | Leu | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Val | Ala | Glu | Glu | Ser | Thr | Met | Leu | Leu | Met | Leu | Asp | Ile | Gln | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Met | Ser | Thr | Trp | Pro | Arg | Thr | Lys | Asp | Asn | Cys | Ile | Met | Phe | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |
| Asn | Gly | Glu | Met | Ile | Leu | His | Leu | Met | Ala | His | Ser | Lys | Val | Lys | His |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |

Gly Lys

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 798 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..798  
(D) OTHER INFORMATION: / Ceres Seq. ID 1482245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

|            |             |            |             |            |             |     |
|------------|-------------|------------|-------------|------------|-------------|-----|
| aaccatagaa | atcctccaat  | tattcgattc | ccaagccact  | aaggcccttg | gaggaacaac  | 60  |
| agaatccaga | aaccgaaaag  | argcctcact | gctgccgcct  | gggccaagtc | gtcgtcttgc  | 120 |
| tttgccaatc | cgtcgctcca  | cctgaacaca | ccggcggaag  | ggaggcgaag | aagcgatggg  | 180 |
| cgtgaccaag | gaggacgtcg  | aggcggccat | cacctctgct  | ctcagccctt | ccaatctcgt  | 240 |
| ggtgacggac | acgtccggag  | ggtgtggcgc | gagctacgag  | atcgagggtg | tgctcggagaa | 300 |
| gttcgagggg | aagcggctgc  | tggagaggca | ccggatgggtg | aacaccgcgc | tggcgtctca  | 360 |
| catggcggag | atccacgccc  | tctccatcaa | gaaggcgctc  | accccggtc  | aggcccagcc  | 420 |
| ccagggccca | gccggagccc  | gccgccgata | agccccaggc  | ttaagtgttt | aacaccccc   | 480 |
| aaaacggttt | gatcccatat  | gccgatgcac | gattacattg  | gctatctgct | tgaataatgc  | 540 |
| gggcgggatg | acttgctaaa  | ttgcaggatg | ttatccttga  | ctgattagaa | acttctgcac  | 600 |
| cgtgcattta | acttctgtgt  | cactgtgtgt | gtgttctgga  | tgtttctgcc | ctggtcgttt  | 660 |
| gctcgagact | gtgtgtttga  | gttcatgctg | ttaatgttct  | gccagggtgg | ggttttcagt  | 720 |
| cctggaattt | ttatatattga | ctgttgctat | gtctttcctt  | gctttagagg | gtaagggggt  | 780 |
| tattctttta | ccttgtgg    |            |             |            |             |     |

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..47  
(D) OTHER INFORMATION: / Ceres Seq. ID 1482246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ile | Glu | Ile | Leu | Gln | Leu | Phe | Asp | Ser | Gln | Ala | Thr | Lys | Ala | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Gly | Gly | Thr | Thr | Glu | Ser | Arg | Asn | Arg | Lys | Xaa | Ala | Ser | Leu | Leu | Pro |

20 25 30  
Pro Gly Pro Ser Arg Arg Leu Ala Leu Pro Ile Arg Arg Ser Thr  
35 40 45

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

Met Gly Val Thr Lys Glu Asp Val Glu Ala Ala Ile Thr Ser Ala Leu  
1 5 10 15  
Ser Pro Ser Asn Leu Val Val Thr Asp Thr Ser Gly Gly Cys Gly Ala  
20 25 30  
Ser Tyr Glu Ile Glu Val Val Ser Glu Lys Phe Glu Gly Lys Arg Leu  
35 40 45  
Leu Glu Arg His Arg Met Val Asn Thr Ala Leu Ala Ser His Met Ala  
50 55 60  
Glu Ile His Ala Val Ser Ile Lys Lys Ala Leu Thr Pro Ala Gln Ala  
65 70 75 80  
Gln Pro Gln Gly Pro Ala Gly Ala Gly Arg Arg  
85 90

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..572
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

atgggtggtc cgcactccgc accggtaccg cacaaccccc acaccgcgag catccccatt 60  
tctccgtccc aaaaccctag gctagtcccc ccacacctgg atccatcggg tcggaggcca 120  
tgacgacggc gaggtccga tcctcgccct cctccgcggg ggctctcctc cgccacttct 180  
ccgtgggtcc cgcctcgact ccgcgcgccg tctcccgggt ccagatttc caggttcctc 240  
agtctattat gtggaggcat ttgcgaacgt ccaggcctaa ttctcttgca agacgcgaca 300  
actttggtct gatggcctgt ttgcacgctc agatacgatg cgcttcgcag gctgctgctg 360  
tgaaagaaac cgaatccagt agcagcaaga taagcatcgg gcccaaacca aaacagatca 420  
aggaggatga cgaggatgct aacctggtat accaagggcc aatatcatcg accataaaga 480  
aagtgaagct tctctccctg tccacctgct gcctctccgt gtcgctgggg ccagtggtaa 540  
cattcatgac ttgcctgac atgaatgtga tc

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151



(D) OTHER INFORMATION: / Ceres Seq. ID 1482249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

Met Thr Thr Ala Arg Leu Arg Ser Ser Ala Ser Leu Arg Gly Ala Leu  
1 5 10 15  
Leu Arg His Phe Ser Val Gly Pro Ala Ser Thr Pro Arg Ala Val Ser  
20 25 30  
Arg Val Pro Asp Phe Gln Val Pro Gln Ser Ile Met Trp Arg His Phe  
35 40 45  
Ala Thr Ser Arg Pro Asn Ser Leu Ala Arg Arg Asp Asn Phe Gly Leu  
50 55 60  
Met Ala Cys Leu His Ala Gln Ile Arg Cys Ala Ser Gln Ala Ala Ala  
65 70 75 80  
Val Lys Glu Thr Glu Ser Ser Ser Ser Lys Ile Ser Ile Gly Pro Lys  
85 90 95  
Pro Lys Gln Ile Lys Glu Asp Asp Glu Asp Ala Asn Leu Val Tyr Gln  
100 105 110  
Gly Pro Ile Ser Ser Thr Ile Lys Lys Val Lys Leu Leu Ser Leu Ser  
115 120 125  
Thr Cys Cys Leu Ser Val Ser Leu Gly Pro Val Val Thr Phe Met Thr  
130 135 140  
Ser Pro Asp Met Asn Val Ile  
145 150

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1482250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

Met Trp Arg His Phe Ala Thr Ser Arg Pro Asn Ser Leu Ala Arg Arg  
1 5 10 15  
Asp Asn Phe Gly Leu Met Ala Cys Leu His Ala Gln Ile Arg Cys Ala  
20 25 30  
Ser Gln Ala Ala Ala Val Lys Glu Thr Glu Ser Ser Ser Ser Lys Ile  
35 40 45  
Ser Ile Gly Pro Lys Pro Lys Gln Ile Lys Glu Asp Asp Glu Asp Ala  
50 55 60  
Asn Leu Val Tyr Gln Gly Pro Ile Ser Ser Thr Ile Lys Lys Val Lys  
65 70 75 80  
Leu Leu Ser Leu Ser Thr Cys Cys Leu Ser Val Ser Leu Gly Pro Val  
85 90 95  
Val Thr Phe Met Thr Ser Pro Asp Met Asn Val Ile  
100 105

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1482251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

Met Ala Cys Leu His Ala Gln Ile Arg Cys Ala Ser Gln Ala Ala Ala  
1 5 10 15  
Val Lys Glu Thr Glu Ser Ser Ser Ser Lys Ile Ser Ile Gly Pro Lys  
20 25 30  
Pro Lys Gln Ile Lys Glu Asp Asp Glu Asp Ala Asn Leu Val Tyr Gln  
35 40 45  
Gly Pro Ile Ser Ser Thr Ile Lys Lys Val Lys Leu Leu Ser Leu Ser  
50 55 60  
Thr Cys Cys Leu Ser Val Ser Leu Gly Pro Val Val Thr Phe Met Thr  
65 70 75 80  
Ser Pro Asp Met Asn Val Ile  
85

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..519
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

aaggctcact gctcagtgt cactgtctac tagctaaaaa catctccttt cttatccatg 60  
gaganggcag cgctcacctc ccactccctg cagcgcccag cagcagcagc agctgtctcc 120  
gcgcatggcc agcngcggag ggtcggagcg gcgggcctgc ggcaccggca gccgcgcgcc 180  
ggcggcagga tccggggccct gccttcggcg gaggtcatca gcgagatcct gagccccaag 240  
ctggtgcccc gctcgcccg cgacaccggc gacgtctcct cgctcgctcc ggtcagtgcc 300  
ctgatgtgct tcttctactt cgtgtccaac tgggtggtgc ccgagctgct cctgaagggc 360  
ctcaacgagc ccaagcccga ggacgaagcg tccacgtcct tcgccgcgtc cgcnacaac 420  
gccgccgccg ctggcccagc agacgacggc ggcaccggta agatccgcct caaggtcaag 480  
aagaagaaga acgggaaagc gaccatcgtc aaggtctag

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

Gly Ser Leu Leu Ser Ala His Cys Ser Leu Ala Lys Asn Ile Ser Phe  
1 5 10 15  
Leu Ile His Gly Xaa Gly Ser Ala His Leu Pro Leu Pro Ala Ala Pro  
20 25 30  
Ser Ser Ser Ser Ser Cys Ser Arg Ala Trp Pro Xaa Ala Glu Gly Arg  
35 40 45  
Ser Gly Gly Pro Ala Ala Pro Ala Ala Arg Arg Arg Gln Asp Pro  
50 55 60  
Gly Pro Ala Phe Gly Gly Gly His Gln Arg Asp Pro Glu Pro Gln Ala  
65 70 75 80  
Gly Ala Arg Leu Ala Arg Arg His Arg Arg Arg Leu Leu Ala Arg Pro  
85 90 95  
Gly Gln Cys Pro Asp Ala Ala Leu Leu Leu Arg Val Gln Leu Gly Gly

100 105 110  
Ala Arg Ala Ala Pro Glu Gly Pro Gln Arg Ala Gln Ala Arg Gly Arg  
115 120 125  
Ser Val His Val Leu Arg Arg Val Arg Xaa Gln Arg Arg Arg Arg Trp  
130 135 140  
Pro Ser Arg Arg Arg Arg His Arg  
145 150

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

Met Glu Xaa Ala Ala Leu Thr Ser His Ser Leu Gln Arg Pro Ala Ala  
1 5 10 15  
Ala Ala Ala Ala Pro Ala His Gly Gln Xaa Arg Arg Val Gly Ala Ala  
20 25 30  
Gly Leu Arg His Arg Gln Pro Arg Ala Gly Gly Arg Ile Arg Ala Leu  
35 40 45  
Pro Ser Ala Glu Val Ile Ser Glu Ile Leu Ser Pro Lys Leu Val Pro  
50 55 60  
Gly Ser Pro Ala Asp Thr Gly Asp Val Ser Ser Leu Val Pro Val Ser  
65 70 75 80  
Ala Leu Met Leu Leu Phe Tyr Phe Val Ser Asn Trp Val Val Pro Glu  
85 90 95  
Leu Leu Leu Lys Gly Leu Asn Glu Pro Lys Pro Glu Asp Glu Ala Ser  
100 105 110  
Thr Ser Phe Ala Ala Ser Ala Xaa Asn Ala Ala Ala Gly Pro Ala  
115 120 125  
Asp Asp Gly Gly Thr Gly Lys Ile Arg Leu Lys Val Lys Lys Lys Lys  
130 135 140  
Asn Gly Lys Ala Thr Ile Val Lys Val  
145 150

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..278
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

artgcaagca tatrgngcgc cgtgccagcc tgctcctcgc cgcrgcgtg ctgcgtgccg 60  
tcgctgccgc ggcgggtgccs cgacgtgcga gcgcacgag tgcccggcgt acgaggtggt 120  
ggacagcgcc aacgggttcg agatccggcg gtacacggac gccatgtgga tcaccacggc 180  
gcccacgag gacatctcct tcgtcgccgc cagcgcacc ggcttcctac agctgttcga 240  
ctacatcbag ggcaagaacg cgtacaacca gacgatcg

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..92
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1482258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Xaa | Ala | Ser | Ile | Xaa | Xaa | Ala | Val | Pro | Ala | Cys | Ser | Ser | Pro | Xaa | Arg |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Cys | Ser | Ser | Pro | Ser | Leu | Pro | Arg | Arg | Cys | Xaa | Asp | Val | Arg | Ala | His |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg | Val | Pro | Gly | Val | Arg | Gly | Gly | Gly | Gln | Arg | Gln | Arg | Val | Arg | Asp |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Pro | Ala | Val | His | Gly | Arg | His | Val | Asp | His | His | Gly | Ala | His | Arg | Gly |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| His | Leu | Leu | Arg | Arg | Arg | His | Ala | His | Arg | Leu | Pro | Thr | Ala | Val | Arg |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Leu | His | Xaa | Gly | Gln | Glu | Arg | Val | Gln | Pro | Asp | Asp |     |     |     |     |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:441:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 92 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..92
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1482259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Xaa | Gln | Ala | Tyr | Xaa | Ala | Pro | Cys | Gln | Pro | Ala | Pro | Arg | Arg | Xaa | Ala |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Ala | Arg | Arg | Arg | Arg | Cys | Arg | Gly | Gly | Ala | Xaa | Thr | Cys | Glu | Arg | Ile |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Glu | Cys | Pro | Ala | Tyr | Glu | Val | Val | Asp | Ser | Ala | Asn | Gly | Phe | Glu | Ile |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | Arg | Tyr | Thr | Asp | Ala | Met | Trp | Ile | Thr | Thr | Ala | Pro | Ile | Glu | Asp |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ile | Ser | Phe | Val | Ala | Ala | Thr | Arg | Thr | Gly | Phe | Leu | Gln | Leu | Phe | Asp |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Tyr | Ile | Xaa | Gly | Lys | Asn | Ala | Tyr | Asn | Gln | Thr | Ile |     |     |     |     |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:442:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 92 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..92
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1482260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Cys | Lys | His | Xaa | Xaa | Arg | Arg | Ala | Ser | Leu | Leu | Ala | Xaa | Ala | Leu |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |

Leu Val Ala Val Ala Ala Ala Val Xaa Arg Arg Ala Ser Ala Ser  
20 25 30  
Ser Ala Arg Arg Thr Arg Trp Trp Thr Ala Pro Thr Gly Ser Arg Ser  
35 40 45  
Gly Gly Thr Arg Thr Pro Cys Gly Ser Pro Arg Arg Pro Ser Arg Thr  
50 55 60  
Ser Pro Ser Ser Pro Pro Arg Ala Pro Ala Ser Tyr Ser Cys Ser Thr  
65 70 75 80  
Thr Xaa Arg Ala Arg Thr Arg Thr Thr Arg Arg Ser  
85 90

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..931
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

gaattcctcg ccgccgtctt cgtccaccag aaccatggcc tccgacaccg cctcggcagt 60  
tccgtcgtct gtggtctcag ctgccgagga gacgctcgga tataccgaat ccgtagggac 120  
catctctccc atctgctcgc ggcggcgccg gcggaccccc acgccgtggc cgagctccca 180  
cccccttccc gggcgcgccg tttccttgcc ttggcgccag ccgcgacctc ccttctcgga 240  
gttcggttaa ggtgttcggg agttgacct gacgagcacc ccatcagaaa ggagtttgaa 300  
aggttaagcc taatgcagga gaagttaa atcaattgaga actgggacaa agcaccactt 360  
cgcccttcta ctacactaaa tacacaagca gcagcaaggt tcattggaca ctcaatttcc 420  
catctgacat ctgatcagaa gaggagcatg catgaaataa gtagaggaga aaggcggagt 480  
tggtctgggc agaagagaaa gcctgaacct tcagtagaaa agaagtctgt tcgtgctgct 540  
gcagaagagt tccttgcaaa ggcttctcag gaacttattg gacatagtga tagcagggtc 600  
aagggtcctg ttatactcat ttctgatgaa gatgaggact agatcaaaaa aatgggcgct 660  
taccagatta catgcctgat tcacgcgcta ggcaaaggaa ggtagaagtt cctggtgatg 720  
aagataaact tacgtacatt gctgtggtga tgaagatgaa tttatctgca ttgctgtggt 780  
gttctacatg taacagggaa tggagcaaa ctgcataggc ttgcttaagt cccagttct 840  
gggagcaatt ggctcgaa cttgagtga atttatctga gtttctttcc ggaaagaatt 900  
ttgacattct atttgctagt ggaactggag c

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

Glu Phe Leu Ala Ala Val Phe Val His Gln Asn His Gly Leu Arg His  
1 5 10 15  
Arg Leu Gly Ser Ser Val Val Cys Gly Leu Ser Cys Arg Gly Asp Ala  
20 25 30  
Arg Ile Tyr Arg Ile Arg Arg Asp His Leu Ser His Leu Leu Ala Ala  
35 40 45  
Ala Ala Ala Asp Pro Asp Ala Val Ala Glu Leu Pro Pro Leu Leu Arg  
50 55 60  
Ala Arg Ala Phe Leu Ala Leu Ala Gln Ala Ala Thr Ser Leu Leu Gly

65 70 75 80  
Val Arg Leu Arg Cys Ser Gly Val Asp Pro Asp Glu His Pro Ile Arg  
85 90 95  
Lys Glu Phe Glu Arg Leu Ser Leu Met Gln Glu Lys Leu Asn Gln Phe  
100 105 110  
Glu Asn Trp Asp Lys Ala Pro Leu Arg Pro Ser Thr Thr Leu Asn Thr  
115 120 125  
Gln Ala Ala Ala Arg Phe Ile Gly His Ser Leu Ser His Leu Thr Ser  
130 135 140  
Asp Gln Lys Arg Ser Met His Glu Ile Ser Arg Gly Glu Arg Arg Ser  
145 150 155 160  
Trp Ser Gly Gln Lys Arg Lys Pro Glu Pro Ser Val Glu Lys Lys Ser  
165 170 175  
Val Arg Ala Ala Ala Glu Glu Phe Leu Ala Lys Ala Ser Gln Glu Leu  
180 185 190  
Ile Gly His Ser Asp Ser Arg Val Lys Gly Pro Val Ile Leu Ile Ser  
195 200 205  
Asp Glu Asp Glu Asp  
210

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

Met Gln Glu Lys Leu Asn Gln Phe Glu Asn Trp Asp Lys Ala Pro Leu  
1 5 10 15  
Arg Pro Ser Thr Thr Leu Asn Thr Gln Ala Ala Arg Phe Ile Gly  
20 25 30  
His Ser Leu Ser His Leu Thr Ser Asp Gln Lys Arg Ser Met His Glu  
35 40 45  
Ile Ser Arg Gly Glu Arg Arg Ser Trp Ser Gly Gln Lys Arg Lys Pro  
50 55 60  
Glu Pro Ser Val Glu Lys Lys Ser Val Arg Ala Ala Ala Glu Glu Phe  
65 70 75 80  
Leu Ala Lys Ala Ser Gln Glu Leu Ile Gly His Ser Asp Ser Arg Val  
85 90 95  
Lys Gly Pro Val Ile Leu Ile Ser Asp Glu Asp Glu Asp  
100 105

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..600
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

actgacagct cgccgarrrg ccgcgccgcg ctcgaraccc gtcgatggcg aggcggagct 60  
ggcggtcgac gcaaccgcag gcgccgcac cggggttcgg ttcgcgccca cctccaataa 120

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| cctgctcgtc  | tcctcatggg  | attcggggct | gcgggtgtac | gatgccgacg | agggcacgct | 180 |
| caggggtcaac | gtggagtcag  | aggcggcatt | cctcgactgc | tgcttcgagg | atgagtctgc | 240 |
| agcggttgcc  | tgcggtctctg | atggatctgt | gagaaggtac | gacttcact  | caggttcgca | 300 |
| ggatacgggtg | gggtcccatg  | aagatgcact | agcctgcatt | gagttctctt | cactgaccgg | 360 |
| tcagattatg  | acaggcagcc  | ttgacaagaa | gctaaagctt | tgggattcaa | aaacaagaaa | 420 |
| tgtaaagccc  | agcggcacca  | taaccttaaa | ttcagatgtg | gcctcaattt | ctatatgcgg | 480 |
| catttacata  | ttagctgcag  | ttgagagaaa | tgtttatctt | tatgacatga | ggaatctaac | 540 |
| aagaccagtt  | gatgaaaaaa  | gactgtcctc | tggattatca | aattcgatgc | cttcatactt | 600 |

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..199
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Thr | Ala | Arg | Arg | Xaa | Ala | Ala | Pro | Arg | Ser | Xaa | Pro | Val | Asp | Gly |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Glu | Ala | Glu | Leu | Ala | Val | Asp | Ala | Thr | Ala | Gly | Ala | Ala | Ser | Arg | Val |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg | Phe | Ala | Pro | Thr | Ser | Asn | Asn | Leu | Leu | Val | Ser | Ser | Trp | Asp | Ser |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Gly | Leu | Arg | Leu | Tyr | Asp | Ala | Asp | Glu | Gly | Thr | Leu | Arg | Val | Asn | Val |  |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Glu | Ser | Glu | Ala | Ala | Phe | Leu | Asp | Cys | Cys | Phe | Glu | Asp | Glu | Ser | Ala |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Ala | Phe | Ala | Cys | Gly | Ser | Asp | Gly | Ser | Val | Arg | Arg | Tyr | Asp | Phe | His |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Ser | Gly | Ser | Gln | Asp | Thr | Val | Gly | Leu | His | Glu | Asp | Ala | Leu | Ala | Cys |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ile | Glu | Phe | Ser | Ser | Leu | Thr | Gly | Gln | Ile | Met | Thr | Gly | Ser | Leu | Asp |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Lys | Lys | Leu | Lys | Leu | Trp | Asp | Ser | Lys | Thr | Arg | Asn | Val | Ser | Pro | Ser |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Gly | Thr | Ile | Thr | Leu | Asn | Ser | Asp | Val | Ala | Ser | Ile | Ser | Ile | Cys | Gly |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |
| Ile | Tyr | Ile | Leu | Ala | Val | Glu | Arg | Asn | Val | Tyr | Leu | Tyr | Asp | Met |     |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |  |
| Arg | Asn | Leu | Thr | Arg | Pro | Val | Asp | Glu | Lys | Arg | Leu | Ser | Ser | Gly | Leu |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Ser | Asn | Ser | Met | Pro | Ser | Tyr |     |     |     |     |     |     |     |     |     |  |
|     |     |     | 195 |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..516
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

```
gcgtcaccat ccatttgacg aggcgggttta tccccagca ccccaaccaa cctttccacg 60
taccaccggg tttctgtccg cgccccgcc ttcaaaagca ggtccgcacg ccggccggcg 120
agacagacga caccaccacg ccgggacggg aggcacaggt gcggtctgcg tcgagagttg 180
gtccactggc aggccggaat gaagaagtgc gcgtcggagc tggagctgga ggcgttcac 240
cgggagagcg gcgaggacgc ccgcgccgcc gccggaggta gcagtccggg gtgcggtgga 300
tcaagcgatc ccggagggag cggcgtcttc tcacccggct tcggtttcgc cgactcggac 360
accatggatg gaggcagttg gtggtacggg aacgtccgca cgccgaacct agtcatgtcg 420
caggcggcgt ccatatccgc tagccccggg ctaaccacct cagccaatca tgctcttgaa 480
agcgagtcag actccgacag cgaatcactg tatgag
```

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

```
Arg His His Pro Phe Asp Glu Ala Val Tyr Pro Pro Ala Pro Gln Pro
1 5 10 15
Thr Phe Pro Arg Thr Thr Gly Phe Leu Ser Ala Pro Arg Pro Ser Lys
 20 25 30
Ala Gly Pro His Ala Gly Arg Arg Asp Arg Arg His His Ala Gly
 35 40 45
Thr Gly Gly Thr Gly Ala Val Cys Val Glu Ser Trp Ser Thr Gly Arg
50 55 60
Pro Glu
65
```

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

```
Val Thr Ile His Leu Thr Arg Arg Phe Ile Pro Gln His Pro Asn Gln
1 5 10 15
Pro Phe His Val Pro Pro Gly Phe Cys Pro Arg Pro Ala Leu Gln Lys
 20 25 30
Gln Val Arg Thr Pro Ala Gly Glu Thr Asp Asp Thr Thr Thr Pro Gly
 35 40 45
Arg Glu Ala Gln Val Arg Ser Ala Ser Arg Val Gly Pro Leu Ala Gly
50 55 60
Arg Asn Glu Glu Val Arg Val Gly Ala Gly Ala Gly Gly Val His Pro
65 70 75 80
Gly Glu Arg Arg Gly Arg Pro Arg Arg Arg Arg Arg
 85 90
```

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid



- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..106
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1482273
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

```
Met Lys Lys Cys Ala Ser Glu Leu Glu Leu Glu Ala Phe Ile Arg Glu
1 5 10 15
Ser Gly Glu Asp Ala Arg Ala Ala Ala Gly Gly Ser Ser Pro Gly Cys
 20 25 30
Gly Gly Ser Ser Asp Pro Gly Gly Ser Gly Val Phe Ser Pro Gly Phe
 35 40 45
Gly Phe Ala Asp Ser Asp Thr Met Asp Gly Gly Ser Trp Trp Tyr Gly
 50 55 60
Asn Val Arg Thr Pro Asn Pro Val Met Ser Gln Ala Ala Ser Ile Ser
65 70 75 80
Ala Ser Pro Gly Leu Thr Thr Ser Ala Asn His Ala Leu Glu Ser Glu
 85 90 95
Ser Asp Ser Asp Ser Glu Ser Leu Tyr Glu
 100 105
```

(2) INFORMATION FOR SEQ ID NO:452:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 561 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..561
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1482274
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

```
aagatggaca ggctctgtcg ccaactgctac accagtacac cctgcacgcg ctgcgggcgt 60
ttccgcgcgc tttgtgcctc ctctgccctc cccggggcgt cgccctccgt ccacgctcaa 120
gctcgctccg tcccggcgcc tcgaactcgt cgctcctcgt tccgctgtcg ccaccgcgaa 180
gcatgaggag gcgtcctggg atcactggct tgcagaatgt ggcggtact ctcgaactat 240
cagaaccagt tgggactggt cggggacaat atggccaagg tcgggaccga tgtcatgaag 300
aagcagcgac ttgggatggt ccgatcacag ctcgagaaat ttgcttgcaa gcataagggt 360
ttgagcaggt ttggtgcaat ctgattttga acctgctatg gacatcttcc actcaagttc 420
ttgtcaatgg agtgcctgga cagcctataa atctcaagcg tgggttgcaa caagctgctc 480
tgaaacatcc attttctctg kgccatcaat ggatgcttag cacagatcgc ttccacatat 540
cacatgatca atcagtactg g
```

(2) INFORMATION FOR SEQ ID NO:453:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 61 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..61
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1482275
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

```
Lys Met Asp Arg Leu Cys Arg His Cys Tyr Thr Ser Thr Pro Cys Thr
1 5 10 15
Arg Cys Gly Arg Phe Arg Arg Leu Cys Ala Ser Ser Ala Leu Pro Gly
```

20 25 30  
Arg Ser Pro Ser Val His Ala Gln Ala Arg Ser Val Pro Ala Pro Arg  
35 40 45  
Thr Arg Arg Pro Arg Phe Arg Cys Arg His Arg Glu Ala  
50 55 60

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1482276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

Arg Trp Thr Gly Ser Val Ala Thr Ala Thr Pro Val His Pro Ala Arg  
1 5 10 15  
Ala Ala Gly Val Ser Ala Gly Phe Val Pro Pro Leu Pro Ser Pro Gly  
20 25 30  
Ala Arg Pro Pro Ser Thr Leu Lys Leu Ala Pro Ser Arg Arg Leu Glu  
35 40 45  
Leu Val Val Leu Ala Ser Ala Val Ala Thr Ala Lys His Glu Glu Ala  
50 55 60  
Ser Trp Asp His Trp Leu Ala Glu Cys Gly Gly Tyr Ser Arg Thr Ile  
65 70 75 80  
Arg Thr Ser Trp Asp Trp Ser Gly Thr Ile Trp Pro Arg Ser Gly Pro  
85 90 95  
Met Ser

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1482277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

Asp Gly Gln Ala Leu Ser Pro Leu Leu His Gln Tyr Thr Leu His Ala  
1 5 10 15  
Leu Arg Ala Phe Pro Pro Ala Leu Cys Leu Leu Cys Pro Pro Arg Ala  
20 25 30  
Leu Ala Leu Arg Pro Arg Ser Ser Ser Leu Arg Pro Gly Ala Ser Asn  
35 40 45  
Ser Ser Ser Ser Leu Pro Leu Ser Pro Pro Arg Ser Met Arg Arg Arg  
50 55 60  
Pro Gly Ile Thr Gly Leu Gln Asn Val Ala Ala Thr Leu Glu Leu Ser  
65 70 75 80  
Glu Pro Val Gly Thr Gly Arg Gly Gln Tyr Gly Gln Gly Arg Asp Arg  
85 90 95  
Cys His Glu Glu Ala Ala Thr Trp Asp Gly Pro Ile Thr Ala Arg Glu  
100 105 110  
Ile Cys Leu Gln Ala  
115

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..578
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| acctcggctc | gggcgcagag | cgcgcggcgc | cggcgcgtcc | tctcctcctg | ctccgatctc  | 60  |
| tctgcccagc | ccgcctgtg  | cgcttcgcta | ctacgcttcc | tccatgcata | ccctcagcca  | 120 |
| tgtacgcctg | tatttgggaa | gacattagcg | gagttgaatc | cagaagaaga | gccgaagagt  | 180 |
| tatcttagcc | acagccaggt | cgcccgttag | ttgttcgcgg | aaatgtccct | ccgccagctg  | 240 |
| cttcacaaa  | cgcgctcgtg | gcgcgcgctt | gagcagccca | cgaagatgtc | ttgtctcctc  | 300 |
| tccatcttcc | gtgcgtcttc | cattctccgt | tctgaaggct | cggctgagcc | actgcgccga  | 360 |
| tcttcattcg | tgccagcccc | gctgccaaga | agcttgccct | gctccagctc | tgacccccctt | 420 |
| ggccccagat | tcagcatcga | cgtggctgac | tcggaccatt | ggccctcgtc | atttgacttg  | 480 |
| ktgtccgacg | ctgcacggag | caatgaatgc | ccagatgtct | ncgagcaaca | tgaggatgat  | 540 |
| gaactgcmcg | actcttatga | tgagatagat | gacatgag   |            |             |     |

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ser | Ala | Arg | Gln | Ser | Ala | Arg | Arg | Arg | Val | Leu | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |
| Cys | Ser | Asp | Leu | Ser | Ala | Gln | Pro | Arg | Leu | Cys | Ala | Ser | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  | Leu |
| Phe | Leu | His | Ala | Ser | Pro | Gln | Pro | Cys | Thr | Pro | Val | Phe | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  | Lys |
| Leu | Ala | Glu | Leu | Asn | Pro | Glu | Glu | Pro | Lys | Ser | Tyr | Leu | Ser |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     | His |
| Ser | Gln | Val | Ala | Arg |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Leu | Arg | Gln | Leu | Leu | His | Gln | Thr | Arg | Pro | Trp | Arg | Ala | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Glu | Gln | Pro | Thr | Lys | Met | Ser | Cys | Leu | Leu | Ser | Ile | Phe | Arg | Ala | Leu |

20 25 30  
Ser Ile Leu Arg Ser Glu Gly Ser Ala Glu Pro Leu Arg Arg Ser Ser  
35 40 45  
Ser Val Pro Ala Pro Leu Pro Arg Ser Leu Pro Cys Ser Ser Ser Asp  
50 55 60  
Pro Leu Gly Pro Arg Phe Ser Ile Asp Val Val Asp Ser Asp His Trp  
65 70 75 80  
Pro Ser Ser Phe Asp Leu Xaa Ser Asp Ala Arg Ser Asn Glu Cys  
85 90 95  
Pro Asp Val Xaa Glu Gln His Glu Asp Asp Glu Leu Xaa Asp Ser Tyr  
100 105 110  
Asp Glu Ile Asp Asp Met  
115

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1482285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

Met Ser Cys Leu Leu Ser Ile Phe Arg Ala Leu Ser Ile Leu Arg Ser  
1 5 10 15  
Glu Gly Ser Ala Glu Pro Leu Arg Arg Ser Ser Ser Val Pro Ala Pro  
20 25 30  
Leu Pro Arg Ser Leu Pro Cys Ser Ser Ser Asp Pro Leu Gly Pro Arg  
35 40 45  
Phe Ser Ile Asp Val Val Asp Ser Asp His Trp Pro Ser Ser Phe Asp  
50 55 60  
Leu Xaa Ser Asp Ala Ala Arg Ser Asn Glu Cys Pro Asp Val Xaa Glu  
65 70 75 80  
Gln His Glu Asp Asp Glu Leu Xaa Asp Ser Tyr Asp Glu Ile Asp Asp  
85 90 95  
Met

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 881 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..881

(D) OTHER INFORMATION: / Ceres Seq. ID 1482289

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| tctctctttt  | ttccccagca | atgcaattcc | gcagacagac | gcaggcggca | rgcggcaggc | 60  |
| ggcggcgcac  | cgcaccgctt | cttcctcttc | tatctctcat | ctacagcctt | cgctgcgccg | 120 |
| ccatggccac  | caccgccttg | ctgccgtgc  | tccgacgccg | cctcgccgcc | gcaatcgccg | 180 |
| gatcgccctg  | tccctactcc | ctccgaggac | cctcatttcc | tgcaccagca | gctgcagggc | 240 |
| taaggctccct | cctaacagtt | gctggagcga | gcgatactgc | aacagaacct | caggaccaac | 300 |
| agcattccga  | aacaactccc | ccgcgggctt | ctgtcccgcg | accggagtcc | ggtctcaaag | 360 |
| tcagggaac   | ctccaacctg | aagatctcac | caaggcatga | cctcgccatg | atctttacgt | 420 |
| gcaagggtgtg | cgagaccagg | tccatgaaga | tggccagcag | ggactcgtac | gagaacggag | 480 |

(2) INFORMATION FOR SEQ ID NO:461:

(A) LENGTH: 227 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..227

(D) OTHER INFORMATION: / Ceres Seq. ID 1482290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

[illegible]

(2) INFORMATION FOR SEQ ID NO:462:

(A) LENGTH: 221 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..221

(D) OTHER INFORMATION: / Ceres Seq. ID 1482291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

Met Gln Phe Arg Arg Gln Thr Gln Ala Ala Xaa Gly Arg Arg Arg Arg  
1 5 10 15  
Thr Ala Pro Leu Leu Pro Leu Leu Ser Leu Ile Tyr Ser Leu Arg Cys  
20 25 30  
Ala Ala Met Ala Thr Thr Arg Leu Leu Pro Leu Leu Arg Arg Arg Leu  
35 40 45  
Ala Ala Ala Ile Ala Gly Ser Pro Ala Pro Tyr Ser Leu Arg Gly Pro  
50 55 60  
Ser Phe Pro Ala Pro Ala Ala Ala Gly Leu Arg Ser Leu Leu Thr Val  
65 70 75 80  
Ala Gly Ala Ser Asp Thr Ala Thr Glu Pro Gln Asp Gln Gln His Ser  
85 90 95  
Glu Thr Thr Pro Pro Pro Ala Ser Val Pro Thr Pro Glu Ser Gly Leu  
100 105 110  
Lys Val Arg Asp Thr Ser Asn Leu Lys Ile Ser Pro Arg His Asp Leu  
115 120 125  
Ala Met Ile Phe Thr Cys Lys Val Cys Glu Thr Arg Ser Met Lys Met  
130 135 140  
Ala Ser Arg Asp Ser Tyr Glu Asn Gly Val Val Val Val Arg Cys Gly  
145 150 155 160  
Gly Cys Asn Asn Leu His Leu Met Ala Asp Arg Leu Gly Trp Phe Gly  
165 170 175  
Glu Pro Gly Ser Ile Glu Asp Phe Leu Ala Thr Gln Gly Glu Glu Val  
180 185 190  
Lys Lys Gly Ser Thr Asp Thr Ile Ser Phe Thr Leu Asp Asp Leu Ala  
195 200 205  
Gly Ser Gln Val Ser Ser Lys Gly Pro Ser Glu Gln Asn  
210 215 220

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1482292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

Met Ala Thr Thr Arg Leu Leu Pro Leu Leu Arg Arg Arg Arg Leu Ala Ala  
1 5 10 15  
Ala Ile Ala Gly Ser Pro Ala Pro Tyr Ser Leu Arg Gly Pro Ser Phe  
20 25 30  
Pro Ala Pro Ala Ala Ala Gly Leu Arg Ser Leu Leu Thr Val Ala Gly  
35 40 45  
Ala Ser Asp Thr Ala Thr Glu Pro Gln Asp Gln Gln His Ser Glu Thr  
50 55 60  
Thr Pro Pro Pro Ala Ser Val Pro Thr Pro Glu Ser Gly Leu Lys Val  
65 70 75 80  
Arg Asp Thr Ser Asn Leu Lys Ile Ser Pro Arg His Asp Leu Ala Met  
85 90 95  
Ile Phe Thr Cys Lys Val Cys Glu Thr Arg Ser Met Lys Met Ala Ser  
100 105 110  
Arg Asp Ser Tyr Glu Asn Gly Val Val Val Val Arg Cys Gly Gly Cys  
115 120 125  
Asn Asn Leu His Leu Met Ala Asp Arg Leu Gly Trp Phe Gly Glu Pro

130 135 140  
Gly Ser Ile Glu Asp Phe Leu Ala Thr Gln Gly Glu Glu Val Lys Lys  
145 150 155 160  
Gly Ser Thr Asp Thr Ile Ser Phe Thr Leu Asp Asp Leu Ala Gly Ser  
165 170 175  
Gln Val Ser Ser Lys Gly Pro Ser Glu Gln Asn  
180 185

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..671
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| gctctttccc  | ccttgcccc  | ttcccagtt  | ccactctgag | cactctcctc | cgctctgctc  | 60  |
| ctttgctccc  | cacggcaaac | cgtaaaccct | agcctgaggg | gcacccctgt | cgcagccatg  | 120 |
| ggcgccascg  | gaagctgcag | ggcgagatcg | accgcgtcct | gaagaaggtc | caggagggcg  | 180 |
| tcgatgtctt  | tgacagcatc | tggataaagg | tctacgacac | tgagaatgcc | aaccagaagg  | 240 |
| agaagttcga  | ggcggacctc | aagaaggaga | tcaagaagct | gcagcggnta | caggggaccag | 300 |
| atcaagacgt  | ggattcagtc | cagcgagatc | aaggacaaga | aggctctgat | ggatgctcga  | 360 |
| aagcagattg  | aacgagagat | ggaacgattt | aaagtatgtg | agaaggaaac | aaaaactaag  | 420 |
| gcatttctcaa | aagaagggtt | aggtcagcaa | ccaaaaacag | atcccaaaga | aaaggccaaa  | 480 |
| gctgaaacaa  | gagactggct | taataatgtg | gtgtgttgga | atcctgaatt | gctactctta  | 540 |
| tgctcttatg  | ttttcatatc | tgttttttgg | tatactaact | gaaccacact | gttaaatacgc | 600 |
| aacatatgta  | tactattttg | tttgagaata | ccttggatct | ttaattcatt | tccgaggaca  | 660 |
| tggtttgtgt  | c          |            |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Leu | Thr | Ala | Ser | Gly | Ile | Arg | Ser | Thr | Thr | Leu | Arg | Met | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Arg | Arg | Arg | Ser | Ser | Arg | Arg | Thr | Ser | Arg | Arg | Arg | Ser | Arg | Ser |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Ser | Xaa | Tyr | Arg | Asp | Gln | Ile | Lys | Thr | Trp | Ile | Gln | Ser | Ser | Glu |
|     |     |     |     | 35  |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Ile | Lys | Asp | Lys | Lys | Ala | Leu | Met | Asp | Ala | Arg | Lys | Gln | Ile | Glu | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Met | Glu | Arg | Phe | Lys | Val | Cys | Glu | Lys | Glu | Thr | Lys | Thr | Lys | Ala |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Phe | Ser | Lys | Glu | Gly | Leu | Gly | Gln | Gln | Pro | Lys | Thr | Asp | Pro | Lys | Glu |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Ala | Lys | Ala | Glu | Thr | Arg | Asp | Trp | Leu | Asn | Asn | Val | Val | Cys | Trp |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Asn | Pro | Glu | Leu | Leu | Leu | Leu | Cys | Ser | Tyr | Val | Phe | Ile | Ser | Val | Phe |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

Trp Tyr Thr Asn  
130

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

Met Pro Thr Arg Arg Arg Ser Ser Arg Arg Thr Ser Arg Arg Arg Ser  
1 5 10 15  
Arg Ser Cys Ser Xaa Tyr Arg Asp Gln Ile Lys Thr Trp Ile Gln Ser  
20 25 30  
Ser Glu Ile Lys Asp Lys Lys Ala Leu Met Asp Ala Arg Lys Gln Ile  
35 40 45  
Glu Arg Glu Met Glu Arg Phe Lys Val Cys Glu Lys Glu Thr Lys Thr  
50 55 60  
Lys Ala Phe Ser Lys Glu Gly Leu Gly Gln Gln Pro Lys Thr Asp Pro  
65 70 75 80  
Lys Glu Lys Ala Lys Ala Glu Thr Arg Asp Trp Leu Asn Asn Val Val  
85 90 95  
Cys Trp Asn Pro Glu Leu Leu Leu Leu Cys Ser Tyr Val Phe Ile Ser  
100 105 110  
Val Phe Trp Tyr Thr Asn  
115

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

Met Asp Ala Arg Lys Gln Ile Glu Arg Glu Met Glu Arg Phe Lys Val  
1 5 10 15  
Cys Glu Lys Glu Thr Lys Thr Lys Ala Phe Ser Lys Glu Gly Leu Gly  
20 25 30  
Gln Gln Pro Lys Thr Asp Pro Lys Glu Lys Ala Lys Ala Glu Thr Arg  
35 40 45  
Asp Trp Leu Asn Asn Val Val Cys Trp Asn Pro Glu Leu Leu Leu Leu  
50 55 60  
Cys Ser Tyr Val Phe Ile Ser Val Phe Trp Tyr Thr Asn  
65 70 75

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 868 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)



(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..868

(D) OTHER INFORMATION: / Ceres Seq. ID 1482297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

|             |            |            |            |             |            |     |
|-------------|------------|------------|------------|-------------|------------|-----|
| gtccatgcat  | gggcatggaa | tggatggatg | tgaatgccac | gaacgattcc  | gccccgccgg | 60  |
| ccaggtgaga  | gatgagcctc | acggcggcct | tccgtgccac | caaaatcccc  | cgcgtctctc | 120 |
| ctccaaagtg  | cggtgagcct | gccgcctcct | cttcggcctc | ggcgtccggg  | gatccgccgc | 180 |
| cggggggccgt | gaagagtact | aaggcgccgc | cgcgtgggtg | cgtgtacctt  | atagcctcat | 240 |
| cccggatccg  | ccgcacgtac | gtcggcgcta | ccaccgattt | ccctcgccgg  | ctgcggcaac | 300 |
| ataatggtga  | gttaaaagg  | ggtgcaaaag | cttcctctgc | cggcaggcct  | tggaatctcg | 360 |
| catgccttgt  | tgaaggattt | gccaacagaa | gtgaagcctg | tgagtttgaa  | tcgaaatgga | 420 |
| agatcgtctc  | ccgaaaaatt | gcacggaaaa | gaactgagct | tagcatgaag  | tcagtgtctg | 480 |
| aacatcgaga  | agcagctttg | agcagagtgg | aaacattcat | ggattgtagc  | cacctaaaaa | 540 |
| tcaaattggca | gtcaagttga | gaccatttaa | tcacttgcac | tatgcagggtg | gcaggcatct | 600 |
| aacttgagga  | aacatcacca | cttaagaatc | ctcctgtctt | ctagcagctc  | gtagcaaaga | 660 |
| taacttataa  | tcttctgctg | aaccatcaag | atggctgctg | ctatgctttc  | ttaacatgaa | 720 |
| aaaccaagag  | tagccccagt | ggaattctat | gtttgatttt | tttttctatg  | aacaattggt | 780 |
| tccgaacaat  | aatatggatc | atgcgacacc | cgtttgtaaa | tgtaaattat  | acttatgtat | 840 |
| tgtaatcacc  | tatatttctt | ctcattct   |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1482298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Leu | Thr | Ala | Ala | Phe | Arg | Ala | Thr | Lys | Ile | Pro | Arg | Ala | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |  |
| Pro | Pro | Lys | Cys | Gly | Glu | Pro | Ala | Ala | Ser | Ser | Ser | Ala | Ser | Ala | Ser |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Gly | Asp | Pro | Pro | Pro | Gly | Ala | Val | Lys | Ser | Thr | Lys | Ala | Pro | Pro | Pro |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| Trp | Cys | Val | Tyr | Leu | Ile | Ala | Ser | Ser | Arg | Ile | Arg | Arg | Thr | Tyr | Val |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Gly | Val | Thr | Thr | Asp | Phe | Pro | Arg | Arg | Leu | Arg | Gln | His | Asn | Gly | Glu |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Leu | Lys | Gly | Gly | Ala | Lys | Ala | Ser | Ser | Ala | Gly | Arg | Pro | Trp | Asn | Leu |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ala | Cys | Leu | Val | Glu | Gly | Phe | Ala | Asn | Arg | Ser | Glu | Ala | Cys | Glu | Phe |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Glu | Ser | Lys | Trp | Lys | Ile | Val | Ser | Arg | Lys | Ile | Ala | Arg | Lys | Arg | Thr |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Glu | Leu | Ser | Met | Lys | Ser | Val | Leu | Gln | His | Arg | Glu | Ala | Ala | Leu | Ser |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |  |
| Arg | Val | Glu | Thr | Phe | Met | Asp | Cys | Ser | His | Leu | Lys | Ile | Lys | Trp | Gln |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ser | Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 642 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..642

(D) OTHER INFORMATION: / Ceres Seq. ID 1482299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| aaatttttct | ccagccgccg | cgctcctgat | ccttatctct  | gcgcgcgctg | catcggcgcc | 60  |
| cgccgggagg | gagtcgccgc | cgctcgtcc  | atgttggtgg  | tccgcaatat | ccgccgcttc | 120 |
| gtcgacacgg | gcgcggcctt | cggatccgag | gccatcatgg  | aactggagac | taaaaggata | 180 |
| ttgcttgaga | ttttcaagga | gcggcagcgn | gaagagtgcc  | gaggctggtt | ccatcccaag | 240 |
| tttttacaag | aaacctgaag | aaggatccat | tagctctaga  | gttcaaaggt | tggccaagta | 300 |
| caggtttcta | aagaaacaat | cagagcttct | gctgaatgct  | gatgatcttg | atgccatgtg | 360 |
| ggtttgcttc | agagaaaatt | gtgttattga | tgatgctact  | ggtgctgaaa | agatgaatta | 420 |
| tgaagatttc | tgccatatcg | ccacagtctg | cactgagtag  | attggtcaga | aatgcaaacg | 480 |
| atttttcagc | ccttcaaact | tcatgaagtc | tgcacggagc  | acttgcacag | attgtttggc | 540 |
| taattacaag | attatctcag | tgttttggtt | tgaattttaga | gtatacttat | gtatgaaata | 600 |
| ttgattggta | ctcatttata | ttatattaat | tatattatta  | tt         |            |     |

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1482300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Lys | Phe | Phe | Ser | Ser | Arg | Arg | Ala | Pro | Asp | Pro | Tyr | Leu | Cys | Ala | Arg |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Cys | Ile | Gly | Ala | Arg | Arg | Glu | Gly | Val | Pro | Pro | Ala | Ser | Ser | Met | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Trp | Val | Arg | Asn | Ile | Arg | Arg | Phe | Val | Asp | Thr | Gly | Ala | Gly | Leu | Gly |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |  |
| Ser | Glu | Ala | Ile | Met | Glu | Leu | Glu | Thr | Lys | Arg | Ile | Leu | Leu | Glu | Ile |  |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |  |
| Phe | Lys | Glu | Arg | Gln | Xaa | Glu | Glu | Cys | Arg | Gly | Trp | Phe | His | Pro | Lys |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Phe | Leu | Gln | Glu | Thr |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1482301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Phe | Ser | Pro | Ala | Ala | Ala | Leu | Leu | Ile | Leu | Ile | Ser | Ala | Arg | Ala |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ala | Ser | Ala | Pro | Ala | Gly | Arg | Glu | Ser | Arg | Pro | Pro | Arg | Pro | Cys | Cys |  |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |  |
| Gly | Ser | Ala | Ile | Ser | Ala | Ala | Ser | Ser | Thr | Arg | Ala | Pro | Ala | Ser | Asp |  |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 35                                                              | 40  | 45  |
| Pro Arg Pro Ser Trp Asn Trp Arg Leu Lys Gly Tyr Cys Leu Arg Phe |     |     |
| 50                                                              | 55  | 60  |
| Ser Arg Ser Gly Ser Xaa Lys Ser Ala Glu Ala Gly Ser Ile Pro Ser |     |     |
| 65                                                              | 70  | 75  |
| Phe Tyr Lys Lys Pro Glu Glu Gly Ser Ile Ser Ser Arg Val Gln Arg |     | 80  |
|                                                                 | 85  | 90  |
| Leu Ala Lys Tyr Arg Phe Leu Lys Lys Gln Ser Glu Leu Leu Leu Asn |     | 95  |
|                                                                 | 100 | 105 |
| Ala Asp Asp Leu Asp Ala Met Trp Val Cys Leu Arg Glu Asn Cys Val |     | 110 |
|                                                                 | 115 | 120 |
| Ile Asp Asp Ala Thr Gly Ala Glu Lys Met Asn Tyr Glu Asp Phe Cys |     | 125 |
|                                                                 | 130 | 135 |
| His Ile Ala Thr Val Cys Thr Glu                                 |     | 140 |
| 145                                                             | 150 |     |

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..607
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

|         |       |         |        |        |       |        |       |        |        |        |       |     |
|---------|-------|---------|--------|--------|-------|--------|-------|--------|--------|--------|-------|-----|
| aagttc  | gatg  | gaatag  | ctgg   | atccgt | gacc  | gtgca  | accac | ctcaac | cgca   | tttcag | ggggc | 60  |
| aaggtc  | tttca | tcccga  | atcc   | tcggc  | ctcgt | ctccc  | atctc | gtgcc  | ctaca  | taaaat | ccag  | 120 |
| acgccc  | cgct  | ttacccc | ggt    | cacga  | cggct | ccgcg  | cttg  | ggctg  | ttgaa  | gccgc  | ctcca | 180 |
| gtggtt  | ggcg  | aggtg   | ccgga  | tgtgc  | gttg  | tcagt  | ctgcg | gccgc  | caactg | tctcca | caact | 240 |
| ggtgtc  | gtgc  | ttggtt  | tgtg   | gacatt | gaag  | attat  | ctctg | gggc   | cagacg | atgtc  | gttca | 300 |
| tcgctg  | ctgc  | agcttg  | gttg   | cctcc  | gatgg | ctgct  | tgtca | agcgc  | cgggg  | cctca  | gcgct | 360 |
| cgggaca | act   | tgcg    | cgctg  | catcat | ccaa  | ctccat | tccc  | gtcgc  | agtc   | ca     | gcgtg | 420 |
| cacgtgt | aat   | ttga    | agatca | ttctc  | gtacc | tggaa  | tctaa | agtccc | agggt  | caaga  | acagg | 480 |
| taccaca | gga   | tgagg   | ggcat  | ggagg  | tggct | gcgat  | gtgtt | cgtga  | gargt  | ctagg  | tcgtc | 540 |
| gtctccc | agt   | caactt  | tggg   | ttgct  | ggatc | gttgt  | ctcct | tacga  | tgtat  | ttattt | tattt | 600 |
| yatatag |       |         |        |        |       |        |       |        |        |        |       |     |

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| Lys Phe Asp Gly Ile Ala Gly Ser Val Thr Val Gln Pro Pro Gln Pro |    |    |
| 1                                                               | 5  | 10 |
| His Phe Arg Gly Lys Val Phe Ile Pro Asn Pro Arg Pro Arg Leu Pro |    | 15 |
|                                                                 | 20 | 25 |
| Ser Arg Ala Leu His Lys Ile Gln Thr Pro Arg Phe Thr Pro Phe Thr |    | 30 |
|                                                                 | 35 | 40 |
| Thr Ala Pro Arg Leu Gly Leu Leu Lys Pro Pro Val Leu Gly Glu     |    | 45 |
|                                                                 | 50 | 55 |
| Val Pro Asp Val Arg Trp Ser Val Cys Gly Arg His Cys Leu His Thr |    | 60 |

(2) INFORMATION FOR SEQ ID NO:475:

(A) LENGTH: 546 base pairs

(A) LENGTH: 546 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..546

(D) OTHER INFORMATION: / Ceres Seq. ID 1482307

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| aaaccctagc | cattttcttt  | tcttatcccc | agccgccaca | aagacagccg  | gccgcctggg | 60  |
| aacttttttt | tcttttcttc  | ttcctggccg | accgcacctc | ccacttctct  | ctattttttt | 120 |
| tccttgaccc | atggcttggc  | aaacggatct | aggctggctt | cctctctttc  | tgttcttctc | 180 |
| ctgctctggt | ctttgcttct  | ttcttcccca | ccgaacagct | caaaccgggtg | agctagccgc | 240 |
| tgcttgagcg | cgcagcsggc  | tcacatatcc | gaggatgacc | ggattaatgt  | tcaggggcat | 300 |
| gcgggtttta | ccgccgggtgt | gcgcgtcccc | tcggtagggc | gcgccgccgt  | cggtaaaccg | 360 |
| ccgacagatg | tccctgttga  | cagcagagaa | aaggggtcga | cctcttggtc  | gacttctgtg | 420 |
| actgtgcacg | cccagatctt  | atctccctta | cctctttgac | tcgatctcgt  | tctctgtgat | 480 |
| gtagtgatg  | gatctaattgt | aatatcggg  | atcgagttat | gagttgatag  | aacgtagatt | 540 |
| ttctgc     |             |            |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:476:

(A) LENGTH: 81 amino acids

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..81

(D) OTHER INFORMATION: / Ceres Seq. ID 1482308

[illegible]

(2) INFORMATION FOR SEQ ID NO:477:

(A) LENGTH: 49 amino acids

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..49
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1482309
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

```
Thr Leu Ala Ile Phe Phe Ser Tyr Pro Gln Pro Pro Gln Arg Gln Pro
1 5 10 15
Ala Ala Trp Glu Leu Phe Phe Leu Phe Phe Phe Leu Ala Asp Arg Thr
 20 25 30
Ser His Phe Ser Leu Phe Phe Phe Leu Ala Pro Trp Leu Gly Lys Arg
 35 40 45
Ile
```

(2) INFORMATION FOR SEQ ID NO:478:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 742 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..742
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1482322
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

```
atttgctcac cagcggcagc accgcagcta gtccattgca ttgacgcctc gatcagggct 60
agcgacggac gaaagaaagc tctgcatgca gcgcctcgcc gccgccgtcg tccccagcct 120
ggtgccgccc ctctacctgt ccatggccgc ctccgcccgt gccggctggt ttccagcaga 180
agcagccggc agtagtagcc ggacgacgac gtcgacgccg acgccgacgc ggcggccatt 240
attagcgcas cgccgtggcg ggtggtgcta ctgacgtccc tgctgctggc gccgagctgc 300
tgccaggcga cgcgaggcat gcagccgttc aggggcaagc cgctgcggcc aggcaccgcc 360
aaccatttcc tggggttctt gccgcgggga ccggcgccct cgtccggccc ctgcggcag 420
cacaactcca tcggagcgca ggatcaaagc catccctgac ggcgaccgca ggactgaagc 480
gtggaagaag cagggccgcc gtcgtgtcga tgctcgatc cgaggagtaa gatctccacc 540
aatcaagag agttcgcata accatggatt aggttccttg tcaaaagggt aagctcgtag 600
tattgattat ttagctagtt tcgtagcact agcagcaata gatgtatact cggagagggga 660
acgaagaaaa ggcacgttct ttgtaggacg atgtacatga ggctatatatt tttttgttgg 720
ggatgggtgt ggtggcgtct cg
```

(2) INFORMATION FOR SEQ ID NO:479:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 64 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..64
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1482323
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

```
Ile Cys Ser Pro Arg Pro Ala Pro Gln Leu Val His Cys Ile Asp Ala
1 5 10 15
Ser Ile Arg Ala Ser Asp Gly Arg Lys Lys Ala Leu His Ala Ala Pro
 20 25 30
Arg Arg Arg Arg Arg Pro Gln Pro Gly Ala Ala Ala Leu Pro Val His
 35 40 45
```

Gly Arg Leu Arg Arg Cys Arg Leu Phe Ser Ser Arg Ser Ser Arg Gln  
50 55 60

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1482324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

Met Gln Arg Leu Ala Ala Val Val Pro Ser Leu Val Pro Pro Leu  
1 5 10 15  
Tyr Leu Ser Met Ala Ala Ser Ala Ala Ala Gly Cys Phe Pro Ala Glu  
20 25 30  
Ala Ala Gly Ser Ser Ser Arg Thr Thr Thr Ser Thr Pro Thr Pro Thr  
35 40 45  
Arg Arg Pro Leu Leu Ala Xaa Arg Arg Gly Gly Trp Cys Tyr  
50 55 60

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..46

(D) OTHER INFORMATION: / Ceres Seq. ID 1482325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

Met Gln Pro Phe Arg Gly Lys Pro Leu Arg Pro Gly Thr Ala Asn His  
1 5 10 15  
Phe Leu Gly Phe Leu Pro Arg Gly Pro Ala Pro Pro Ser Gly Pro Ser  
20 25 30  
Arg Gln His Asn Ser Ile Gly Ala Gln Asp Gln Ser His Pro  
35 40 45

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..587

(D) OTHER INFORMATION: / Ceres Seq. ID 1482334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| acgacccaca ccgctgccgc caccgctgcc gacgtakbca cggccgctcc cggacccaca | 60  |
| cctcgacta tgtsscccc accgcccgcg cctcccctct agatcctcaa tgcactgcta   | 120 |
| ggtcccgtcc acagccgctc actgccgcca cctctaacgc gcctaggacc atcgccacct | 180 |
| ccacatctag cttctggagt cgagatccat ggctgactcc cctggaggag cccggatctg | 240 |
| gcctaccggg caggtctcg agctttaggc gtctcagcag gcagcgcggt gtactccgtc  | 300 |

atcgcccaat ggagcagccg accaagcaag aactctatcc gtgctcgtgc cgaggcgtg 360  
tctctactct ctactccatc tgttctgttc ccgcgcctgc gcgtcgtcct ctacggatcc 420  
gtccaccgcc gcgccasacc atgtgaactg agacacgcct cmacctatgc atccaagaca 480  
casctctgca tctgcgtccg tgcactggct acactggatc gattacggag tggagggtgt 540  
tctttacaaa gaaagcttgt accttaaac aggaggatag aagaagt

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

Asp Pro His Arg Cys Arg His Arg Cys Arg Arg Xaa His Gly Arg Ser  
1 5 10 15  
Pro Thr His Thr Ser His Tyr Xaa Xaa Pro Thr Ala Ala Ala Ser Pro  
20 25 30  
Leu Asp Pro Gln Cys Thr Ala Arg Ser Arg Pro Gln Pro Leu Thr Ala  
35 40 45  
Ala Thr Ser Asn Ala Pro Arg Thr Ile Ala Thr Ser Thr Ser Ser Phe  
50 55 60  
Trp Ser Arg Asp Pro Trp Ser Thr Pro Leu Glu Pro Gly Ser Gly  
65 70 75 80  
Leu Pro Gly Thr Val Ser Ser Phe Arg Arg Leu Ser Arg Gln Arg Gly  
85 90 95  
Val Leu Arg His Arg Pro Met Glu Gln Pro Thr Lys Gln Glu Leu Tyr  
100 105 110  
Pro Cys Ser Cys Arg Gly Ala Val Ser Thr Leu Tyr Ser Ile Cys Ser  
115 120 125  
Val Pro Ala Pro Ala Arg Arg Pro Leu Arg Ile Arg Pro Pro Pro Arg  
130 135 140  
Xaa Thr Met  
145

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..543
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

gcttgtgaag acagaaaacg attcctctcc cctccctccc agctctggac gcgtgamgct 60  
cggcggcggc cgcacccctc gctcctcgcc tcacctcccg gtccatcctc gccgctctgc 120  
gcgtgccctca cctcgacacc agccttccct cgtgacacga ctgcaacctc gctgacggag 180  
agtacgtcct cgtgccggag caaggtattg ctcaggaggt agccccaga tccagcacca 240  
gagcctgcac cagaggatct gcctgccact gctttggaag gttctttgga ggacatggtt 300  
gctggagtga cttggccgct catcttgcca ccgggttgga cagtcgagtg ggatcctgcc 360  
tcggctgagg aggagcatga ggagtgatgg gacaggcttc cccatccctc catttaatta 420  
tcgttagttt tattgccgct gcacttcgaa caatgatggc aacttttgaa aaactccgat 480  
ggtgatgtaa taatttagta ctccttgatg tatgatttta tgtcttattg tatttgctct 540  
gtg

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

Ala Cys Glu Asp Arg Lys Arg Phe Leu Ser Pro Pro Ser Gln Leu Trp  
1 5 10 15  
Thr Arg Xaa Ala Arg Arg Arg Pro His Pro Arg Leu Leu Ala Ser Pro  
20 25 30  
Pro Gly Pro Ser Ser Pro Leu Cys Ala Cys Leu Thr Ser Thr Pro Ala  
35 40 45  
Phe Pro Arg Asp Thr Thr Ala Thr Ser Leu Thr Glu Ser Thr Ser Ser  
50 55 60  
Cys Arg Ser Lys Val Leu Leu Arg Arg  
65 70

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..57
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

Leu Val Lys Thr Glu Asn Asp Ser Ser Pro Leu Pro Pro Ser Ser Gly  
1 5 10 15  
Arg Val Xaa Leu Gly Gly Gly Arg Ile Leu Gly Ser Ser Pro His Leu  
20 25 30  
Pro Val His Pro Arg Arg Ser Ala Arg Ala Ser Pro Arg His Gln Pro  
35 40 45  
Ser Leu Val Thr Arg Leu Gln Pro Arg  
50 55

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..633
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| acgccgagca ctccttctcc tcctcctctg tcggcggtcg tgggagacgt acacggcgat  | 60  |
| taggaggcac gtcgtccacc agtctcctcg cagggatgtc gaagagcacg gaaatcgag   | 120 |
| ataaagcaat catcttgatg caggatcatg ccaagcatat ctatcgtatt tgcaatgaga  | 180 |
| agctaataatt gggtaaagga ttgactgcat ttgaggtcaa agaacttcgt gaagcacttg | 240 |
| aattcgccgc cgaaggattg gaccagggct cccttttttg ccaagaggaa ttggatgcaa  | 300 |



```
ctgttaagga ggaacaattg gagcatgacg agaaggtggc ttcacagatg attgaaagcc 360
cacttccttc tcctgattcg gactgcttcc tatcccttga agagcacatt gagaagtttt 420
ggggcggttg ttacaactcg gaccagatgc ctagctactc cgactaggct cagagtttat 480
ggtgctgtga aattctagat gtttggtgt aatggtatgt tggatgtgta tgtgaactgt 540
aattctggat gtgtggatgt aatggtgaac tgactgaatg gtgtcttggtg taatggtatt 600
ttggatgtct atgtgaactc tagctctggg ttt
```

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

```
Ala Glu His Ser Phe Ser Ser Ser Ser Val Gly Gly Arg Gly Arg Arg
1 5 10 15
Thr Arg Arg Leu Gly Gly Thr Ser Ser Thr Ser Leu Leu Ala Gly Met
20 25 30
Ser Lys Ser Thr Glu Ile Ala Asp Lys Ala Ile Ile Leu Met Gln Asp
35 40 45
His Ala Lys His Ile Tyr Arg Ile Cys Asn Glu Lys Leu Ile Leu Gly
50 55 60
Lys Gly Leu Thr Ala Phe Glu Val Lys Glu Leu Arg Glu Ala Leu Glu
65 70 75 80
Phe Ala Ala Glu Gly Leu Asp Gln Gly Ser Leu Phe Cys Gln Glu Glu
85 90 95
Leu Asp Ala Thr Val Lys Glu Glu Gln Leu Glu His Asp Glu Lys Val
100 105 110
Ala Ser Gln Met Ile Glu Ser Pro Leu Pro Ser Pro Asp Ser Asp Cys
115 120 125
Phe Leu Ser Leu Glu Glu His Ile Glu Lys Phe Trp Gly Val Asp Tyr
130 135 140
Asn Ser Asp Gln Met Pro Ser Tyr Ser Asp
145 150
```

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

```
Met Ser Lys Ser Thr Glu Ile Ala Asp Lys Ala Ile Ile Leu Met Gln
1 5 10 15
Asp His Ala Lys His Ile Tyr Arg Ile Cys Asn Glu Lys Leu Ile Leu
20 25 30
Gly Lys Gly Leu Thr Ala Phe Glu Val Lys Glu Leu Arg Glu Ala Leu
35 40 45
Glu Phe Ala Ala Glu Gly Leu Asp Gln Gly Ser Leu Phe Cys Gln Glu
50 55 60
Glu Leu Asp Ala Thr Val Lys Glu Glu Gln Leu Glu His Asp Glu Lys
```

65 70 75 80  
Val Ala Ser Gln Met Ile Glu Ser Pro Leu Pro Ser Pro Asp Ser Asp  
85 90 95  
Cys Phe Leu Ser Leu Glu Glu His Ile Glu Lys Phe Trp Gly Val Asp  
100 105 110  
Tyr Asn Ser Asp Gln Met Pro Ser Tyr Ser Asp  
115 120

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1482342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

Met Gln Asp His Ala Lys His Ile Tyr Arg Ile Cys Asn Glu Lys Leu  
1 5 10 15  
Ile Leu Gly Lys Gly Leu Thr Ala Phe Glu Val Lys Glu Leu Arg Glu  
20 25 30  
Ala Leu Glu Phe Ala Ala Glu Gly Leu Asp Gln Gly Ser Leu Phe Cys  
35 40 45  
Gln Glu Glu Leu Asp Ala Thr Val Lys Glu Glu Gln Leu Glu His Asp  
50 55 60  
Glu Lys Val Ala Ser Gln Met Ile Glu Ser Pro Leu Pro Ser Pro Asp  
65 70 75 80  
Ser Asp Cys Phe Leu Ser Leu Glu Glu His Ile Glu Lys Phe Trp Gly  
85 90 95  
Val Asp Tyr Asn Ser Asp Gln Met Pro Ser Tyr Ser Asp  
100 105

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..827

(D) OTHER INFORMATION: / Ceres Seq. ID 1482346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

cctaatacgaa aaatcgaaaa cccaccgcac cctttcatca gcctgcctgt ccactgttgg 60  
cttgggtgact tcttccgctc cgctccgctc ccctccgctc ccgaacggtc gatctttgca 120  
tggcagcagc agctggctcc aaggggcggg cgatcgctgg aagcttcgtc agccgcgtcc 180  
tcgccggcaa ggccgcctcg ccgaggaggg ccgtgcacgc ctccggcgta gacaagaacc 240  
tggaggacca ggtgcgccc ggcgttcgtgc cggacgatgt gatcggcagc gccggnagac 300  
cccgaacaagt actggagccc ccaccccaag accggcgctc tcggcccggc ggcggtggac 360  
cccaagctgg ccgctgggtg cgccgccgga cgccggcgcg gawtgcctga ggaggcacgg 420  
tgctggacca gaaggtgtgg ttccgcccgc tcgaggacgt cgagaagccg cccccgccg 480  
cgtgagccgc gcggcgctgc taggccagcc cacactgctg ctcgctcata aaaagggcgg 540  
cgggagagcc tggcagtggc aggcaactct ctcgtgctcg gccgggctgg gctccctgct 600  
tatatcactg caatattata ctactagtag tgggtgctga tagcagtgtg tggctgtgct 660  
aataccagta taatactggt tctactataa tacagtcgta tcaggcatgg cgtgcatcag 720  
gactggttgt gatagtagca acgtgatgct cgtgcctgta ataagaacaa gcaggcgatg 780  
tgtgcctgtg atgtaccggt gtcgtcagtg ttataagtac ttgggggc

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..212
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

Leu Ile Glu Lys Ser Lys Thr His Arg Thr Leu Ser Ser Ala Cys Leu  
1 5 10 15  
Ser Thr Val Gly Leu Val Thr Ser Ser Ala Pro Leu Arg Ser Pro Pro  
20 25 30  
Leu Pro Asn Gly Arg Ser Leu His Gly Ser Ser Ser Trp Leu Gln Gly  
35 40 45  
Ala Gly Asp Arg Trp Lys Leu Arg Gln Pro Arg Pro Arg Arg Gln Gly  
50 55 60  
Arg Leu Ala Glu Glu Gly Arg Ala Arg Leu Gly Val Arg Gln Glu Pro  
65 70 75 80  
Gly Gly Pro Gly Ala Pro Gly Val Arg Ala Gly Arg Cys Asp Arg Gln  
85 90 95  
Arg Arg Xaa Ala Pro Thr Ser Thr Gly Ala Pro Thr Pro Arg Pro Ala  
100 105 110  
Ser Ser Ala Arg Arg Arg Trp Thr Pro Ser Trp Pro Leu Val Ala Pro  
115 120 125  
Pro Asp Ala Gly Ala Xaa Cys Cys Arg Arg His Gly Ala Gly Pro Glu  
130 135 140  
Gly Val Val Pro Pro Ala Arg Gly Arg Arg Glu Ala Ala Pro Arg Arg  
145 150 155 160  
Val Ser Arg Ala Ala Leu Leu Gly Gln Pro Thr Leu Leu Leu Ala His  
165 170 175  
Lys Lys Gly Gly Arg Ala Trp Gln Trp Gln Ala Leu Cys Ser Cys  
180 185 190  
Ser Ala Gly Leu Gly Ser Leu Leu Ile Ser Leu Gln Tyr Tyr Thr Thr  
195 200 205  
Ser Ser Gly Ala  
210

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

Met Ala Ala Ala Gly Ser Lys Gly Arg Ala Ile Ala Gly Ser Phe  
1 5 10 15  
Val Ser Arg Val Leu Ala Gly Lys Ala Ala Ser Pro Arg Arg Ala Val  
20 25 30  
His Ala Ser Ala Tyr Asp Lys Asn Leu Glu Asp Gln Val Arg Pro Ala  
35 40 45  
Phe Val Pro Asp Asp Val Ile Gly Ser Ala Xaa Glu Pro Arg Gln Val

50 55 60  
Leu Glu Pro Pro Pro Gln Asp Arg Arg Leu Arg Pro Gly Gly Gly Gly  
65 70 75 80  
Pro Gln Ala Gly Arg Trp Trp Arg Arg Arg Thr Pro Ala Arg Xaa Ala  
85 90 95  
Ala Gly Gly Thr Val Leu Asp Gln Lys Val Trp Phe Arg Pro Leu Glu  
100 105 110  
Asp Val Glu Lys Pro Pro Pro Ala Ala  
115 120

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 767 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..767
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

```
awrcctgcac cgcgtccttc tcttcccaac ttcctcgcgt tcatttcttc accccacccg 60
cccccaaacy ccaaatactaa cagcaaaggt ccggaacctt ctagccgcac ctagggtttg 120
gattggcgcc gagcatggcg tacgtcgacc acgccttctc catctccgac gaggacgacc 180
tcgtcggmgy cgccatgggg ggcccgcgcg gggcgcmcgt gaaggagatc gccttcgccg 240
ccgcgtgct cgmcttcggg gcbtcggtta ccatcaggtg gcctgctaata ggctgtcaac 300
cgcgtcggag gggaccgcgc gcacggaatt ttcttcata tggtgggcat tgtaatgttc 360
atccctgggt tctactacac aaggtatgcc tactatgctt acaaagggtta caagggtttc 420
tctttttcga acatcccacc gatctgaagg agtgtgctgc ctgcctggct ggtcatgaag 480
tggtgtcgct ggtttaagag tttgtcgact ctgtcgaatg gctctgtaga cacccttggt 540
ctacatcttt ctgtggccac attctctttg aacactctag aatgaactgg tggatgtgta 600
cagataaatg cagccatagt tgtgtcccat cgctgtttgg ccgattggaa ggttggtttg 660
tgtgctagtg tgaccatgtt caactgatac gcattgctac ttgtgcatta ctatcgtttt 720
tgtcagggac cttaaatacat tatatgggaa taagatctcg tcgttcc
```

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

Xaa Ser His Arg Val Leu Leu Phe Pro Thr Ser Ser Arg Ser Phe Leu  
1 5 10 15  
His Pro Thr Arg Pro Gln Thr Pro Asn Leu Thr Ala Lys Val Arg Asn  
20 25 30  
Leu Leu Ala Ala Pro Arg Val Trp Ile Gly Ala Glu His Gly Val Arg  
35 40 45  
Arg Pro Arg Leu Leu His Leu Arg Arg Gly Arg Pro Arg Arg Xaa Arg  
50 55 60  
His Gly Gly Pro Ala Arg Gly Xaa Arg Glu Gly Asp Arg Leu Arg Arg  
65 70 75 80  
Arg Ala Ala Xaa Leu Arg Gly Xaa Arg Tyr His Gln Val Ala Cys  
85 90 95

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Tyr | Val | Asp | His | Ala | Phe | Ser | Ile | Ser | Asp | Glu | Asp | Asp | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Xaa | Gly | Ala | Met | Gly | Gly | Pro | Arg | Gly | Ala | Xaa | Val | Lys | Glu | Ile |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ala | Phe | Ala | Ala | Ala | Leu | Leu | Xaa | Phe | Gly | Ala | Xaa | Gly | Thr | Ile | Arg |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Trp | Pro | Ala | Asn | Gly | Cys | Gln | Pro | Arg | Arg | Arg | Gly | Pro | Arg | Ala | Arg |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Asn | Phe | Leu | His | Asp | Val | Gly | His | Cys | Asn | Val | His | Pro | Trp | Val | Leu |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Leu | His | Lys | Asp | Arg | Leu | Leu | Cys | Leu | Gln | Arg | Leu | Gln | Gly | Phe | Leu |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Phe | Phe | Glu | His | Pro | Thr | Asp | Leu | Lys | Glu | Cys | Ala | Ala | Cys | Leu | Ala |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Gly | His | Glu | Val | Val | Ser | Leu | Val |     |     |     |     |     |     |     |     |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Gly | Pro | Arg | Gly | Ala | Xaa | Val | Lys | Glu | Ile | Ala | Phe | Ala | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Leu | Leu | Xaa | Phe | Gly | Ala | Xaa | Gly | Thr | Ile | Arg | Trp | Pro | Ala | Asn |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Gly | Cys | Gln | Pro | Arg | Arg | Arg | Gly | Pro | Arg | Ala | Arg | Asn | Phe | Leu | His |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Asp | Val | Gly | His | Cys | Asn | Val | His | Pro | Trp | Val | Leu | Leu | His | Lys | Asp |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Arg | Leu | Leu | Cys | Leu | Gln | Arg | Leu | Gln | Gly | Phe | Leu | Phe | Phe | Glu | His |
| 65  |     |     | 70  |     |     |     | 75  |     |     |     |     |     |     | 80  |     |
| Pro | Thr | Asp | Leu | Lys | Glu | Cys | Ala | Ala | Cys | Leu | Ala | Gly | His | Glu | Val |
|     |     | 85  |     |     |     | 90  |     |     |     |     |     |     | 95  |     |     |
| Val | Ser | Leu | Val |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1072 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1072

(D) OTHER INFORMATION: / Ceres Seq. ID 1482353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

```
acatcacaaa ccgaaaaaarg ccgcgacgag ccgacgatct ctactgcccc cttccggcct 60
tcggcgaccg tgacgagcaa cgacgacgac ggcgacgatg gccgcttcct ccctctgcca 120
cgggcacttg ctccgtgttc tcctcgtgtc cgtcacatcg gcctgcctcg gtaccgcggc 180
asscantcaa gccgggtctg gagagggtca cacgatcgcc ggccgcgtca agatcgatgg 240
catgagttag aagggctatg gtcttcacgc caagacatca aacacaaaag tgatacttaa 300
tgggcgccaa agggttacat ttgccaggcc agacggctac ttgcatctcc acaacgtgcc 360
agctggaact catctgattg aggtctcctc aattggttac ttcttttccc ctgtccgagt 420
tgatataagt gcaaggaatc ctggatatat tcaagcagca ttgactgaaa ccagaagagt 480
tctgaatgag cttgttctgg aacctctgaa agaagagcag tactttgagg ttagggagcc 540
gttctccgtc atgtcacttt tgaagagccc catgggggta atgggttggt ttatggtctt 600
aatggtcttc gtgatgcccc agatgatgga gaacatagat cccgaggaga tgaagcaagc 660
tcaagwacaa atgaggaaca accctgtatc attctctggc ttgctcgcca gagcgaggg 720
ctagagaagt agactgtaga catgaggata ctgcaaaggt caaacattct agaatgtgag 780
taagagcact attaaagtgc ttggcacgtc actcactcgg ggcaatttcc tggggataag 840
aaggaaatcc tttccccctg tttttaccgt atttttagggc tagtttgagg acaccaattt 900
tccaaaggat ttatatcttc ccatgggaaa atgaactaat ttctcttggg aaaatgaaaa 960
tctcttgaaa aattgggggt ccaaactagy ccttaagtta taatttgtct gcggtgtaga 1020
acctctgaaa acctctgagc tagtgatgag tcagattgag atattttgtt cg
```

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..208

(D) OTHER INFORMATION: / Ceres Seq. ID 1482354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

```
Met Ala Ala Ser Ser Leu Cys His Gly His Leu Leu Leu Phe Leu Leu
1 5 10 15
Val Ser Val Thr Ser Ala Cys Leu Gly Thr Ala Ala Xaa Xaa Gln Ala
20 25 30
Gly Ser Gly Glu Gly Tyr Thr Ile Ala Gly Arg Val Lys Ile Asp Gly
35 40 45
Met Ser Glu Lys Gly Tyr Gly Leu Pro Ala Lys Thr Ser Asn Thr Lys
50 55 60
Val Ile Leu Asn Gly Gly Gln Arg Val Thr Phe Ala Arg Pro Asp Gly
65 70 75 80
Tyr Phe Ala Phe His Asn Val Pro Ala Gly Thr His Leu Ile Glu Val
85 90 95
Ser Ser Ile Gly Tyr Phe Phe Ser Pro Val Arg Val Asp Ile Ser Ala
100 105 110
Arg Asn Pro Gly Tyr Ile Gln Ala Ala Leu Thr Glu Thr Arg Arg Val
115 120 125
Leu Asn Glu Leu Val Leu Glu Pro Leu Lys Glu Glu Gln Tyr Phe Glu
130 135 140
Val Arg Glu Pro Phe Ser Val Met Ser Leu Leu Lys Ser Pro Met Gly
145 150 155 160
Leu Met Val Gly Phe Met Val Leu Met Val Phe Val Met Pro Lys Met
165 170 175
Met Glu Asn Ile Asp Pro Glu Glu Met Lys Gln Ala Gln Xaa Gln Met
```

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 180                                                             | 185 | 190 |
| Arg Asn Asn Pro Val Ser Phe Ser Gly Leu Leu Ala Arg Ala Gln Gly |     |     |
| 195                                                             | 200 | 205 |

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Glu | Lys | Gly | Tyr | Gly | Leu | Pro | Ala | Lys | Thr | Ser | Asn | Thr | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ile | Leu | Asn | Gly | Gly | Gln | Arg | Val | Thr | Phe | Ala | Arg | Pro | Asp | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Phe | Ala | Phe | His | Asn | Val | Pro | Ala | Gly | Thr | His | Leu | Ile | Glu | Val |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ser | Ser | Ile | Gly | Tyr | Phe | Phe | Ser | Pro | Val | Arg | Val | Asp | Ile | Ser | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Asn | Pro | Gly | Tyr | Ile | Gln | Ala | Ala | Leu | Thr | Glu | Thr | Arg | Arg | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Asn | Glu | Leu | Val | Leu | Glu | Pro | Leu | Lys | Glu | Glu | Gln | Tyr | Phe | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Arg | Glu | Pro | Phe | Ser | Val | Met | Ser | Leu | Leu | Lys | Ser | Pro | Met | Gly |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Leu | Met | Val | Gly | Phe | Met | Val | Leu | Met | Val | Phe | Val | Met | Pro | Lys | Met |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Met | Glu | Asn | Ile | Asp | Pro | Glu | Met | Lys | Gln | Ala | Gln | Xaa | Gln | Met |     |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Arg | Asn | Asn | Pro | Val | Ser | Phe | Ser | Gly | Leu | Leu | Ala | Arg | Ala | Gln | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..803
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| accaacctca  | cctactgttc  | tgggttgaaa | tcttgcggaa | agtctgccaa | aacaaaaaac | 60  |
| aaaagtcctt  | gcaggtgggt  | tggcaggcta | aacttgacgt | ttgcgttggc | aggaagccgt | 120 |
| ggctgctgta  | atctaactctg | ctgctgcaat | ctccgacccg | tctcccagac | ttgactgtac | 180 |
| ctgaaaccac  | tattgaaaca  | atcggtgaga | gcgagagaga | aaattaaaga | gaaacccgac | 240 |
| aaaaaccaac  | caaccaagca  | gctctccgtt | ccatatagcc | gctgcatcag | atccattcaa | 300 |
| gaactagagc  | caagccacca  | acaataaatt | cctctggccg | gcctgcctca | tcagctcggt | 360 |
| tcaaaaaaaaa | caaaaaaaaa  | agaagtcgca | gcggcagtag | taaactgcag | tgacatacgg | 420 |
| agcactactg  | tactgtactg  | tagtaacata | ctactactgc | tgctgctcac | agcaagaaca | 480 |

aggatacgcgta aaaaaagaac caaggcaaaa agctaagggtc ctgttttgga acaaagtttt 540  
tgaaaaccac agtttttgaa atactatact atactttagt tataacaata ccgtagttta 600  
taataccgca gttttgaaaa ctgaggtcca gagctaagtt tagaatgcct taaaacaact 660  
atagtatttg caatacttca gttttgaaaa cagagatttt acctagcttg ccaaacacca 720  
ttatgtatat aatactgcag tatttgagaa tactgcagta ttcttccaaa actgcagaaa 780  
aactttgttc ccaaacaccc cct

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..57
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

Thr Asn Leu Thr Tyr Cys Ser Gly Leu Lys Ser Cys Gly Lys Ser Ala  
1 5 10 15  
Lys Thr Lys Asn Lys Ser Pro Cys Arg Trp Phe Gly Arg Leu Asn Leu  
20 25 30  
Thr Phe Ala Leu Ala Gly Ser Arg Gly Cys Cys Asn Leu Ile Cys Cys  
35 40 45  
Cys Asn Leu Arg Pro Val Ser Gln Thr  
50 55

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

Gln Pro His Leu Leu Phe Trp Val Glu Ile Leu Arg Lys Val Cys Gln  
1 5 10 15  
Asn Lys Lys Gln Lys Ser Leu Gln Val Val Trp Gln Ala Lys Leu Asp  
20 25 30  
Val Cys Val Gly Arg Lys Pro Trp Leu Leu  
35 40

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..517
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

gtagacgacg tgcattgtgtr gccggccaat ttacgcgcgc ccacatgctc tgctcgccca 60  
tcgctttcga gctttgtgta aatggactag agcggaaggc atagcatgca taggaatagg 120  
agcaactaac caccggcctc tcgctccctc gctgcgccat aaggctgcga ctgcgagagc 180



```
cagccgcacc cgcaccagtc cataggccgg cctcctctct taccttccca cacccttct 240
cgaccgtacg tagcctagtt gtgcttggtta gccagccaga aggtcgtcgg ccgatgatgg 300
gaggaagaac agtggccccg ccgctcgtcc tcgcgctggt gaccatcatc gccatcggcg 360
gcggccgarg gggacgaggt gaagtgtggc gggtrctctc cgtrcrgcgg crccgactgc 420
mcggtgctgt acccgthnmm gcscrcrcg ccgtactact actacagcmc tmccccaccc 480
gcgacctacc ccggggagtc ctggtcatatc taccagc
```

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

```
Met Cys Xaa Arg Pro Ile Tyr Ala Pro Pro His Ala Leu Leu Ala His
1 5 10 15
Arg Phe Arg Ala Leu Cys Lys Trp Thr Arg Ala Glu Gly Ile Ala Cys
 20 25 30
Ile Gly Ile Gly Ala Thr Asn His Arg Pro Leu Ala Pro Ser Leu Arg
 35 40 45
His Lys Ala Ala Thr Ala Arg Ala Ser Arg Thr Arg Thr Ser Pro
 50 55 60
```

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

```
Met Met Gly Gly Arg Thr Val Ala Pro Pro Leu Val Leu Ala Leu Val
1 5 10 15
Thr Ile Ile Ala Ile Gly Gly Gly Arg Xaa Gly Arg Gly Glu Val Trp
 20 25 30
Arg Xaa Leu Ser Xaa Xaa Arg Xaa Arg Leu Xaa Gly Ala Val Pro Xaa
 35 40 45
Xaa Xaa Pro Xaa Ala Val Leu Leu Leu Gln Xaa Xaa Pro Thr Arg Asp
 50 55 60
Leu Pro Arg Gly Val Leu Val Ile Leu Pro
65 70
```

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482362

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 449 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..449

(D) OTHER INFORMATION: / Ceres Seq. ID 1482363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO:1000 |            |            |            |            |            |  |  |     |
|-------------------------------------------|------------|------------|------------|------------|------------|--|--|-----|
| aaagagaag                                 | tttattacga | tgtaggtgca | tattcaaggc | ccgttgatgg | atgaactttt |  |  | 60  |
| gtagttgtgg                                | tccaaaggtg | tacgtatgtg | ggacgggcat | aaaaaatatg | attttgatct |  |  | 120 |
| acgtgctttg                                | ttattggcga | acaggcgagt | gagtgaagag | agaagccatg | cctctttcgt |  |  | 180 |
| gtgaggcaag                                | cgatgaacga | gtagatgctg | ccattcaaca | agggattcag | ggtctgcacc |  |  | 240 |
| tattgtttag                                | atgagatcgt | tatcttgtat | ctacatcatt | gtagagaagt | tatttacatg |  |  | 300 |
| ggccatcgtc                                | gatttcttgg | aaacacccaa | taagaagaaa | aggcaagcat | tgaaatgcac |  |  | 360 |
| aagtagacca                                | tcgtgccaaa | gcctattccc | caaaggagca | accttgattt | ccagatggta |  |  | 420 |
| taqaacttaa                                | atgtagtgtg | tgggaaatcg |            |            |            |  |  |     |

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..33

(D) OTHER INFORMATION: / Ceres Seq. ID 1482364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

[illegible]

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..32

(D) OTHER INFORMATION: / Ceres Seq. ID 1482365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

```
Met Trp Asp Gly His Lys Lys Tyr Asp Phe Asp Leu Arg Ala Leu Leu
1 5 10 15
Leu Ala Asn Arg Arg Val Ser Glu Glu Arg Ser His Ala Ser Phe Val
 20 25 30
```

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..42

(D) OTHER INFORMATION: / Ceres Seq. ID 1482366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

```
Met Leu Pro Phe Asn Lys Gly Phe Arg Val Cys Thr Tyr Cys Leu Asp
1 5 10 15
Glu Ile Gly Ile Leu Tyr Leu His His Cys Arg Glu Val Ile Tyr Met
 20 25 30
Gly His Arg Arg Phe Leu Val Asn Thr Lys
 35 40
```

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 757 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..757

(D) OTHER INFORMATION: / Ceres Seq. ID 1482371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

```
tgattggttt gatgaacagc tagagaacta cttagatgat gattatcttg tgtttgattg 60
ccctggccag attgaactct tcacacatgt tccagttctg cggaactttg tcgagcacct 120
gaaacgaaaa aatttcaacg tttgcgctgt ttaccttctt gattcacagt ttgtcagcga 180
tgtaacaaaa tacatcagtg gttgcatggc ttctctatct gctatgattc agcttgaact 240
tcctcatatc aacatccttt caaagatgga tctggtctcc aacaaaaaag atgtagaaga 300
gtacctggac ccgaatgcac aggttcttct ttcacagctg aatcggcaga tggcacctcg 360
gtttggcaag ttgaacaagt gtttagctga actggttgat gattacagca tggttaattt 420
cattccactt gatttgagaa aggaaagcag catacaatat gtgctatctt ctatcgacac 480
ctgtatccag tatggggaag atgcagatgt gaaggtcagg gacttcgaag aagacgaaga 540
ctaaccactg gcaactggatg ctgtaggagg tgcaaactgg ttgctagcag tcgtgtagtg 600
cggagtgaga ctttgggact gtgtakgggt gcgcaggcat gcaaaaacgt cgtaggatgc 660
tgatgacagc tawctggcct atgtaagacg aactaawgca gatatttggc aagtcctagt 720
aaaatgtgtg wgcrccttga tggctmyctrw tctcccc
```

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..180

(D) OTHER INFORMATION: / Ceres Seq. ID 1482372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

```
Asp Trp Phe Asp Glu Gln Leu Glu Asn Tyr Leu Asp Asp Asp Tyr Leu
1 5 10 15
Val Phe Asp Cys Pro Gly Gln Ile Glu Leu Phe Thr His Val Pro Val
 20 25 30
Leu Arg Asn Phe Val Glu His Leu Lys Arg Lys Asn Phe Asn Val Cys
 35 40 45
Ala Val Tyr Leu Leu Asp Ser Gln Phe Val Ser Asp Val Thr Lys Tyr
 50 55 60
Ile Ser Gly Cys Met Ala Ser Leu Ser Ala Met Ile Gln Leu Glu Leu
 65 70 75 80
Pro His Ile Asn Ile Leu Ser Lys Met Asp Leu Val Ser Asn Lys Lys
 85 90 95
Asp Val Glu Glu Tyr Leu Asp Pro Asn Ala Gln Val Leu Leu Ser Gln
 100 105 110
Leu Asn Arg Gln Met Ala Pro Arg Phe Gly Lys Leu Asn Lys Cys Leu
 115 120 125
Ala Glu Leu Val Asp Asp Tyr Ser Met Val Asn Phe Ile Pro Leu Asp
 130 135 140
Leu Arg Lys Glu Ser Ser Ile Gln Tyr Val Leu Ser Ser Ile Asp Thr
 145 150 155 160
Cys Ile Gln Tyr Gly Glu Asp Ala Asp Val Lys Val Arg Asp Phe Glu
 165 170 175
Glu Asp Glu Asp
 180
```

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1482373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

```
Met Ala Ser Leu Ser Ala Met Ile Gln Leu Glu Leu Pro His Ile Asn
1 5 10 15
Ile Leu Ser Lys Met Asp Leu Val Ser Asn Lys Lys Asp Val Glu Glu
 20 25 30
Tyr Leu Asp Pro Asn Ala Gln Val Leu Leu Ser Gln Leu Asn Arg Gln
 35 40 45
Met Ala Pro Arg Phe Gly Lys Leu Asn Lys Cys Leu Ala Glu Leu Val
 50 55 60
Asp Asp Tyr Ser Met Val Asn Phe Ile Pro Leu Asp Leu Arg Lys Glu
 65 70 75 80
Ser Ser Ile Gln Tyr Val Leu Ser Ser Ile Asp Thr Cys Ile Gln Tyr
 85 90 95
Gly Glu Asp Ala Asp Val Lys Val Arg Asp Phe Glu Glu Asp Glu Asp
 100 105 110
```

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..106
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1482374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Gln | Leu | Leu | Pro | His | Ile | Asn | Ile | Leu | Ser | Lys | Met | Asp |     |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Leu | Val | Ser | Asn | Lys | Lys | Asp | Val | Glu | Glu | Tyr | Leu | Asp | Pro | Asn | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Val | Leu | Leu | Ser | Gln | Leu | Asn | Arg | Gln | Met | Ala | Pro | Arg | Phe | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Leu | Asn | Lys | Cys | Leu | Ala | Glu | Leu | Val | Asp | Asp | Tyr | Ser | Met | Val |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Asn | Phe | Ile | Pro | Leu | Asp | Leu | Arg | Lys | Glu | Ser | Ser | Ile | Gln | Tyr | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Ser | Ser | Ile | Asp | Thr | Cys | Ile | Gln | Tyr | Gly | Glu | Asp | Ala | Asp | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Val | Arg | Asp | Phe | Glu | Glu | Asp | Glu | Asp |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:516:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 617 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..617
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1482375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| agaatcccc   | gtmgacgcgc | acggcagagc  | tccgcatccg | caccggccgc | cggcggstgg | 60  |
| atggggaagc  | tctccgccct | gaagcgggaa  | gcggtcggag | tggactaggc | gctcggtgac | 120 |
| ttcctagttt  | agaagcggta | rgtgaggcg   | atgcggggcg | gggcgatgaa | ggccctgcgg | 180 |
| cgatccagca  | cctcctcggc | gccatcgcca  | agggtgccgt | cttccccgcg | gtcttattcg | 240 |
| tggatccacc  | gccggtcgct | tctcgttacc  | tygccggcct | cgccggmgmc | gtcctctgtg | 300 |
| tctgaatcgg  | cgaatttgcc | cgcggagggt  | tcggattcag | cgccagcktc | agtggtgga  | 360 |
| gcttcctcgt  | cgccctcgct | ggctgcttcg  | tctccgaaca | tggaatggtg | gggctatcct | 420 |
| gtccggattt  | ctcctcgtgc | tgcattgggtc | gcttcaaaat | ggggaataat | tggtgggcta | 480 |
| cttgatattt  | cccaacaacg | attcgcgcac  | ttattcccaa | aattatgctg | ttctggtagc | 540 |
| acagtgggaag | tggtagtttg | ttcgggtacta | ttattcttat | aagatttgct | ttagtctctt | 600 |
| agattaaaaa  | aaagctg    |             |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:517:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 143 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..143
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1482376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

Met Arg Gly Gly Ala Met Lys Ala Leu Arg Arg Ser Ser Thr Ser Ser

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   | 5   | 10  | 15  |     |     |     |     |     |     |     |     |     |     |     |     |
| Ala | Pro | Ser | Pro | Arg | Val | Pro | Ser | Ser | Pro | Arg | Ser | Tyr | Ser | Trp | Ile |
|     | 20  |     |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Arg | Arg | Ser | Leu | Leu | Val | Thr | Xaa | Pro | Ala | Ser | Pro | Xaa | Xaa | Ser |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Val | Ser | Glu | Ser | Ala | Asn | Leu | Pro | Ala | Glu | Gly | Ser | Asp | Ser | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Xaa | Ser | Val | Val | Ala | Ala | Ser | Ser | Ser | Pro | Ser | Leu | Ala | Ala | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Pro | Asn | Met | Glu | Trp | Trp | Gly | Tyr | Pro | Val | Arg | Ile | Ser | Pro | Arg |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Ala | Trp | Val | Ala | Ser | Lys | Trp | Gly | Ile | Ile | Val | Gly | Leu | Leu | Asp |
|     | 100 |     |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Ser | Gln | Gln | Arg | Phe | Ala | His | Leu | Phe | Pro | Lys | Leu | Cys | Cys | Ser |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Ser | Thr | Val | Glu | Val | Val | Cys | Ser | Val | Leu | Leu | Phe | Leu |     |     |
| 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ala | Leu | Arg | Arg | Ser | Ser | Thr | Ser | Ser | Ala | Pro | Ser | Pro | Arg |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Pro | Ser | Ser | Pro | Arg | Ser | Tyr | Ser | Trp | Ile | His | Arg | Arg | Ser | Leu |
|     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Leu | Val | Thr | Xaa | Pro | Ala | Ser | Pro | Xaa | Xaa | Ser | Ser | Val | Ser | Glu | Ser |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ala | Asn | Leu | Pro | Ala | Glu | Gly | Ser | Asp | Ser | Ala | Pro | Xaa | Ser | Val | Val |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ala | Ala | Ser | Ser | Ser | Pro | Ser | Leu | Ala | Ala | Ser | Ser | Pro | Asn | Met | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Trp | Trp | Gly | Tyr | Pro | Val | Arg | Ile | Ser | Pro | Arg | Ala | Ala | Trp | Val | Ala |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Lys | Trp | Gly | Ile | Ile | Val | Gly | Leu | Asp | Ile | Ser | Gln | Gln | Arg |     |
|     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Phe | Ala | His | Leu | Phe | Pro | Lys | Leu | Cys | Cys | Ser | Gly | Ser | Thr | Val | Glu |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Val | Val | Val | Cys | Ser | Val | Leu | Leu | Phe | Leu |     |     |     |     |     |     |
| 130 |     |     |     |     | 135 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..585
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

```
aattcattac cggaagagaa aaaaataact cggaaaagaa ggagacgccg aaaattcgaa 60
aggggagggg aaagcaaagc tgatggcgga ggaccagggg aaagcaaagc aaatggcgga 120
ggccccgagc aagatcgaat ccatgaggaa gtgggtcgtc gagcacaagc tccgagccgt 180
aggttgccctc tggctagggtg ggatcagcag ttcgatcgcc tacaactggt cgcggcccaa 240
tatgaagcct agcgtcaaga tcatccacgc aaggttgcac gctcaagctc taaccctggc 300
tgcattagtt ggttctgcat gcgtggagta ctatgatcag aagtatgggt cttctgggcc 360
aaaggtggac aaatacaca gccaatacct ggcccattcg cataaagatt aaaggtcgcc 420
atggttggttc ctgcatgccg gattaatttt gggctcatct cgggttgctc atgaccgcc 480
catggatgct ggatgtttat tctttttttg tcttcataat tacaaaatgg tgggtgtactt 540
gccaggcaaa tgtaatatgag ggtataatgc agatattgtc gtcgc
```

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

```
Met Ala Glu Asp Gln Gly Lys Ala Lys Gln Met Ala Glu Ala Pro Ser
1 5 10 15
Lys Ile Glu Ser Met Arg Lys Trp Val Val Glu His Lys Leu Arg Ala
 20 25 30
Val Gly Cys Leu Trp Leu Gly Gly Ile Ser Ser Ser Ile Ala Tyr Asn
 35 40 45
Trp Ser Arg Pro Asn Met Lys Pro Ser Val Lys Ile Ile His Ala Arg
 50 55 60
Leu His Ala Gln Ala Leu Thr Leu Ala Ala Leu Val Gly Ser Ala Cys
65 70 75 80
Val Glu Tyr Tyr Asp Gln Lys Tyr Gly Ser Ser Gly Pro Lys Val Asp
 85 90 95
Lys Tyr Thr Ser Gln Tyr Leu Ala His Ser His Lys Asp
 100 105
```

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

```
Met Ala Glu Ala Pro Ser Lys Ile Glu Ser Met Arg Lys Trp Val Val
1 5 10 15
Glu His Lys Leu Arg Ala Val Gly Cys Leu Trp Leu Gly Gly Ile Ser
 20 25 30
Ser Ser Ile Ala Tyr Asn Trp Ser Arg Pro Asn Met Lys Pro Ser Val
 35 40 45
Lys Ile Ile His Ala Arg Leu His Ala Gln Ala Leu Thr Leu Ala Ala
 50 55 60
Leu Val Gly Ser Ala Cys Val Glu Tyr Tyr Asp Gln Lys Tyr Gly Ser
65 70 75 80
Ser Gly Pro Lys Val Asp Lys Tyr Thr Ser Gln Tyr Leu Ala His Ser
```

85

90

95

His Lys Asp

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1482381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

Met Arg Lys Trp Val Val Glu His Lys Leu Arg Ala Val Gly Cys Leu  
1 5 10 15  
Trp Leu Gly Gly Ile Ser Ser Ser Ile Ala Tyr Asn Trp Ser Arg Pro  
20 25 30  
Asn Met Lys Pro Ser Val Lys Ile Ile His Ala Arg Leu His Ala Gln  
35 40 45  
Ala Leu Thr Leu Ala Ala Leu Val Gly Ser Ala Cys Val Glu Tyr Tyr  
50 55 60  
Asp Gln Lys Tyr Gly Ser Ser Gly Pro Lys Val Asp Lys Tyr Thr Ser  
65 70 75 80  
Gln Tyr Leu Ala His Ser His Lys Asp  
85

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 769 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..769

(D) OTHER INFORMATION: / Ceres Seq. ID 1482382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

caaaaaaaaaac caatcggacg gaaacgaaaa aggcctcact catctccgtc cgtccgccgc 60  
accgtcgccg agcgccgctc cgcgccggag acgtcctgtt tttttgccgc ctacgagcgc 120  
tgtccctctt ttctttccgc ggttctgccc caacttctgc atccgaatct cccacgaagt 180  
tgtcacggcg atggcagcga cggcgggcgt ttcaactgac gatatcccga tcctgcaagc 240  
agagaacctc accagcaacg tcaagtccgt ccactacagt cgaacattct tgcgatcat 300  
tggtggagtt gttgctggaa tctggggatt cacaggcttg acgggatttg tcttctactt 360  
tctgataatg atggttgcat ctatcgggct cttagcaaag tcaaagtttt cagtgcagac 420  
atacttcgat agttggacca ggatttcaat tgaaggagtt tttggtggcc ttatgtcatt 480  
cgtgctgttc tggacatttg cttatgacat tgttcatatc ttctgatgga cgtagaaaga 540  
gctaccctcc aaagaaaata tggaatttca tctgatgtcg aacattccca atgggctctt 600  
tgtacactca gtttttattt tggttaattgt tgatataata ttttgtgata ctatatcggt 660  
ggacctaaagc agagctcata aactgatgta gcaactcctt cgcttgatg atctgtagca 720  
gttgtgattt gtcatttcca gtaatgaatg taaactttga ttgatggac

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Lys | Asn | Gln | Ser | Asp | Gly | Asn | Glu | Lys | Gly | Leu | Thr | His | Leu | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Ser | Ala | Ala | Pro | Ser | Pro | Ser | Ala | Pro | Arg | Arg | Arg | Arg | Pro |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Val | Phe | Leu | Pro | Pro | Thr | Ser | Ala | Val | Pro | Leu | Phe | Phe | Pro | Arg | Phe |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Pro | Asn | Phe | Cys | Ile | Arg | Ile | Ser | His | Glu | Val | Val | Thr | Ala | Met |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Ala | Thr | Gly | Gly | Val | Ser | Thr | Asp | Asp | Ile | Pro | Ile | Leu | Gln | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Asn | Leu | Thr | Ser | Asn | Val | Lys | Ser | Val | His | Tyr | Ser | Arg | Thr | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Ser | Ile | Ile | Gly | Gly | Val | Val | Ala | Gly | Ile | Trp | Gly | Phe | Thr | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Thr | Gly | Phe | Val | Phe | Tyr | Phe | Leu | Ile | Met | Met | Val | Ala | Ser | Ile |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Gly | Leu | Leu | Ala | Lys | Ser | Lys | Phe | Ser | Val | Gln | Thr | Tyr | Phe | Asp | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Trp | Thr | Arg | Ile | Ser | Ile | Glu | Gly | Val | Phe | Gly | Gly | Leu | Met | Ser | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Leu | Phe | Trp | Thr | Phe | Ala | Tyr | Asp | Ile | Val | His | Ile | Phe |     |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Lys | Thr | Asn | Arg | Thr | Glu | Thr | Lys | Lys | Ala | Ser | Leu | Ile | Ser | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Pro | Pro | His | Arg | Arg | Arg | Ala | Pro | Leu | Arg | Ala | Gly | Asp | Val | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Phe | Cys | Arg | Leu | Arg | Ala | Leu | Ser | Leu | Phe | Ser | Phe | Arg | Gly | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Pro | Thr | Ser | Ala | Ser | Glu | Ser | Pro | Thr | Lys | Leu | Ser | Arg | Arg | Trp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Arg | Pro | Ala | Ala | Phe | Gln | Leu | Thr | Ile | Ser | Arg | Ser | Cys | Lys | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Arg | Thr | Ser | Pro | Ala | Thr | Ser | Ser | Pro | Ser | Thr | Thr | Val | Glu | His | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Cys | Arg | Ser | Leu | Val | Glu | Leu | Leu | Leu | Glu | Ser | Gly | Asp | Ser | Gln | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..111  
(D) OTHER INFORMATION: / Ceres Seq. ID 1482385  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:  
Met Ala Ala Thr Gly Gly Val Ser Thr Asp Asp Ile Pro Ile Leu Gln  
1 5 10 15  
Ala Glu Asn Leu Thr Ser Asn Val Lys Ser Val His Tyr Ser Arg Thr  
20 25 30  
Phe Leu Ser Ile Ile Gly Gly Val Val Ala Gly Ile Trp Gly Phe Thr  
35 40 45  
Gly Leu Thr Gly Phe Val Phe Tyr Phe Leu Ile Met Met Val Ala Ser  
50 55 60  
Ile Gly Leu Leu Ala Lys Ser Lys Phe Ser Val Gln Thr Tyr Phe Asp  
65 70 75 80  
Ser Trp Thr Arg Ile Ser Ile Glu Gly Val Phe Gly Gly Leu Met Ser  
85 90 95  
Phe Val Leu Phe Trp Thr Phe Ala Tyr Asp Ile Val His Ile Phe  
100 105 110

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 767 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..767  
(D) OTHER INFORMATION: / Ceres Seq. ID 1482386  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

agtcagacat agagaatcct tctagacaca gcgatgtgcc ggtgccccag caattcattg 60  
tggcatttcg caccacatc aacccttca cacacgaacc agatcagaaa agccactact 120  
gctttctctc tctctctcac acacacacag acacaaataa aagaaatcag tagttcgatt 180  
tctcctctca cctttattta cacatatctc tgtattttaca aattagggtg ttgatgtagg 240  
ctgtacgcac ctgctagttt gctactcgat cctatatatc gtccaatcct atctgacctc 300  
tcgacatctg gtccttgatt actcgctcctt tttgcttggt tatatcgtcg ccccggcgcg 360  
ttgagctagc ttcctctagt tctcgcgctc gtcgctcgatc ggttggttgc atagcccacg 420  
gcgagccgaa ggaataatgt cgctcgccgc cctgcagatc gcgcccgtgc cgggagcatg 480  
tgtgctacgt gcaactgcaac ttctgcaaca caattctcgc ggtaaaccac ctcatctctc 540  
tgtttgctcc cctccctcct ttgaattccc agttctcgat cggcatgcat gcctctgaag 600  
tgcagatcta caaaggggag atgcacatga aatgattgst gcgcgcgcgc atgcatcata 660  
cagttttattt tgtaggattt ggctgtcccc tcttgctgga tttcttcttc ttcttcttta 720  
tttttttgct ctataaattg ttttgtaaag gttgaatgaa atttctg

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..56  
(D) OTHER INFORMATION: / Ceres Seq. ID 1482387  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

Ser Asp Ile Glu Asn Pro Ser Arg His Ser Asp Val Pro Val Pro Gln  
1 5 10 15  
Gln Phe Ile Val Ala Phe Arg Thr His Ile Asn Pro Phe Thr His Glu  
20 25 30  
Pro Asp Gln Lys Ser His Tyr Cys Phe Leu Ser Leu Ser His Thr His  
35 40 45  
Thr Asp Thr Asn Lys Arg Asn Gln  
50 55

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1482388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

Met Cys Arg Cys Pro Ser Asn Ser Leu Trp His Phe Ala Pro Thr Ser  
1 5 10 15  
Thr Pro Ser His Thr Asn Gln Ile Arg Lys Ala Thr Thr Ala Phe Ser  
20 25 30  
Leu Ser Leu Thr His Thr Gln Thr Gln Ile Lys Glu Ile Ser Ser Ser  
35 40 45  
Ile Ser Pro Leu Thr Phe Ile Tyr Thr Tyr Leu Cys Ile Tyr Lys Leu  
50 55 60  
Gly Cys  
65

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1482389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

Met Ser Ser Ala Pro Leu Gln Ile Ala Pro Val Pro Gly Ala Cys Val  
1 5 10 15  
Leu Arg Ala Leu Gln Leu Leu Gln His Asn Ser Arg Gly Lys His Pro  
20 25 30  
His Leu Ser Val Cys Pro Pro Pro Ser Phe Glu Phe Pro Val Leu Asp  
35 40 45  
Arg His Ala Cys Leu  
50

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1023 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1023

(D) OTHER INFORMATION: / Ceres Seq. ID 1482398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

|            |            |             |            |             |             |      |
|------------|------------|-------------|------------|-------------|-------------|------|
| atttgcctat | ttccggtgca | ggcagtcctgg | cagagcgagc | aggcarrcaa  | ctggggccaga | 60   |
| rtcagacagg | cctgcccgcc | acgccgtccc  | gacggccatg | gcccgaccct  | tctcttcccc  | 120  |
| acacatcccc | tcttcacct  | gggtgactcg  | ccgccctcct | ccctggacct  | cctcaccgtc  | 180  |
| cgtctccacc | acgagaacta | gcgcctcgtc  | tattaccgcg | tgacagaccgc | gccgcagggc  | 240  |
| agtcgcgccg | gcggcctccc | tccacctcgg  | cccgggggag | atcgccgagc  | tcgcgcgcaa  | 300  |
| caaggttttr | attgcggcga | cagtrgcgag  | cgcgatcggg | cagctgtcca  | agcccttcac  | 360  |
| ctcggtaaac | aatggggggc | tcggcgccgg  | ccttgacctc | aggaccgtct  | tccgctccgg  | 420  |
| agggatgccc | tccayycaat | ccgcgagtg   | tggtgcagtt | gctacttcgc  | ttgggctaga  | 480  |
| aaggggggtt | rcagactcca | tatttggaat  | gtcagtrgw  | tttkcagcaa  | ttgtaatgta  | 540  |
| tgatgctcag | ggagtaagaa | gagaaktggg  | caaccacgcc | aagatcttga  | acaggttttg  | 600  |
| gacctcaaaa | gagaaggtac | ctctggagta  | ttctgaagt  | gacatggcag  | ctcctgggtt  | 660  |
| tgtttcggtc | accgaggaag | cgagctccaa  | cgcgagcccc | tccttgaagc  | gcggttctag  | 720  |
| caccgaatca | ccaaggggtg | atgggctccg  | tggtgcagag | cctgagctga  | cagagctgaa  | 780  |
| gcaggtctgc | gtagaggagg | attaccgggt  | gagtgaatct | ggtggccaca  | cggagcttca  | 840  |
| ggcacagtc  | ggcgccctgt | tggtttttgc  | tgtaagctta | gcagtgatg   | caacactgta  | 900  |
| acggaccttt | tcatatcacg | tccttgattg  | attacacatt | tacacttttt  | tttacacaga  | 960  |
| aacaatacat | gcggtttatt | gttcccaccg  | tttaaatac  | aaatgcctat  | gctagctcgt  | 1020 |
| ttc        |            |             |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..299

(D) OTHER INFORMATION: / Ceres Seq. ID 1482399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ala | Tyr | Phe | Arg | Cys | Arg | Gln | Ser | Gly | Arg | Ala | Ser | Arg | Xaa | Xaa |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     |     | 15  |     |
| Thr | Gly | Pro | Xaa | Ser | Asp | Arg | Pro | Ala | Arg | His | Ala | Val | Pro | Thr | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Ala | Arg | Pro | Phe | Ser | Ser | Pro | His | Ile | Pro | Ser | Ser | Ser | Trp | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Arg | Arg | Pro | Pro | Pro | Trp | Thr | Ser | Ser | Pro | Ser | Val | Ser | Thr | Thr |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Thr | Ser | Ala | Ser | Ser | Ile | Thr | Ala | Cys | Arg | Pro | Arg | Arg | Arg | Ala |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Val | Ala | Pro | Ala | Ala | Ser | Leu | His | Leu | Gly | Pro | Gly | Glu | Ile | Ala | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Ala | Arg | Asn | Lys | Val | Xaa | Ile | Ala | Ala | Thr | Xaa | Ala | Ser | Ala | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Gln | Leu | Ser | Lys | Pro | Phe | Thr | Ser | Val | Lys | Asn | Gly | Gly | Val | Gly |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Ala | Gly | Leu | Asp | Leu | Arg | Thr | Val | Phe | Arg | Ser | Gly | Gly | Met | Pro | Ser |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Xaa | His | Ser | Ala | Ser | Val | Val | Ala | Val | Ala | Thr | Ser | Leu | Gly | Leu | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Arg | Gly | Phe | Xaa | Asp | Ser | Ile | Phe | Gly | Met | Ser | Xaa | Xaa | Phe | Xaa | Ala |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ile | Val | Met | Tyr | Asp | Ala | Gln | Gly | Val | Arg | Arg | Glu | Xaa | Gly | Asn | His |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ala | Lys | Ile | Leu | Asn | Arg | Phe | Trp | Ile | Leu | Lys | Glu | Lys | Val | Pro | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |

Glu Tyr Ser Glu Val Asp Met Ala Ala Pro Gly Phe Val Ser Val Thr  
210 215 220  
Glu Glu Ala Ser Ser Asn Ala Ser Pro Ser Leu Lys Arg Gly Ser Ser  
225 230 235 240  
Thr Glu Ser Pro Arg Val Asn Gly Leu Arg Gly Ser Glu Pro Glu Leu  
245 250 255  
Thr Glu Leu Lys Gln Ala Cys Val Glu Glu Asp Tyr Arg Leu Ser Glu  
260 265 270  
Ser Val Gly His Thr Glu Leu Gln Val Thr Val Gly Ala Leu Leu Gly  
275 280 285  
Phe Ala Val Ser Leu Ala Val Tyr Ala Thr Leu  
290 295

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..267
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

Met Ala Arg Pro Phe Ser Ser Pro His Ile Pro Ser Ser Ser Trp Val  
1 5 10 15  
Thr Arg Arg Pro Pro Pro Trp Thr Ser Ser Pro Ser Val Ser Thr Thr  
20 25 30  
Arg Thr Ser Ala Ser Ser Ile Thr Ala Cys Arg Pro Arg Arg Arg Ala  
35 40 45  
Val Ala Pro Ala Ala Ser Leu His Leu Gly Pro Gly Glu Ile Ala Glu  
50 55 60  
Leu Ala Arg Asn Lys Val Xaa Ile Ala Ala Thr Xaa Ala Ser Ala Ile  
65 70 75 80  
Gly Gln Leu Ser Lys Pro Phe Thr Ser Val Lys Asn Gly Gly Val Gly  
85 90 95  
Ala Gly Leu Asp Leu Arg Thr Val Phe Arg Ser Gly Gly Met Pro Ser  
100 105 110  
Xaa His Ser Ala Ser Val Val Ala Val Ala Thr Ser Leu Gly Leu Glu  
115 120 125  
Arg Gly Phe Xaa Asp Ser Ile Phe Gly Met Ser Xaa Xaa Phe Xaa Ala  
130 135 140  
Ile Val Met Tyr Asp Ala Gln Gly Val Arg Arg Glu Xaa Gly Asn His  
145 150 155 160  
Ala Lys Ile Leu Asn Arg Phe Trp Ile Leu Lys Glu Lys Val Pro Leu  
165 170 175  
Glu Tyr Ser Glu Val Asp Met Ala Ala Pro Gly Phe Val Ser Val Thr  
180 185 190  
Glu Glu Ala Ser Ser Asn Ala Ser Pro Ser Leu Lys Arg Gly Ser Ser  
195 200 205  
Thr Glu Ser Pro Arg Val Asn Gly Leu Arg Gly Ser Glu Pro Glu Leu  
210 215 220  
Thr Glu Leu Lys Gln Ala Cys Val Glu Glu Asp Tyr Arg Leu Ser Glu  
225 230 235 240  
Ser Val Gly His Thr Glu Leu Gln Val Thr Val Gly Ala Leu Leu Gly  
245 250 255  
Phe Ala Val Ser Leu Ala Val Tyr Ala Thr Leu  
260 265

(2) INFORMATION FOR SEQ ID NO:534:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 158 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..158  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1482401  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

Met Pro Ser Xaa His Ser Ala Ser Val Val Ala Val Ala Thr Ser Leu  
1                   5                   10                   15  
Gly Leu Glu Arg Gly Phe Xaa Asp Ser Ile Phe Gly Met Ser Xaa Xaa  
                  20                   25                   30  
Phe Xaa Ala Ile Val Met Tyr Asp Ala Gln Gly Val Arg Arg Glu Xaa  
                  35                   40                   45  
Gly Asn His Ala Lys Ile Leu Asn Arg Phe Trp Ile Leu Lys Glu Lys  
50                   55                   60  
Val Pro Leu Glu Tyr Ser Glu Val Asp Met Ala Ala Pro Gly Phe Val  
65                   70                   75                   80  
Ser Val Thr Glu Glu Ala Ser Ser Asn Ala Ser Pro Ser Leu Lys Arg  
                  85                   90                   95  
Gly Ser Ser Thr Glu Ser Pro Arg Val Asn Gly Leu Arg Gly Ser Glu  
                  100                   105                   110  
Pro Glu Leu Thr Glu Leu Lys Gln Ala Cys Val Glu Glu Asp Tyr Arg  
                  115                   120                   125  
Leu Ser Glu Ser Val Gly His Thr Glu Leu Gln Val Thr Val Gly Ala  
130                   135                   140  
Leu Leu Gly Phe Ala Val Ser Leu Ala Val Tyr Ala Thr Leu  
145                   150                   155

(2) INFORMATION FOR SEQ ID NO:535:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 524 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..524  
(D) OTHER INFORMATION: / Ceres Seq. ID 1482402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

ttccggctcc gctcagtcag gcctcagatc ggtcgaatcc agcaccacct ccagatttgc 60  
gtcaccaatc ttctttttct tccgcgcgcg ccgcgcgtcc cccacaagga ggtagctgc 120  
tatcccaaaa tcgattcatc aatcatccgt gtccttccat ttcattccag tcggtcgcgcg 180  
cagcacggac cgagaacaga gcatcacgtc acatcaaact aacctaacca gcctcgtccc 240  
tcgctgcgta tctgctgcac tttcatcaac accagtcttt ctctccttg attgcattgc 300  
ccaggcaaga gaacgcacgc acaccgaccg gaatagccat gatcttctga tccaatccaa 360  
gatgggcctc aaggagcagc agctagacgc cactgaccaa actcgtgatg ccgccaactc 420  
cctcgcttct gtttctgacg agcaccacga gggaccctgt gtctcaagct gcagcaccga 480  
caaggattct ggccttccaa gttgccgagt ctgccattgc gtgg

(2) INFORMATION FOR SEQ ID NO:536:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 174 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..174

(D) OTHER INFORMATION: / Ceres Seq. ID 1482403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Ser | Ala | Gln | Ser | Gly | Leu | Arg | Ser | Val | Glu | Ser | Ser | Thr | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Arg | Phe | Ala | Ser | Pro | Ile | Phe | Phe | Phe | Arg | Arg | Arg | Arg | Arg | Arg |
|     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Ser | Pro | Thr | Arg | Arg | Leu | Ala | Ala | Ile | Pro | Lys | Ser | Ile | His | Gln | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ser | Val | Ser | Phe | His | Phe | Ile | Pro | Val | Gly | Arg | Arg | Ser | Thr | Asp | Arg |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Glu | Gln | Ser | Ile | Thr | Ser | His | Gln | Thr | Asn | Leu | Thr | Ser | Leu | Val | Pro |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Cys | Val | Ser | Ala | Leu | Ser | Ser | Thr | Pro | Val | Phe | Leu | Leu | Leu |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |     |
| Asp | Cys | Ile | Ala | Gln | Ala | Arg | Glu | Arg | Thr | His | Thr | Asp | Arg | Asn | Ser |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| His | Asp | Leu | Leu | Ile | Gln | Ser | Lys | Met | Gly | Leu | Lys | Glu | Gln | Gln | Leu |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Asp | Ala | Thr | Asp | Gln | Thr | Arg | Asp | Ala | Ala | Asn | Ser | Leu | Ala | Ser | Val |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Ser | Asp | Glu | His | His | Glu | Gly | Pro | Arg | Val | Ser | Ser | Cys | Ser | Thr | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Asp | Ser | Gly | Leu | Pro | Ser | Cys | Arg | Val | Cys | His | Cys | Val |     |     |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 451 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..451

(D) OTHER INFORMATION: / Ceres Seq. ID 1482404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gtggacgact | ggcgcggtgg | tgatacgctt | gttactctcc | caggtcgccc | gtcgagtcga | 60  |
| gcttctgcgt | ggagtcgctt | ctgcctctgc | acaccgccac | cgccggtgca | cgcatgacgt | 120 |
| ccatgctcgc | cgctcctggc | caaggcctcg | gctggctcac | ccaaggatct | gatgaaacta | 180 |
| gatgaagagc | agccggggaa | agctgaaact | gacggagtat | aacgccccct | gcgggtactt | 240 |
| taggaaccag | gacatcaatt | gtgcttcgag | ttcttgtgtg | cctggaggaa | acaggaagag | 300 |
| ttgattggaa | aaagaaaaaa | tgggatgtgt | ttttcttttt | gttcatgtga | actgagatac | 360 |
| gacttaataa | actagatctt | cgaatgatgc | tctgaccccc | ccccccccct | tttgtaaatg | 420 |
| ctttttcatt | gactaaaacg | gttatgtaat | g          |            |            |     |

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..38

(D) OTHER INFORMATION: / Ceres Seq. ID 1482405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

Val Asp Asp Trp Arg Gly Gly Asp Thr Leu Val Thr Leu Pro Gly Arg  
1 5 10 15  
Pro Ser Ser Arg Ala Ser Ala Trp Ser Arg Phe Cys Leu Cys Thr Pro  
20 25 30  
Pro Pro Pro Val His Ala  
35

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

Trp Thr Thr Gly Ala Val Val Ile Arg Leu Leu Leu Ser Gln Val Ala  
1 5 10 15  
Arg Arg Val Glu Leu Leu Arg Gly Val Ala Ser Ala Ser Ala His Arg  
20 25 30  
His Arg Arg Cys Thr His Asp Val His Ala Arg Arg Ser Trp Pro Arg  
35 40 45  
Pro Arg Leu Ala His Pro Arg Ile  
50 55

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..40
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

Met Lys Ser Ser Arg Gly Lys Leu Lys Leu Thr Glu Tyr Asn Ala Pro  
1 5 10 15  
Cys Gly Tyr Phe Arg Asn Gln Asp Ile Asn Cys Ala Ser Ser Ser Cys  
20 25 30  
Val Pro Gly Gly Asn Arg Lys Ser  
35 40

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..553
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

aaagacgaag gtaatttgat cagcaccggg agacgagacg agagagagag aacgggggaa 60  
acaacaccgc cgccaggagt gtccaccggg gggaaatgat ggcgggagca ttgccaaggt 120  
ctcgccgtgc ttctccggct gcaggatggg tccgccgtgg agcatggaca gcctcgtaag 180



|            |             |            |             |             |            |     |
|------------|-------------|------------|-------------|-------------|------------|-----|
| tgccttcac  | gccgggttaga | aattctcttt | agagttcgta  | catgtattag  | cttcatacca | 240 |
| caccgtgtga | gggggaaagg  | caccatcacg | ccccgcgtgt  | ngttggtcgg  | caatggcacc | 300 |
| gctacctgcg | ctgccggcta  | gctatacccg | aggaagaaga  | atagtgccag  | ccaatgatct | 360 |
| agaaaaagag | ggcccggatt  | agagactagg | tgaccgcttt  | ggctcgggtca | agctggaccg | 420 |
| ttgattttct | gttaaaccgt  | catgtgtgca | tacctgtgcg  | caatagaatg  | tgagccattg | 480 |
| atctgtgac  | cgaggatcta  | cagatcatat | cgtttgggtga | ccctggagat  | ctaatatgtg | 540 |
| ccatccgtgc | gtg         |            |             |             |            |     |

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asp | Glu | Gly | Asn | Leu | Ile | Ser | Thr | Gly | Arg | Arg | Asp | Glu | Arg | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Arg | Thr | Gly | Glu | Thr | Thr | Pro | Pro | Pro | Gly | Val | Phe | Thr | Gly | Gly | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Ala | Tyr | Leu | Cys | Ala | Ile | Glu | Cys | Glu | Pro | Leu | Ile | Cys | Asp |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Pro | Arg | Ile | Tyr | Arg | Ser | Tyr | Arg | Leu | Val | Thr | Leu | Glu | Ile |     |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..809
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| aagtgcatta | attagtgcc  | actgcagtag | ctactagcta  | gcacagttca | tcgacctcgc | 60  |
| tcgtggcccg | caagcaatcg | ctcaagctaa | gccatggcgc  | ctcgcagccg | cctcctcgac | 120 |
| ctggagaggc | acgacgtgct | cttcttctac | ggcgatgggtg | cctaccacca | gagcgagagc | 180 |
| kncgtcgtcc | ttgtcgtcgt | cgtcgccgcc | ctgctcctcc  | tcctcgtcgc | gccgctccc  | 240 |
| cacgccgctg | ccgtctgcgg | ggcgctctac | gtcgcctact  | gcttcctcct | cgaccgcgca | 300 |
| gcraagngcg | agcagctcca | gctcgtcgtg | tccttcact   | gacactgccg | cgccgccggc | 360 |

```
ggcagacgcc tctcgcccca ctactcgggg cacggtggca ggctatatga tcgtgcagaa 420
gcagaattga agtcgcaatg gtcagcatgc ttatattacc agttaccatg cttaattgca 480
tagttgcact gtagtgatca ccgcaggaag atggctctgt gtggaataga gtagtaggct 540
taagcacatt tcgtattaca ggaaaagagt ttgtgggtcag aggtcttccc acgtatatag 600
ctgtctcttg agactctgca tggactctgc aatckggata tgcatgcact ataatcactt 660
cgaaataggg ccacagttga caaatcagcc aggaaacata tgtaatctgg attcttttca 720
aaaaaaaaatt gtaatacggc tactcttctc aggaatatat atgaatggac tgcacggttt 780
tctttcagtc tgttgcctgt tcttcagcc
```

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

```
Met Ala Pro Arg Ser Arg Leu Leu Asp Leu Glu Arg His Asp Val Leu
1 5 10 15
Phe Phe Tyr Gly Asp Gly Ala Tyr His Gln Ser Glu Ser Xaa Val Val
 20 25 30
Leu Val Val Val Val Ala Ala Leu Leu Leu Leu Val Ala Pro Leu
 35 40 45
Pro His Ala Ala Ala Val Cys Gly Ala Leu Tyr Val Ala Tyr Cys Phe
 50 55 60
Leu Leu Asp Arg Ala Xaa Lys Xaa Glu Gln Leu Gln Leu Val Val Ser
65 70 75 80
Phe His
```

(2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

```
Met Val Pro Thr Thr Arg Ala Arg Xaa Xaa Ser Ser Leu Ser Ser Ser
1 5 10 15
Ser Pro Pro Cys Ser Ser Ser Ser Ser Arg Arg Ser Arg Thr Pro Leu
 20 25 30
Pro Ser Ala Gly Arg Ser Thr Ser Pro Thr Ala Ser Ser Thr Ala
 35 40 45
Gln Xaa Xaa Ala Ser Ser Ser Ser Ser Cys Pro Ser Thr Asp Thr
 50 55 60
Ala Ala Pro Pro Ala Ala Asp Ala Ser Arg Pro Thr Thr Arg Gly Thr
65 70 75 80
Val Ala Gly Tyr Met Ile Val Gln Lys Gln Asn
 85 90
```

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..63  
(D) OTHER INFORMATION: / Ceres Seq. ID 1482414  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:  
Met Asp Ser Ala Ile Xaa Ile Cys Met His Tyr Asn His Phe Glu Ile  
1 5 10 15  
Gly Pro Gln Leu Thr Asn Gln Pro Gly Asn Ile Cys Asn Leu Asp Ser  
20 25 30  
Phe Gln Lys Lys Ile Val Ile Arg Leu Leu Phe Ser Gly Ile Tyr Met  
35 40 45  
Asn Gly Leu His Gly Phe Leu Ser Val Cys Cys Leu Phe Phe Ser  
50 55 60

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 871 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..871  
(D) OTHER INFORMATION: / Ceres Seq. ID 1482415

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

atatatacgc acacgcggtg ggagtrggag ggggagactc tgccctgacc acagcaaaca 60  
acctctcttt tcctttccat ccatcggacc atcgatcaca attttcatgg cggtaagga 120  
ctgcr gcggg cacaagggt gcgagtgcga gcgggagcgr ctgtaccggc ggtgctgcgc 180  
ggcggtcgtg gctctgatcc tcctggctct cttcatcgtg ctcgtcgtgt ggtggtgct 240  
gcgccccac aagccccggt tctacctgca ggacctgtcg gtgctgtgcc tgaacgtgac 300  
gccgccggt ccacgtacct gttcacgacg atgcaggcga cgggtggcgg gcgcaaccgc 360  
aacgagcgcg tgggcgtgta ctacgaccag gcggacgcgt acgcggaggt acaagggcgt 420  
ggcgatcacg gtgccgacgc ggctgcccgt gcagtaccag gggccccggg acgcgtccgt 480  
gtggtccccg ttcctgcgcg ccccggaagg cggcgtgcag ytcccgcgc agctggccgt 540  
ggcstggcgc aggacgagac ggcgggctac gtgcntstcg acgtccgcgt cgacggctgg 600  
gtccgctgga aggtcggtac cagctggatc tggggtcact accacctccg cgtcaactgc 660  
cncgcgctgc tcaccgtcaa cgacggcagg ggcagctacg gcgccaacac cggcggcggc 720  
accggatact tccgcttcca gcaggcagsg catgcgccgt agacgtctag cagtgtcttc 780  
tctctctctg taccagctag ctgtgtttgc caattcgtcg atcgaatcaa aggacgatgc 840  
ttccttcgtc ggtgttcac actcacgcac t

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..290  
(D) OTHER INFORMATION: / Ceres Seq. ID 1482416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

Tyr Ile Arg Thr Arg Gly Gly Ser Xaa Arg Gly Arg Leu Cys Pro Asp  
1 5 10 15  
His Ser Lys Gln Pro Pro Leu Ser Phe Pro Ser Ile Gly Pro Ser Ile

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 20                                                              | 25  | 30  |
| Thr Ile Phe Met Ala Val Lys Asp Cys Xaa Gly His Lys Gly Cys Glu |     |     |
| 35                                                              | 40  | 45  |
| Cys Glu Arg Glu Xaa Leu Tyr Arg Arg Cys Cys Ala Ala Val Val Ala |     |     |
| 50                                                              | 55  | 60  |
| Leu Ile Leu Leu Val Leu Phe Ile Val Leu Val Trp Leu Val Leu     |     |     |
| 65                                                              | 70  | 75  |
| Arg Pro His Lys Pro Arg Phe Tyr Leu Gln Asp Leu Ser Val Leu Cys |     |     |
| 85                                                              | 90  | 95  |
| Leu Asn Val Thr Pro Pro Xaa Pro Arg Thr Cys Ser Arg Arg Cys Arg |     |     |
| 100                                                             | 105 | 110 |
| Arg Arg Trp Arg Arg Ala Thr Arg Thr Ser Ala Trp Ala Cys Thr Thr |     |     |
| 115                                                             | 120 | 125 |
| Thr Arg Arg Thr Arg Thr Arg Arg Tyr Lys Gly Val Ala Ile Thr Val |     |     |
| 130                                                             | 135 | 140 |
| Pro Thr Arg Leu Pro Val Gln Tyr Gln Gly Pro Arg Asp Ala Ser Val |     |     |
| 145                                                             | 150 | 155 |
| Trp Ser Pro Phe Leu Arg Ala Pro Glu Gly Gly Val Gln Xaa Pro Pro |     |     |
| 165                                                             | 170 | 175 |
| Gln Leu Ala Val Xaa Trp Arg Arg Thr Arg Arg Arg Ala Thr Cys Xaa |     |     |
| 180                                                             | 185 | 190 |
| Ser Thr Ser Ala Ser Thr Ala Gly Ser Ala Gly Arg Ser Val Pro Ala |     |     |
| 195                                                             | 200 | 205 |
| Gly Ser Arg Val Thr Thr Thr Ser Ala Ser Thr Ala Xaa Arg Cys Ser |     |     |
| 210                                                             | 215 | 220 |
| Pro Ser Thr Thr Ala Gly Ala Ala Thr Ala Pro Thr Pro Ala Ala Ala |     |     |
| 225                                                             | 230 | 235 |
| Pro Asp Thr Ser Ala Ser Ser Arg Gln Xaa Met Arg Arg Arg Arg Leu |     |     |
| 245                                                             | 250 | 255 |
| Ala Val Leu Ser Leu Ser Leu Tyr Gln Leu Ala Val Phe Ala Asn Ser |     |     |
| 260                                                             | 265 | 270 |
| Ser Ile Glu Ser Lys Asp Asp Ala Ser Phe Val Gly Val His His Ser |     |     |
| 275                                                             | 280 | 285 |
| Arg Thr                                                         |     |     |
| 290                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..255
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| Met Ala Val Lys Asp Cys Xaa Gly His Lys Gly Cys Glu Cys Glu Arg |    |    |
| 1                                                               | 5  | 10 |
| Glu Xaa Leu Tyr Arg Arg Cys Cys Ala Val Val Ala Leu Ile Leu     |    |    |
| 20                                                              | 25 | 30 |
| Leu Val Leu Phe Ile Val Leu Val Val Trp Leu Val Leu Arg Pro His |    |    |
| 35                                                              | 40 | 45 |
| Lys Pro Arg Phe Tyr Leu Gln Asp Leu Ser Val Leu Cys Leu Asn Val |    |    |
| 50                                                              | 55 | 60 |
| Thr Pro Pro Xaa Pro Arg Thr Cys Ser Arg Arg Cys Arg Arg Arg Trp |    |    |
| 65                                                              | 70 | 75 |
| Arg Arg Ala Thr Arg Thr Ser Ala Trp Ala Cys Thr Thr Thr Arg Arg |    |    |
| 85                                                              | 90 | 95 |

Thr Arg Thr Arg Arg Tyr Lys Gly Val Ala Ile Thr Val Pro Thr Arg  
100 105 110  
Leu Pro Val Gln Tyr Gln Gly Pro Arg Asp Ala Ser Val Trp Ser Pro  
115 120 125  
Phe Leu Arg Ala Pro Glu Gly Gly Val Gln Xaa Pro Pro Gln Leu Ala  
130 135 140  
Val Xaa Trp Arg Arg Thr Arg Arg Arg Ala Thr Cys Xaa Ser Thr Ser  
145 150 155 160  
Ala Ser Thr Ala Gly Ser Ala Gly Arg Ser Val Pro Ala Gly Ser Arg  
165 170 175  
Val Thr Thr Thr Ser Ala Ser Thr Ala Xaa Arg Cys Ser Pro Ser Thr  
180 185 190  
Thr Ala Gly Ala Ala Thr Ala Pro Thr Pro Ala Ala Ala Pro Asp Thr  
195 200 205  
Ser Ala Ser Ser Arg Gln Xaa Met Arg Arg Arg Arg Leu Ala Val Leu  
210 215 220  
Ser Leu Ser Leu Tyr Gln Leu Ala Val Phe Ala Asn Ser Ser Ile Glu  
225 230 235 240  
Ser Lys Asp Asp Ala Ser Phe Val Gly Val His His Ser Arg Thr  
245 250 255

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..725
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| aggaacttgt aacctggctc gcagcggtgc gtgaaggacc tcgcgcgcgc tctcctctac   | 60  |
| tgtcttggtcg tctcggttgcc ccggccgaac atccaagcct ctccatgtct ggcccttcga | 120 |
| aggagcagcg cgnccatgccg gcaactgggt gctggctaata ggctgtcggc accttcgct  | 180 |
| tggccttcac ctggtcgtgc ttcttcggct ccgggttgct ctgctcagcc acctactccg   | 240 |
| agatacaggt gatcggcgtg catgggcgca cgggttcgggt gtggacgctg ctgtcgtgca  | 300 |
| ccctctgctt cctgtgcgcc ttcaacctca ccagcanagc cgctgtacgc ggccaccttc   | 360 |
| ctgtccttcg tctacgcctt cgggtacctg agcaccgagt gcatgggtgta ccacaccatg  | 420 |
| agtgcagcta gtctcgctccc gttcaccttc atcgctgtca catccatggt ctggatgctg  | 480 |
| attcaatgga actcggatgg tcacggcccc cgtcttcttc atgggtctac tgcctccaag   | 540 |
| cagccatgac ttcgcaggtt ctctcaccta tggcttcctt caactacata cggttcagtg   | 600 |
| catgcaagca ccatggaatt atggaatatc tgtaatactt tgtaataatc gtttctatgt   | 660 |
| ccgcaggtc agtgaatgaa actagcaagc tatcatctgt gataaatttg taattttacc    | 720 |
| actct                                                               |     |

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

Glu Leu Val Thr Trp Leu Ala Ala Leu Arg Glu Gly Pro Arg Ala Arg  
1 5 10 15

Ser Pro Leu Leu Leu Gly Arg Leu Val Ala Pro Ala Glu His Pro Ser  
20 25 30  
Leu Ser Met Ser Gly Pro Ser Lys Glu Gln Arg Xaa Met Pro Ala Leu  
35 40 45  
Gly Cys Trp Leu Met Ala Val Gly Thr Phe Arg Leu Ala Phe Thr Trp  
50 55 60  
Ser Cys Phe Phe Gly Ser Gly Xaa Leu Cys Ser Ala Thr Tyr Ser Glu  
65 70 75 80  
Ile Gln Val Ile Gly Val His Gly Arg Thr Val Ala Val Trp Thr Leu  
85 90 95  
Leu Ser Cys Thr Leu Cys Phe Leu Cys Ala Phe Asn Leu Thr Ser Xaa  
100 105 110  
Ala Ala Val Arg Gly His Leu Pro Val Leu Arg Leu Arg Leu Arg Val  
115 120 125  
Pro Glu His Arg Val His Gly Val Pro His His Glu Cys Ser  
130 135 140

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

Met Ser Gly Pro Ser Lys Glu Gln Arg Xaa Met Pro Ala Leu Gly Cys  
1 5 10 15  
Trp Leu Met Ala Val Gly Thr Phe Arg Leu Ala Phe Thr Trp Ser Cys  
20 25 30  
Phe Phe Gly Ser Gly Xaa Leu Cys Ser Ala Thr Tyr Ser Glu Ile Gln  
35 40 45  
Val Ile Gly Val His Gly Arg Thr Val Ala Val Trp Thr Leu Leu Ser  
50 55 60  
Cys Thr Leu Cys Phe Leu Cys Ala Phe Asn Leu Thr Ser Xaa Ala Ala  
65 70 75 80  
Val Arg Gly His Leu Pro Val Leu Arg Leu Arg Leu Arg Val Pro Glu  
85 90 95  
His Arg Val His Gly Val Pro His His Glu Cys Ser  
100 105

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

Met Pro Ala Leu Gly Cys Trp Leu Met Ala Val Gly Thr Phe Arg Leu  
1 5 10 15  
Ala Phe Thr Trp Ser Cys Phe Phe Gly Ser Gly Xaa Leu Cys Ser Ala  
20 25 30  
Thr Tyr Ser Glu Ile Gln Val Ile Gly Val His Gly Arg Thr Val Ala

(2) INFORMATION FOR SEQ ID NO:555:

(A) LENGTH: 119 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- ```
(A) NAME/KEY: -
(B) LOCATION: 1..119
(D) OTHER INFORMATION: / Ceres Seq. ID 1482422
```

(X1) SEQUENCE DESCRIPTION: SEQ ID NUMBER:
aaccgcaagc tcaagcaaaa acacaaagcg cttaaaccac actcaaacca accgccagcc
aacaacacagg cctcctagtc ccgaccagaa ctgcgtcgta gccccgagaa cccgacagc

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..39
(D) OTHER INFORMATION: / Ceres Seq. ID 1482423

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..297
(D) OTHER INFORMATION: / Ceres Seq. ID 1482424

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO:10334 | | | | | | |
|--|------------|------------|------------|------------|------------|-----|
| attttttgcc | cgcgcccc | agtcgcgac | cgaagctgtg | cctcgtagca | tttcgatcca | 60 |
| atggcgccga | cgtcgaagct | gtcgacgggc | atcaagcgcg | cttcgcggtc | gcacgcgtac | 120 |
| catcgccgtg | ggctgtgggc | catgatgaac | ttgagcgcaa | gaagagtata | ccgcttgtag | 180 |
| ttactctgta | acgtacgcag | gcagagagcg | cgcgttcacg | cgtatacgtg | cacgtagacg | 240 |
| tagtacgtac | atgtactacc | cgttacttgc | tctccaatcg | agttgcagtt | gcagccc | |

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..59
 (D) OTHER INFORMATION: / Ceres Seq. ID 1482425
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:
Ile Phe Arg Pro Pro Pro Pro Val Pro Ile Arg Ser Cys Ala Ser Tyr
1 5 10 15
His Phe Asp Pro Met Ala Pro Thr Ser Lys Leu Ser Thr Gly Ile Lys
 20 25 30
Arg Ala Ser Arg Ser His Ala Tyr His Arg Arg Gly Leu Trp Ala Met
 35 40 45
Met Asn Leu Ser Ala Arg Arg Val Tyr Arg Leu
50 55

(2) INFORMATION FOR SEQ ID NO:559:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 47 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..47
 (D) OTHER INFORMATION: / Ceres Seq. ID 1482426
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:
Phe Phe Ala Arg Arg Pro Gln Ser Arg Ser Glu Ala Val Pro Arg Thr
1 5 10 15
Ile Ser Ile Gln Trp Arg Arg Arg Arg Ser Cys Arg Arg Ala Ser Ser
 20 25 30
Ala Leu Arg Gly Arg Thr Arg Thr Ile Ala Val Gly Cys Gly Pro
 35 40 45

(2) INFORMATION FOR SEQ ID NO:560:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..62
 (D) OTHER INFORMATION: / Ceres Seq. ID 1482427
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:
Phe Ser Pro Ala Ala Pro Ser Pro Asp Pro Lys Leu Cys Leu Val Pro
1 5 10 15
Phe Arg Ser Asn Gly Ala Asp Val Glu Ala Val Asp Gly His Gln Ala
 20 25 30
Arg Phe Ala Val Ala Arg Val Pro Ser Pro Trp Ala Val Gly His Asp
 35 40 45
Glu Leu Glu Arg Lys Lys Ser Ile Pro Leu Val Val Thr Leu
50 55 60

(2) INFORMATION FOR SEQ ID NO:561:
 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..606
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

| | |
|--|-----|
| gtctcacaaa ctttttttta gtctatcggt aaccgcgttc agctagcgag cattgagcag | 60 |
| tctgcagtcg ccgagccgcg tgtccgcccg gccggcggtt accaagctca ccaaaaatct | 120 |
| ttccagggttc gaggcgccc atgttcgcct gcaggtctct cctcgcaagg gatcatattg | 180 |
| tcgaaataag ttggcctcat tcgtgatgga aggggcgcaa ggatcaagca ttgtgacaaa | 240 |
| acacaataaa aggcagtctc ctgtgcagag atggaggcca gtttcaacag aagcagttcc | 300 |
| ccagcatcac caagatgaca ttattgagac atcaaattct ggaagcaaga aaattataga | 360 |
| ggattgcata gcttctagtg agaatttgcc accagatgga acaaccaatg ttgttgaagt | 420 |
| taccgccaat gatgcttcat cgtcaaaaaa taattttaagt tttgggtaca gttcaactaa | 480 |
| agtagttata gaagaccatg cggagttatc tggcttcaat aaggatctag ctgggtccaa | 540 |
| tgtcttcggg acacattcct yctctgttga ggcggtkcaa agtcgacagc ttgactactc | 600 |
| tcattt | |

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..133
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gly | Ala | Gln | Gly | Ser | Ser | Ile | Val | Thr | Lys | His | Asn | Lys | Arg |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gln | Ser | Pro | Val | Gln | Arg | Trp | Arg | Pro | Val | Ser | Thr | Glu | Ala | Val | Pro |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Gln | His | His | Gln | Asp | Asp | Ile | Ile | Glu | Thr | Ser | Asn | Ser | Gly | Ser | Lys |
| | | | 35 | | | | 40 | | | | 45 | | | | |
| Lys | Ile | Ile | Glu | Asp | Cys | Ile | Ala | Ser | Ser | Glu | Asn | Leu | Pro | Pro | Asp |
| | 50 | | | | | 55 | | | | 60 | | | | | |
| Gly | Thr | Thr | Asn | Val | Val | Glu | Val | Thr | Ala | Asn | Asp | Ala | Ser | Ser | Ser |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Lys | Asn | Asn | Leu | Ser | Phe | Gly | Tyr | Ser | Ser | Thr | Lys | Val | Val | Ile | Glu |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Asp | His | Ala | Glu | Leu | Ser | Gly | Phe | Asn | Lys | Asp | Leu | Ala | Gly | Ser | Asn |
| | | 100 | | | | | | 105 | | | | 110 | | | |
| Val | Phe | Gly | Thr | His | Ser | Xaa | Ser | Val | Glu | Ala | Xaa | Gln | Ser | Arg | Gln |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Leu | Asp | Tyr | Ser | His | | | | | | | | | | | |
| | 130 | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..451

(D) OTHER INFORMATION: / Ceres Seq. ID 1482430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| gaaaacggcg | atgttggccg | tcccattttg | taagctcccc | ttccccgtct | ggcgcgtctcg | 60 |
| actgccccag | tcctttctca | gatccatgtc | taccagaat | ctgctaactg | gcgcgtgcac | 120 |
| gagctccgcc | ccgaccccg | ccgagggcga | ggaaggggac | aggacgcctt | tggctgacgc | 180 |
| tgcgaacgcg | gcggaagagc | tgtaccgcct | ccgtgacacc | tttttccgcg | gggacccttc | 240 |
| cgagaaagtc | gccgcactcc | gcgcccgcgc | cgacgccgcc | ctcgcgctcc | tcgacgcctt | 300 |
| cccgtccgaa | caaaagaagt | ctcgacaact | gcgtggtgtt | tatgaatttt | tgaggggaaa | 360 |
| aatactggat | gtctttcctg | attatcataa | ggaggctgaa | gatcatttat | ccaaagcagt | 420 |
| aaagttgaac | ccatctcttg | tagatgcatg | g | | | |

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1482431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Thr | Ala | Met | Leu | Ala | Val | Pro | Phe | Cys | Lys | Leu | Pro | Phe | Pro | Val |
| 1 | | | 5 | | | | | | 10 | | | | | 15 | |
| Trp | Pro | Ser | Arg | Leu | Pro | Gln | Ser | Phe | Leu | Arg | Ser | Met | Ser | Thr | Gln |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Asn | Leu | Leu | Thr | Gly | Ala | Cys | Thr | Ser | Ser | Ala | Pro | Thr | Pro | Ser | Glu |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Ala | Glu | Glu | Gly | Asp | Arg | Thr | Pro | Leu | Ala | Asp | Ala | Ala | Asn | Ala | Ala |
| | | | 50 | | | 55 | | | | 60 | | | | | |
| Glu | Glu | Leu | Tyr | Arg | Leu | Arg | Asp | Thr | Phe | Phe | Pro | Arg | Asp | Pro | Ser |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Glu | Lys | Val | Ala | Ala | Leu | Arg | Ala | Arg | Ala | Asp | Ala | Ala | Leu | Ala | Leu |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Leu | Asp | Ala | Phe | Pro | Ser | Glu | Gln | Lys | Lys | Ser | Arg | Gln | Leu | Arg | Gly |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Val | Tyr | Glu | Phe | Leu | Arg | Gly | Lys | Ile | Leu | Asp | Val | Phe | Pro | Asp | Tyr |
| | | | 115 | | | | 120 | | | | | 125 | | | |
| His | Lys | Glu | Ala | Glu | Asp | His | Leu | Ser | Lys | Ala | Val | Lys | Leu | Asn | Pro |
| | | | 130 | | | | 135 | | | | | 140 | | | |
| Ser | Leu | Val | Asp | Ala | Trp | | | | | | | | | | |
| 145 | | | | | 150 | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1482432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ala | Val | Pro | Phe | Cys | Lys | Leu | Pro | Phe | Pro | Val | Trp | Pro | Ser |
| 1 | | | 5 | | | | | 10 | | | | | 15 | | |
| Arg | Leu | Pro | Gln | Ser | Phe | Leu | Arg | Ser | Met | Ser | Thr | Gln | Asn | Leu | Leu |

(2) INFORMATION FOR SEQ ID NO:566:

(A) LENGTH: 122 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1482433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Thr | Gln | Asn | Leu | Leu | Thr | Gly | Ala | Cys | Thr | Ser | Ser | Ala | Pro |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Thr | Pro | Ser | Glu | Ala | Glu | Glu | Gly | Asp | Arg | Thr | Pro | Leu | Ala | Asp | Ala |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ala | Asn | Ala | Ala | Glu | Glu | Leu | Tyr | Arg | Leu | Arg | Asp | Thr | Phe | Phe | Pro |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Arg | Asp | Pro | Ser | Glu | Lys | Val | Ala | Ala | Leu | Arg | Ala | Arg | Ala | Asp | Ala |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ala | Leu | Ala | Leu | Leu | Asp | Ala | Phe | Pro | Ser | Glu | Gln | Lys | Lys | Ser | Arg |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Gln | Leu | Arg | Gly | Val | Tyr | Glu | Phe | Leu | Arg | Gly | Lys | Ile | Leu | Asp | Val |
| | | | | 85 | | | | | | 90 | | | | 95 | |
| Phe | Pro | Asp | Tyr | His | Lys | Glu | Ala | Glu | Asp | His | Leu | Ser | Lys | Ala | Val |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Lys | Leu | Asn | Pro | Ser | Leu | Val | Asp | Ala | Trp | | | | | | |
| | | 115 | | | | | 120 | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:567:

(A) LENGTH: 463 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..463

(D) OTHER INFORMATION: / Ceres Seq. ID 1482434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| ataccgggat | gggcgccatg | ggcatcgctg | tcagagcgtg | ggcgccctcc | gctcttgccg | 60 |
| ccgcggccgc | gccggcacc | tccggctcca | gggacaccgg | tcaggccccag | cggaggagca | 120 |

agccctcgag gaccggccgc gtgcgcgtgc tcggcgccac tggccgtgtc ggaggatcca 180
cgccaccgc actctccaaa ctccgcccc aacttggcat cctcgtcggg ggcaggaacc 240
gggagaaagg cgagtccatt gcagccaagc ttggggggcca gtctgagttc gtccaggctg 300
acaccgcgaa cacaggcatg ttggaggaag cgctgcaggt ggtagctgtt cgcggagttg 360
ccaaaccgga ggcagctgcg acgcccgcga ggcgctcgcg ccccatccct ctggcttccg 420
tggccgtgtg gagtctggtt gccactggcg ccgcaaattgc tgc

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1482435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

Thr Gly Met Gly Ala Met Gly Ile Val Val Arg Ala Trp Ala Pro Pro
1 5 10 15
Ala Leu Ala Ala Ala Ala Pro Ala Pro Ser Gly Ser Arg Asp Thr
20 25 30
Gly Gln Ala Gln Arg Arg Ser Lys Pro Ser Arg Thr Gly Arg Val Arg
35 40 45
Val Leu Gly Gly Thr Gly Arg Val Gly Gly Ser Thr Ala Thr Ala Leu
50 55 60
Ser Lys Leu Arg Pro Lys Leu Gly Ile Leu Val Gly Gly Arg Asn Arg
65 70 75 80
Glu Lys Gly Glu Ser Ile Ala Ala Lys Leu Gly Gly Gln Ser Glu Phe
85 90 95
Val Gln Val Asp Thr Arg Asn Thr Gly Met Leu Glu Glu Ala Leu Gln
100 105 110
Val Val Ala Val Arg Gly Val Ala Lys Pro Glu Ala Ala Thr Pro
115 120 125
Ala Arg Arg Ser Arg Pro Ile Pro Leu Ala Ser Val Ala Val Trp Ser
130 135 140
Leu Val Ala Thr Gly Ala Ala Asn Ala
145 150

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1482436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

Met Gly Ala Met Gly Ile Val Val Arg Ala Trp Ala Pro Pro Ala Leu
1 5 10 15
Ala Ala Ala Ala Ala Pro Ala Pro Ser Gly Ser Arg Asp Thr Gly Gln
20 25 30
Ala Gln Arg Arg Ser Lys Pro Ser Arg Thr Gly Arg Val Arg Val Leu
35 40 45
Gly Gly Thr Gly Arg Val Gly Gly Ser Thr Ala Thr Ala Leu Ser Lys
50 55 60
Leu Arg Pro Lys Leu Gly Ile Leu Val Gly Gly Arg Asn Arg Glu Lys

(2) INFORMATION FOR SEQ ID NO:570:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:570:

Gly Ile Val Val Arg Ala Trp Ala Pro Pro A

(2) INFORMATION FOR SEQ ID NO:571:

(A) LENGTH: 511 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..511

(D) OTHER INFORMATION: / Ceres Seq. ID 1482438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| aaacgacgcc | gagggtttct | aacaacgtaa | aaagaagaag | gaaagaacag | catttggtct | 60 |
| cgtcctgtacg | tacaggggaa | aggacaaaag | gcttcggggc | gtggcggccg | cgctggtcga | 120 |
| cgatcgttca | gagcgcgggg | agggagaaga | ggtcgymgyc | kscsatgtmt | sykrarcsgc | 180 |
| agccgtcgac | tcctggccac | atcgggaggc | tgccgaggtc | gagcgcgggg | tcsgcggcsa | 240 |

```
ggtagtcgag gccgagctgc ggmgtgggca agtcgtcgtc gaacgggacg ccgccgtaaa 300
gagaacgcgt cctcgccgag ctggggcagg agcgcgtcat cggcggaraa cgggkwkagg 360
ccgccsgggc cgtcgggcgc ktctttcttg gtcgcacaac cggmggcggm gtycgyykat 420
tttyggcggc agartckcac gcgccgtctc gtcgggcatt gcccgaggga cggagaccgg 480
cgagccnacc accakctggg actcgtcgca g
```

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

```
Thr Thr Pro Arg Val Ser Asn Asn Val Lys Arg Arg Arg Lys Glu Gln
1          5          10          15
His Leu Ala Pro Ser Val Arg Thr Gly Glu Arg Thr Lys Gly Phe Gly
          20          25          30
Arg Trp Arg Pro Arg Trp Ser Thr Ile Val Gln Ser Ala Gly Arg Glu
          35          40          45
Lys Arg Ser Xaa Xaa Xaa Met Xaa Xaa Xaa Xaa Gln Pro Ser Thr Pro
          50          55          60
Gly His Ile Gly Arg Leu Pro Arg Ser Ser Ala Gly Xaa Ala Xaa Arg
65          70          75          80
```

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 613 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..613
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

```
mrgtsccaag aatgtttctca cgaagctgat taaatcattg aaccttagat taactgctgt 60
gcaactaatt gattcccacg tatgttgtag tcccgggaac tacgtaagtt cgctacttct 120
ctccttatcc acaatgcttc acatggaact cccacatgtc aatatattgt ctaaaatcga 180
tctgattgga agctacggga agctagcttt caatttagat ttctataaccg atgttcaaga 240
cttgtcatac ttggagcacc atcttagtca agatcctcgc tctgctaagt acagaaaact 300
aacaaaagag ctatgtagtg tcattgaaga ttacagtctt gttaatttta caaccttgga 360
tattcaggat aaagaaagtg ttgggggatct agtaaagctc atcgacaaga gcaatggata 420
catatttgcc ggcattgatg caagtgtggt tgaatacagc aagattgcaa ttggtcaaac 480
tgattgggat tataacagag tcgcagctgt acaggagaag tacatggaag atgaggaaat 540
acaagactga gaacagtgtc tgaaacttta tatagaagag agctggtcta aaatatctct 600
gaaccaaacc att
```

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..182

(D) OTHER INFORMATION: / Ceres Seq. ID 1482445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

Xaa Xaa Lys Asn Val Leu Thr Lys Leu Ile Lys Ser Leu Asn Leu Arg
1 5 10 15
Leu Thr Ala Val Gln Leu Ile Asp Ser His Leu Cys Cys Asp Pro Gly
20 25 30
Asn Tyr Val Ser Ser Leu Leu Leu Ser Leu Ser Thr Met Leu His Met
35 40 45
Glu Leu Pro His Val Asn Ile Leu Ser Lys Ile Asp Leu Ile Gly Ser
50 55 60
Tyr Gly Lys Leu Ala Phe Asn Leu Asp Phe Tyr Thr Asp Val Gln Asp
65 70 75 80
Leu Ser Tyr Leu Glu His His Leu Ser Gln Asp Pro Arg Ser Ala Lys
85 90 95
Tyr Arg Lys Leu Thr Lys Glu Leu Cys Ser Val Ile Glu Asp Tyr Ser
100 105 110
Leu Val Asn Phe Thr Thr Leu Asp Ile Gln Asp Lys Glu Ser Val Gly
115 120 125
Asp Leu Val Lys Leu Ile Asp Lys Ser Asn Gly Tyr Ile Phe Ala Gly
130 135 140
Ile Asp Ala Ser Val Val Glu Tyr Ser Lys Ile Ala Ile Gly Gln Thr
145 150 155 160
Asp Trp Asp Tyr Asn Arg Val Ala Ala Val Gln Glu Lys Tyr Met Glu
165 170 175
Asp Glu Glu Ile Gln Asp
180

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1482446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

Met Leu His Met Glu Leu Pro His Val Asn Ile Leu Ser Lys Ile Asp
1 5 10 15
Leu Ile Gly Ser Tyr Gly Lys Leu Ala Phe Asn Leu Asp Phe Tyr Thr
20 25 30
Asp Val Gln Asp Leu Ser Tyr Leu Glu His His Leu Ser Gln Asp Pro
35 40 45
Arg Ser Ala Lys Tyr Arg Lys Leu Thr Lys Glu Leu Cys Ser Val Ile
50 55 60
Glu Asp Tyr Ser Leu Val Asn Phe Thr Thr Leu Asp Ile Gln Asp Lys
65 70 75 80
Glu Ser Val Gly Asp Leu Val Lys Leu Ile Asp Lys Ser Asn Gly Tyr
85 90 95
Ile Phe Ala Gly Ile Asp Ala Ser Val Val Glu Tyr Ser Lys Ile Ala
100 105 110
Ile Gly Gln Thr Asp Trp Asp Tyr Asn Arg Val Ala Ala Val Gln Glu
115 120 125
Lys Tyr Met Glu Asp Glu Glu Ile Gln Asp
130 135

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

Met Glu Leu Pro His Val Asn Ile Leu Ser Lys Ile Asp Leu Ile Gly
1 5 10 15
Ser Tyr Gly Lys Leu Ala Phe Asn Leu Asp Phe Tyr Thr Asp Val Gln
20 25 30
Asp Leu Ser Tyr Leu Glu His His Leu Ser Gln Asp Pro Arg Ser Ala
35 40 45
Lys Tyr Arg Lys Leu Thr Lys Glu Leu Cys Ser Val Ile Glu Asp Tyr
50 55 60
Ser Leu Val Asn Phe Thr Thr Leu Asp Ile Gln Asp Lys Glu Ser Val
65 70 75 80
Gly Asp Leu Val Lys Leu Ile Asp Lys Ser Asn Gly Tyr Ile Phe Ala
85 90 95
Gly Ile Asp Ala Ser Val Val Glu Tyr Ser Lys Ile Ala Ile Gly Gln
100 105 110
Thr Asp Trp Asp Tyr Asn Arg Val Ala Val Gln Glu Lys Tyr Met
115 120 125
Glu Asp Glu Glu Ile Gln Asp
130 135

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..518
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

gatttttgaga aaaccatctc actgattagc caagatgtcg tcggctcggt ctgcgatcac 60
aaagctaaag ctggctcgat cctttgggga gagtcagatt ggtgcatcgc gttcgggtggt 120
atcgactcga ggaccggcga ttcggtactt cagtgcgat aaaggctcgt tgctcagcga 180
agaggaacgc gcgaaagaga gcatgtatat ccagaaaatg gagagggaaa gactggagaa 240
gaagaagaaa ctcgagcaag ataagctaga tggtagagaaa ggaagtgcc acaagaaacc 300
tgagacaagc aagccatgag tttatcactc acagtataca gaatccggtc ataaggcaag 360
cagtagtgaa aaacaataat gcctttgacc tatgttctct cttggtatga gagatcttgt 420
acttgtacag agatctttta ccttctgatg tgtgtgtttg tatgttctaa gaaatcaagt 480
ttaaataat cgaaaaaac aaccatattgc gttgattc

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..51
(D) OTHER INFORMATION: / Ceres Seq. ID 1482458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

Asp Phe Glu Lys Thr Ile Ser Leu Ile Ser Gln Asp Val Val Gly Ser
1 5 10 15
Phe Cys Asp His Lys Ala Lys Ala Gly Ser Ile Leu Trp Gly Glu Ser
20 25 30
Asp Trp Cys Ile Ala Phe Gly Gly Ile Asp Ser Arg Thr Gly Asp Ser
35 40 45
Val Leu Gln
50

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..94
(D) OTHER INFORMATION: / Ceres Seq. ID 1482459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

Met Ser Ser Ala Arg Ser Ala Ile Thr Lys Leu Lys Leu Ala Arg Ser
1 5 10 15
Phe Gly Glu Ser Gln Ile Gly Ala Ser Arg Ser Val Val Ser Thr Arg
20 25 30
Gly Pro Ala Ile Arg Tyr Phe Ser Asp Asp Lys Gly Arg Val Leu Ser
35 40 45
Glu Glu Glu Arg Ala Lys Glu Ser Met Tyr Ile Gln Lys Met Glu Arg
50 55 60
Glu Arg Leu Glu Lys Lys Lys Leu Glu Gln Asp Lys Leu Asp Gly
65 70 75 80
Glu Lys Gly Ser Ala Asn Lys Lys Pro Glu Thr Ser Lys Pro
85 90

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1116
(D) OTHER INFORMATION: / Ceres Seq. ID 1482460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

| | |
|---|-----|
| atagaacatc ctaatcgaaa aacattagtt ttgctgcggt tagtattcaa tttcatcgac | 60 |
| ccaaatcaaa atatatagga tactagataa agagtgcgtg aaggagagaa aaacaaaaat | 120 |
| ggcgattggt tccgtctcta actcttttct cactttcaat tctcccaatc agctccgatt | 180 |
| tagccgaaga agattctctg ccattgcttc ttcaactact ggagtgcgag tgcgtgaagg | 240 |
| agaaggcaat ttgccaatac tagtccttac ttctcctcag aacagcgagg ctgagatata | 300 |
| tctcttcgga ggctgcatta cttcttgga agttgcgagc ggtaaagatc ttctttttgt | 360 |
| cagaccagat gctgtcttca ataagattaa gccattagc ggagggattc cacattgttt | 420 |
| tccacagttt ggacctgggc taattcaaca gcatgggttt ggaaggaaca tggactggtc | 480 |
| tggtgtcgat tcccagaatg cagatgacaa tgctgctggt actcttgagc ttaaggatgg | 540 |
| tccctatagt cgagccatgt gggactttgc tttccaggct ctatacaagg tcattgttgg | 600 |
| cgcggactcc ctttccactg agctaaagat tacaaacaca gacgataaac cattttcttt | 660 |

```
cagcactgcg ctgcatactt acttccgtgc ttcttctgcg ggggcctccg tgagaggtct 720
aaaggggtgt aaaaccctca ataaggatcc agaccctaag aaccctaag agggtaaaga 780
agacagggat gcagtcactt ttcctggatt tgtggatacc gtctatcttg atgctcccaa 840
tgaattgcag tttgataatg gcttgggtga taaaataatc atcaaaaaca caaattggtc 900
ggatgcggtc ttgtggaacc cgcatactca gatggaggct tgttacagag actttgtgtg 960
cgtggaaaat gcaaagcttg gggatgtcaa gctagagccg ggacagtctt ggactgcaac 1020
acaacttctc agcatcagtt gaaaacattg tacttttaac ttataatgtc cagtggatcc 1080
attttcttaa gcaataaaag ttttatttcc tctccc
```

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 307 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..307

(D) OTHER INFORMATION: / Ceres Seq. ID 1482461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

```
Met Ala Ile Val Ser Val Ser Asn Ser Phe Leu Thr Phe Asn Ser Pro
1          5          10          15
Asn Gln Leu Arg Phe Ser Arg Arg Arg Phe Ser Ala Met Ala Ser Ser
          20          25          30
Thr Thr Gly Val Arg Val Ala Glu Gly Glu Gly Asn Leu Pro Lys Leu
          35          40          45
Val Leu Thr Ser Pro Gln Asn Ser Glu Ala Glu Ile Tyr Leu Phe Gly
          50          55          60
Gly Cys Ile Thr Ser Trp Lys Val Ala Ser Gly Lys Asp Leu Leu Phe
65          70          75          80
Val Arg Pro Asp Ala Val Phe Asn Lys Ile Lys Pro Ile Ser Gly Gly
          85          90          95
Ile Pro His Cys Phe Pro Gln Phe Gly Pro Gly Leu Ile Gln Gln His
          100          105          110
Gly Phe Gly Arg Asn Met Asp Trp Ser Val Val Asp Ser Gln Asn Ala
          115          120          125
Asp Asp Asn Ala Ala Val Thr Leu Glu Leu Lys Asp Gly Pro Tyr Ser
          130          135          140
Arg Ala Met Trp Asp Phe Ala Phe Gln Ala Leu Tyr Lys Val Ile Val
          145          150          155          160
Gly Ala Asp Ser Leu Ser Thr Glu Leu Lys Ile Thr Asn Thr Asp Asp
          165          170          175
Lys Pro Phe Ser Phe Ser Thr Ala Leu His Thr Tyr Phe Arg Ala Ser
          180          185          190
Ser Ala Gly Ala Ser Val Arg Gly Leu Lys Gly Cys Lys Thr Leu Asn
          195          200          205
Lys Asp Pro Asp Pro Lys Asn Pro Ile Glu Gly Lys Glu Asp Arg Asp
          210          215          220
Ala Val Thr Phe Pro Gly Phe Val Asp Thr Val Tyr Leu Asp Ala Pro
          225          230          235          240
Asn Glu Leu Gln Phe Asp Asn Gly Leu Gly Asp Lys Ile Ile Ile Lys
          245          250          255
Asn Thr Asn Trp Ser Asp Ala Val Leu Trp Asn Pro His Thr Gln Met
          260          265          270
Glu Ala Cys Tyr Arg Asp Phe Val Cys Val Glu Asn Ala Lys Leu Gly
          275          280          285
Asp Val Lys Leu Glu Pro Gly Gln Ser Trp Thr Ala Thr Gln Leu Leu
          290          295          300
Ser Ile Ser
```

305

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..279
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

Met Ala Ser Ser Thr Thr Gly Val Arg Val Ala Glu Gly Glu Gly Asn
1 5 10 15
Leu Pro Lys Leu Val Leu Thr Ser Pro Gln Asn Ser Glu Ala Glu Ile
20 25 30
Tyr Leu Phe Gly Gly Cys Ile Thr Ser Trp Lys Val Ala Ser Gly Lys
35 40 45
Asp Leu Leu Phe Val Arg Pro Asp Ala Val Phe Asn Lys Ile Lys Pro
50 55 60
Ile Ser Gly Gly Ile Pro His Cys Phe Pro Gln Phe Gly Pro Gly Leu
65 70 75 80
Ile Gln Gln His Gly Phe Gly Arg Asn Met Asp Trp Ser Val Val Asp
85 90 95
Ser Gln Asn Ala Asp Asp Asn Ala Ala Val Thr Leu Glu Leu Lys Asp
100 105 110
Gly Pro Tyr Ser Arg Ala Met Trp Asp Phe Ala Phe Gln Ala Leu Tyr
115 120 125
Lys Val Ile Val Gly Ala Asp Ser Leu Ser Thr Glu Leu Lys Ile Thr
130 135 140
Asn Thr Asp Asp Lys Pro Phe Ser Phe Ser Thr Ala Leu His Thr Tyr
145 150 155 160
Phe Arg Ala Ser Ser Ala Gly Ala Ser Val Arg Gly Leu Lys Gly Cys
165 170 175
Lys Thr Leu Asn Lys Asp Pro Asp Pro Lys Asn Pro Ile Glu Gly Lys
180 185 190
Glu Asp Arg Asp Ala Val Thr Phe Pro Gly Phe Val Asp Thr Val Tyr
195 200 205
Leu Asp Ala Pro Asn Glu Leu Gln Phe Asp Asn Gly Leu Gly Asp Lys
210 215 220
Ile Ile Ile Lys Asn Thr Asn Trp Ser Asp Ala Val Leu Trp Asn Pro
225 230 235 240
His Thr Gln Met Glu Ala Cys Tyr Arg Asp Phe Val Cys Val Glu Asn
245 250 255
Ala Lys Leu Gly Asp Val Lys Leu Glu Pro Gly Gln Ser Trp Thr Ala
260 265 270
Thr Gln Leu Leu Ser Ile Ser
275

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..190

(D) OTHER INFORMATION: / Ceres Seq. ID 1482463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

Met Asp Trp Ser Val Val Asp Ser Gln Asn Ala Asp Asp Asn Ala Ala
1 5 10 15
Val Thr Leu Glu Leu Lys Asp Gly Pro Tyr Ser Arg Ala Met Trp Asp
20 25 30
Phe Ala Phe Gln Ala Leu Tyr Lys Val Ile Val Gly Ala Asp Ser Leu
35 40 45
Ser Thr Glu Leu Lys Ile Thr Asn Thr Asp Asp Lys Pro Phe Ser Phe
50 55 60
Ser Thr Ala Leu His Thr Tyr Phe Arg Ala Ser Ser Ala Gly Ala Ser
65 70 75 80
Val Arg Gly Leu Lys Gly Cys Lys Thr Leu Asn Lys Asp Pro Asp Pro
85 90 95
Lys Asn Pro Ile Glu Gly Lys Glu Asp Arg Asp Ala Val Thr Phe Pro
100 105 110
Gly Phe Val Asp Thr Val Tyr Leu Asp Ala Pro Asn Glu Leu Gln Phe
115 120 125
Asp Asn Gly Leu Gly Asp Lys Ile Ile Ile Lys Asn Thr Asn Trp Ser
130 135 140
Asp Ala Val Leu Trp Asn Pro His Thr Gln Met Glu Ala Cys Tyr Arg
145 150 155 160
Asp Phe Val Cys Val Glu Asn Ala Lys Leu Gly Asp Val Lys Leu Glu
165 170 175
Pro Gly Gln Ser Trp Thr Ala Thr Gln Leu Leu Ser Ile Ser
180 185 190

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1430
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

ccwagaamca tcctaatacaa aaaacaattc ccgaaattct ctcaaatacac agatccctttt 60
aggggtttttc cactgttttct aggtttttttt tattgtctcaa atctgatcaa tggatagttg 120
tctctctaata caaacggcgc ttcagtttct cccgtcgcgt tccaggagac agagcggcga 180
tggaggcgggt ggttttggtta ttccggcgaa gaggaagatc cagtatagtt cgatggttgt 240
ggttgcggcg gcgggacaga gtcggtgtga gcctggaagc agtctaaacg cgccgcttga 300
gccacgatcg gcgcagggga ggtttctgag aagcgtgttg ctaaacaacac ggcagctatt 360
tcattacgcc gccgctgatg agctaaagca actggctgat gatagggaag ctgcttttagc 420
tcgtatgtct ctcagctctg gttccgatga ggcttctctc cacagaagga tagctgaact 480
caaggaacgc tactgtaaaa ctgcagtcca agacataatg tacatgttaa tcttttataca 540
atactccgag ataagagtcc ctcttggtcc aaagctatcc agatgcatct ataatggaag 600
actcgagatc tggccttcaa aagactggga gttagagtca atttacagct gcgataccct 660
tgagatcatc aaagaacacg ttagcgcagt catcggatta cgggtcaact catgtgtgac 720
tgacaattgg gcaacaacgc agatacagaa actgcattctc aggaaagtat atgctgcctc 780
gatcttgtag ggttacttct tgaaatcagc ttccctaagg caccagcttg agtgttcctt 840
atcagatatt catggaagcg gatattctgaa aagtcccatc tttggatgct cattcacaac 900
gggcaactgca cagatctcca acaagcagca gctgagacat tacatctcag actttgatcc 960
cgagacattg cagagatgcg caaaaccaag gacagaggag gcaaggaatc tgatagagaa 1020
gcaaagtttg gctctttttg gcacggaaga gagtgatgag accatagtga catcgttttc 1080
gagtcctgaag cggttgggtc tcgaggctgt ggcgtttggg acattcctgt gggacacgga 1140
attgtatgta gatggtgcat ataagctgaa ggagaatggg aatgcagaag aacaagaagg 1200
aaagaaaagc atatgatgaa caagtctggt tagaagaaaa gcttcatgat cttctggtag 1260

tgtatatata gagaaatgta tctgccgaat ctctcaggca gttgttcagt tcaatgtata 1320
gatcttgctt agaaatattt tgatttctga ataagaatgt ggtgtggtta taaggaataa 1380
gagatactgt agttgggttc aattttatgt tatgtgttaa gtttccttgt

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..368
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Asp | Ser | Cys | Leu | Ser | Asn | Gln | Thr | Ala | Leu | Gln | Phe | Leu | Pro | Ser | |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | | |
| Arg | Ser | Arg | Arg | Gln | Ser | Gly | Asp | Gly | Gly | Gly | Gly | Phe | Val | Ile | Pro | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Ala | Lys | Arg | Lys | Ile | Gln | Tyr | Ser | Ser | Met | Val | Val | Val | Ala | Ala | Ala | |
| | | | 35 | | | | 40 | | | | | 45 | | | | |
| Gly | Gln | Ser | Arg | Cys | Glu | Pro | Gly | Ser | Ser | Leu | Asn | Ala | Pro | Leu | Glu | |
| | | | 50 | | | 55 | | | | | 60 | | | | | |
| Pro | Arg | Ser | Ala | Gln | Gly | Arg | Phe | Leu | Arg | Ser | Val | Leu | Leu | Asn | Lys | |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | | |
| Arg | Gln | Leu | Phe | His | Tyr | Ala | Ala | Ala | Asp | Glu | Leu | Lys | Gln | Leu | Ala | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Asp | Asp | Arg | Glu | Ala | Ala | Leu | Ala | Arg | Met | Ser | Leu | Ser | Ser | Gly | Ser | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Asp | Glu | Ala | Ser | Leu | His | Arg | Arg | Ile | Ala | Glu | Leu | Lys | Glu | Arg | Tyr | |
| | | | 115 | | | | 120 | | | | | 125 | | | | |
| Cys | Lys | Thr | Ala | Val | Gln | Asp | Ile | Met | Tyr | Met | Leu | Ile | Phe | Tyr | Lys | |
| | | | 130 | | | 135 | | | | | 140 | | | | | |
| Tyr | Ser | Glu | Ile | Arg | Val | Pro | Leu | Val | Pro | Lys | Leu | Ser | Arg | Cys | Ile | |
| 145 | | | | 150 | | | | | | 155 | | | | 160 | | |
| Tyr | Asn | Gly | Arg | Leu | Glu | Ile | Trp | Pro | Ser | Lys | Asp | Trp | Glu | Leu | Glu | |
| | | | | 165 | | | | 170 | | | | | | 175 | | |
| Ser | Ile | Tyr | Ser | Cys | Asp | Thr | Leu | Glu | Ile | Ile | Lys | Glu | His | Val | Ser | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Ala | Val | Ile | Gly | Leu | Arg | Val | Asn | Ser | Cys | Val | Thr | Asp | Asn | Trp | Ala | |
| | | | 195 | | | | 200 | | | | | 205 | | | | |
| Thr | Thr | Gln | Ile | Gln | Lys | Leu | His | Leu | Arg | Lys | Val | Tyr | Ala | Ala | Ser | |
| | | | 210 | | | 215 | | | | | 220 | | | | | |
| Ile | Leu | Tyr | Gly | Tyr | Phe | Leu | Lys | Ser | Ala | Ser | Leu | Arg | His | Gln | Leu | |
| 225 | | | | 230 | | | | | 235 | | | | | 240 | | |
| Glu | Cys | Ser | Leu | Ser | Asp | Ile | His | Gly | Ser | Gly | Tyr | Leu | Lys | Ser | Pro | |
| | | | | 245 | | | | 250 | | | | | | 255 | | |
| Ile | Phe | Gly | Cys | Ser | Phe | Thr | Thr | Gly | Thr | Ala | Gln | Ile | Ser | Asn | Lys | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Gln | Gln | Leu | Arg | His | Tyr | Ile | Ser | Asp | Phe | Asp | Pro | Glu | Thr | Leu | Gln | |
| | | | 275 | | | | 280 | | | | | 285 | | | | |
| Arg | Cys | Ala | Lys | Pro | Arg | Thr | Glu | Glu | Ala | Arg | Asn | Leu | Ile | Glu | Lys | |
| | | | 290 | | | 295 | | | | | 300 | | | | | |
| Gln | Ser | Leu | Ala | Leu | Phe | Gly | Thr | Glu | Glu | Ser | Asp | Glu | Thr | Ile | Val | |
| 305 | | | | 310 | | | | | 315 | | | | | 320 | | |
| Thr | Ser | Phe | Ser | Ser | Leu | Lys | Arg | Leu | Val | Leu | Glu | Ala | Val | Ala | Phe | |
| | | | | 325 | | | | 330 | | | | | | 335 | | |
| Gly | Thr | Phe | Leu | Trp | Asp | Thr | Glu | Leu | Tyr | Val | Asp | Gly | Ala | Tyr | Lys | |
| | | | 340 | | | | 345 | | | | | | 350 | | | |

Leu Lys Glu Asn Gly Asn Ala Glu Glu Gln Glu Gly Lys Lys Ser Ile
355 360 365

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..327

(D) OTHER INFORMATION: / Ceres Seq. ID 1482483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

Met Val Val Val Ala Ala Ala Gly Gln Ser Arg Cys Glu Pro Gly Ser
1 5 10 15
Ser Leu Asn Ala Pro Leu Glu Pro Arg Ser Ala Gln Gly Arg Phe Leu
20 25 30
Arg Ser Val Leu Leu Asn Lys Arg Gln Leu Phe His Tyr Ala Ala Ala
35 40 45
Asp Glu Leu Lys Gln Leu Ala Asp Asp Arg Glu Ala Ala Leu Ala Arg
50 55 60
Met Ser Leu Ser Ser Gly Ser Asp Glu Ala Ser Leu His Arg Arg Ile
65 70 75 80
Ala Glu Leu Lys Glu Arg Tyr Cys Lys Thr Ala Val Gln Asp Ile Met
85 90 95
Tyr Met Leu Ile Phe Tyr Lys Tyr Ser Glu Ile Arg Val Pro Leu Val
100 105 110
Pro Lys Leu Ser Arg Cys Ile Tyr Asn Gly Arg Leu Glu Ile Trp Pro
115 120 125
Ser Lys Asp Trp Glu Leu Glu Ser Ile Tyr Ser Cys Asp Thr Leu Glu
130 135 140
Ile Ile Lys Glu His Val Ser Ala Val Ile Gly Leu Arg Val Asn Ser
145 150 155 160
Cys Val Thr Asp Asn Trp Ala Thr Thr Gln Ile Gln Lys Leu His Leu
165 170 175
Arg Lys Val Tyr Ala Ala Ser Ile Leu Tyr Gly Tyr Phe Leu Lys Ser
180 185 190
Ala Ser Leu Arg His Gln Leu Glu Cys Ser Leu Ser Asp Ile His Gly
195 200 205
Ser Gly Tyr Leu Lys Ser Pro Ile Phe Gly Cys Ser Phe Thr Thr Gly
210 215 220
Thr Ala Gln Ile Ser Asn Lys Gln Gln Leu Arg His Tyr Ile Ser Asp
225 230 235 240
Phe Asp Pro Glu Thr Leu Gln Arg Cys Ala Lys Pro Arg Thr Glu Glu
245 250 255
Ala Arg Asn Leu Ile Glu Lys Gln Ser Leu Ala Leu Phe Gly Thr Glu
260 265 270
Glu Ser Asp Glu Thr Ile Val Thr Ser Phe Ser Ser Leu Lys Arg Leu
275 280 285
Val Leu Glu Ala Val Ala Phe Gly Thr Phe Leu Trp Asp Thr Glu Leu
290 295 300
Tyr Val Asp Gly Ala Tyr Lys Leu Lys Glu Asn Gly Asn Ala Glu Glu
305 310 315 320
Gln Glu Gly Lys Lys Ser Ile
325

(2) INFORMATION FOR SEQ ID NO:587:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 263 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..263
 (D) OTHER INFORMATION: / Ceres Seq. ID 1482484
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

Met Ser Leu Ser Ser Gly Ser Asp Glu Ala Ser Leu His Arg Arg Ile
1 5 10 15
Ala Glu Leu Lys Glu Arg Tyr Cys Lys Thr Ala Val Gln Asp Ile Met
 20 25 30
Tyr Met Leu Ile Phe Tyr Lys Tyr Ser Glu Ile Arg Val Pro Leu Val
 35 40 45
Pro Lys Leu Ser Arg Cys Ile Tyr Asn Gly Arg Leu Glu Ile Trp Pro
 50 55 60
Ser Lys Asp Trp Glu Leu Glu Ser Ile Tyr Ser Cys Asp Thr Leu Glu
65 70 75 80
Ile Ile Lys Glu His Val Ser Ala Val Ile Gly Leu Arg Val Asn Ser
 85 90 95
Cys Val Thr Asp Asn Trp Ala Thr Thr Gln Ile Gln Lys Leu His Leu
 100 105 110
Arg Lys Val Tyr Ala Ala Ser Ile Leu Tyr Gly Tyr Phe Leu Lys Ser
 115 120 125
Ala Ser Leu Arg His Gln Leu Glu Cys Ser Leu Ser Asp Ile His Gly
 130 135 140
Ser Gly Tyr Leu Lys Ser Pro Ile Phe Gly Cys Ser Phe Thr Thr Gly
145 150 155 160
Thr Ala Gln Ile Ser Asn Lys Gln Gln Leu Arg His Tyr Ile Ser Asp
 165 170 175
Phe Asp Pro Glu Thr Leu Gln Arg Cys Ala Lys Pro Arg Thr Glu Glu
 180 185 190
Ala Arg Asn Leu Ile Glu Lys Gln Ser Leu Ala Leu Phe Gly Thr Glu
 195 200 205
Glu Ser Asp Glu Thr Ile Val Thr Ser Phe Ser Ser Leu Lys Arg Leu
 210 215 220
Val Leu Glu Ala Val Ala Phe Gly Thr Phe Leu Trp Asp Thr Glu Leu
225 230 235 240
Tyr Val Asp Gly Ala Tyr Lys Leu Lys Glu Asn Gly Asn Ala Glu Glu
 245 250 255
Gln Glu Gly Lys Lys Ser Ile
 260

(2) INFORMATION FOR SEQ ID NO:588:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 662 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..662
 (D) OTHER INFORMATION: / Ceres Seq. ID 1482490
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

atcgaaaaag atcgaaaaaa aatcgagaag cgaatagcgg aagaacagaa aaagggaaat
tctgagaatc aaatcggaaa ggtagaagaa tcgagtcgga aaaatggaaa cgacgaaaag

60
120

| | | | | | | |
|------------|------------|------------|--------------|------------|------------|-----|
| taacagcagc | gagtcgatg | tcaacgccaa | atgggacgct | tgtctcgatc | tcactgctcg | 180 |
| tcgctttgtc | tactcttccc | tcggcggcgc | tttcgccggt | cttctcttct | tcaggagtcc | 240 |
| ggttacgaga | tgggcgtcga | ttgcttttgg | tgctggaatt | ggatttggtt | ctgcatacac | 300 |
| agattgttct | cgtgtttttg | atgcgtcttc | ttcaacttca | gctactttat | tagcagctcc | 360 |
| caagagtaca | gagacttctg | tatctcaggc | agcagaagag | tgaagacaac | gaggaagctt | 420 |
| ggaggtaaaa | aaccaaacad | tgataggggt | acattacgaa | atggtaattg | atcttgagg | 480 |
| acaaggcttt | tgagataacg | ccattgttaa | aaaaaaaaactt | ttgcttctca | gtgtgggttt | 540 |
| gtacactgat | gtcaaaattg | ttaatgaccc | actcattttt | ttttgttttg | aaaaatctta | 600 |
| tgctctttta | cttgagaaat | aattcctccg | ttgatttggt | tgctctact | gttccttcat | 660 |
| tc | | | | | | |

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Thr | Thr | Lys | Ser | Asn | Ser | Ser | Glu | Ser | Asp | Val | Asn | Ala | Lys | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Trp | Asp | Ala | Cys | Leu | Asp | Leu | Thr | Ala | Arg | Arg | Phe | Val | Tyr | Ser | Ser | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Leu | Gly | Gly | Ala | Phe | Ala | Gly | Leu | Phe | Phe | Arg | Ser | Pro | Val | Thr | | |
| | | 35 | | | | | 40 | | | | 45 | | | | | |
| Arg | Trp | Ala | Ser | Ile | Ala | Phe | Gly | Ala | Gly | Ile | Gly | Ile | Gly | Ser | Ala | |
| | 50 | | | | 55 | | | | | 60 | | | | | | |
| Tyr | Thr | Asp | Cys | Ser | Arg | Val | Phe | Asp | Ala | Ser | Ser | Ser | Thr | Ser | Ala | |
| 65 | | | | 70 | | | | 75 | | | | | | 80 | | |
| Thr | Leu | Leu | Ala | Ala | Pro | Lys | Ser | Thr | Glu | Thr | Ser | Val | Ser | Gln | Ala | |
| | | | 85 | | | | | 90 | | | | | | 95 | | |
| Ala | Glu | Glu | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Thr | Pro | Asn | Gly | Thr | Leu | Val | Ser | Ile | Ser | Leu | Leu | Val | Ala | |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | | |
| Leu | Ser | Thr | Leu | Pro | Ser | Ala | Ala | Leu | Ser | Pro | Val | Phe | Ser | Ser | Ser | |
| | | | 20 | | | | 25 | | | | | 30 | | | | |
| Gly | Val | Arg | Leu | Arg | Asp | Gly | Arg | Arg | Leu | Leu | Leu | Val | Leu | Glu | Leu | |
| | | 35 | | | | 40 | | | | | 45 | | | | | |
| Val | Leu | Val | Leu | His | Thr | Gln | Ile | Val | Leu | Val | Phe | Leu | Met | Arg | Leu | |
| | 50 | | | | 55 | | | | | 60 | | | | | | |
| Leu | Gln | Leu | Gln | Leu | Leu | Tyr | | | | | | | | | | |
| 65 | | | | 70 | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:591:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..56
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Arg | Leu | Ser | Arg | Ser | His | Cys | Ser | Ser | Leu | Cys | Leu | Leu | Phe |
| 1 | | | 5 | | | | | 10 | | | | 15 | | | |
| Pro | Arg | Arg | Arg | Phe | Arg | Arg | Ser | Ser | Leu | Leu | Gln | Glu | Ser | Gly | Tyr |
| | | 20 | | | | | 25 | | | | 30 | | | | |
| Glu | Met | Gly | Val | Asp | Cys | Phe | Trp | Cys | Trp | Asn | Trp | Tyr | Trp | Phe | Cys |
| | | 35 | | | | | 40 | | | | 45 | | | | |
| Ile | His | Arg | Leu | Phe | Ser | Cys | Phe | | | | | | | | |
| | 50 | | | | | 55 | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:592:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 853 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..853
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|-----|
| ccattaccwa | kaacatccta | atcgaaaagt | aatcggagtt | caggcttcag | cattctctct | 60 |
| tcttctctct | cgcagccgta | gtttttgata | ttctcttcaa | ttctctctcc | tgatggccac | 120 |
| gtccgcggtc | ctctccggtg | ccagatcgat | gcttcgagct | gcttcctcac | gcagcgccgc | 180 |
| tgcttctaact | ggccgcttcg | cctctcaagc | gaaatccgct | ccaccattgt | ttagagccac | 240 |
| tgccagaaga | agcccactgc | tttctcctct | ccgaaatcct | gtggaactga | gcttctgtgt | 300 |
| ggagtcattg | ttaccatata | actcggctac | agcttcagcg | ctaatagact | caaagctttc | 360 |
| tatctctggc | caaacctatg | gctggctctc | tgacggctga | cacaagtgtg | gatgaagaca | 420 |
| acgaagccaa | gatctgggta | taaacgatta | gaacgggttt | caggcaataa | gataggcttt | 480 |
| agatacacat | caagcaatgg | ttgatgctgc | atttgtgttt | aaaagaactg | gttctttacat | 540 |
| atcttcttaa | aaaaaataca | tgtaccggga | aaagtgcctt | cttttcttgd | tggttatagc | 600 |
| atttgagtta | ttactgattg | gtcttatact | cccagcttgc | aatgatgatg | tgtgatgatg | 660 |
| tagccagagg | aacaatgaag | ctacagttta | tgtacaaaac | tctacctttt | aaagcctttc | 720 |
| ttcttaaaaa | acttaggaac | gaaaaccctc | ttaattttgt | ttctgagttt | cttgagagagc | 780 |
| ttttgtttgt | tttcagccta | ttaagtaaga | catgttgtat | tggttggacg | agtaactgat | 840 |
| gtttggtata | att | | | | | |

(2) INFORMATION FOR SEQ ID NO:593:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..95
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

Met Ala Thr Ser Ala Val Leu Ser Gly Ala Arg Ser Met Leu Arg Ala

| | | | |
|---|----|----|----|
| 1 | 5 | 10 | 15 |
| Ala Ser Ser Arg Ser Ala Ala Ala Ser Thr Gly Arg Phe Ala Ser Gln | | | |
| | 20 | 25 | 30 |
| Ala Lys Ser Ala Pro Pro Leu Phe Arg Ala Thr Ala Arg Arg Ser Pro | | | |
| | 35 | 40 | 45 |
| Leu Leu Ser Pro Leu Arg Asn Pro Val Glu Leu Ser Phe Cys Val Glu | | | |
| | 50 | 55 | 60 |
| Ser Leu Leu Pro Tyr His Ser Ala Thr Ala Ser Ala Leu Met Thr Ser | | | |
| 65 | 70 | 75 | 80 |
| Lys Leu Ser Ile Ser Gly Gln Thr Tyr Gly Trp Leu Ser Asp Gly | | | |
| | 85 | 90 | 95 |

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

| | | | |
|---|----|----|----|
| Met Leu Arg Ala Ala Ser Ser Arg Ser Ala Ala Ala Ser Thr Gly Arg | | | |
| 1 | 5 | 10 | 15 |
| Phe Ala Ser Gln Ala Lys Ser Ala Pro Leu Phe Arg Ala Thr Ala | | | |
| | 20 | 25 | 30 |
| Arg Arg Ser Pro Leu Leu Ser Pro Leu Arg Asn Pro Val Glu Leu Ser | | | |
| | 35 | 40 | 45 |
| Phe Cys Val Glu Ser Leu Leu Pro Tyr His Ser Ala Thr Ala Ser Ala | | | |
| | 50 | 55 | 60 |
| Leu Met Thr Ser Lys Leu Ser Ile Ser Gly Gln Thr Tyr Gly Trp Leu | | | |
| 65 | 70 | 75 | 80 |
| Ser Asp Gly | | | |

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

| | | | |
|---|----|----|----|
| Met Met Met Cys Asp Glu Leu Ala Arg Gly Thr Met Lys Leu Gln Phe | | | |
| 1 | 5 | 10 | 15 |
| Met Tyr Lys Thr Leu Pro Phe Lys Ala Phe Leu Leu Lys Lys Leu Arg | | | |
| | 20 | 25 | 30 |
| Asn Glu Asn Pro Leu Asn Phe Val Ser Glu Phe Leu Gly Glu Leu Leu | | | |
| | 35 | 40 | 45 |
| Phe Val Phe Ser Leu Leu Ser Lys Thr Cys Cys Ile Gly Trp Thr Ser | | | |
| | 50 | 55 | 60 |
| Asn | | | |
| 65 | | | |

(2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1139
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

| | |
|---|------|
| caatcatctg atctttccct ctctcagcaa tgcattgatt tgcattttct atcagtgttc | 60 |
| aaagctgaaa aaaatcgaaac tgggtctgtt gatttcttca ggtctaaaat cagattagat | 120 |
| tagagaagaa gaagaagaat gctggaagct gtagatagct caggagtggg gaatggagga | 180 |
| ttcccgagaa ttacagagctt ttacggcgat tgcagttagt aagaagagtt atcgggtattg | 240 |
| ccacgtcata caaaagtggg ggtcaccgga aacaaccgga cgaatcggt gcttgttggg | 300 |
| cttcaagggtg ttgtcaaaaa agctgtcggt ctcggtgggt ggcattgggt ggttttgaca | 360 |
| aatggaatag aagtaaggtt gcagaggaat gcgcttagtg tccttgaacc tcctactgga | 420 |
| aacgaagaag acgatgatct tgatttcgaa aacacacaga ggaatggctc tgatatgatt | 480 |
| gtttcttttc cagcatctga ggacacactg aagcctcata agtcgaagct aagagggcag | 540 |
| agatcatctc ggtcatctca caagacgatg agcagggtct tatcatctga ctgcgaatca | 600 |
| aaaagtccgg gttttactcc tcctgaaaaac atgaagggtg atcttagcaa attggaaatg | 660 |
| cctgctttac tgaattattg gcgacatttt aaccttgggt atgcaattcc aaatccatca | 720 |
| aaggagcaac taattgacat tgttcaaagg cacttcatgt ctacgcaaat ggatgagctt | 780 |
| caggttattg tggggtttgt ccaagctgca aagagaatga agaaggcttg caagtttcaa | 840 |
| tccaaagaat ccagaaacac tgatcttaac tgcattcagc aaagaaaagc cctgactctt | 900 |
| aacaaatcct gtatgtacgg tacatcaact tgtttaacca tttgtggctt gctaagttta | 960 |
| gttcttctag tgatgtttgg ctaaagggtg gatgttggtt cttctttgct tctgttgttt | 1020 |
| agccaatgta agtaccatca aaaaacccaa ataactctct aaagctccct attggaaact | 1080 |
| atcttgtctg atacgatctg gagtgaccgg tatgttggtt gaatgtaaat atgtttggg | |

(2) INFORMATION FOR SEQ ID NO:597:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 247 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..247
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Glu | Ala | Val | Asp | Ser | Ser | Gly | Val | Val | Asn | Gly | Gly | Phe | Pro |
| 1 | | | 5 | | | | | 10 | | | | | | 15 | |
| Gln | Ile | Gln | Ser | Phe | Tyr | Gly | Asp | Cys | Ser | Ser | Glu | Glu | Glu | Leu | Ser |
| | | | 20 | | | | | 25 | | | | | | 30 | |
| Val | Leu | Pro | Arg | His | Thr | Lys | Val | Val | Val | Thr | Gly | Asn | Asn | Arg | Thr |
| | | | 35 | | | | | 40 | | | | | | 45 | |
| Lys | Ser | Val | Leu | Val | Gly | Leu | Gln | Gly | Val | Val | Lys | Lys | Ala | Val | Gly |
| | | | 50 | | | | | 55 | | | | | | 60 | |
| Leu | Gly | Gly | Trp | His | Trp | Leu | Val | Leu | Thr | Asn | Gly | Ile | Glu | Val | Lys |
| 65 | | | | | | | | 70 | | | | | | 80 | |
| Leu | Gln | Arg | Asn | Ala | Leu | Ser | Val | Leu | Glu | Pro | Pro | Thr | Gly | Asn | Glu |
| | | | 85 | | | | | 90 | | | | | | 95 | |
| Glu | Asp | Asp | Asp | Leu | Asp | Phe | Glu | Asn | Thr | Gln | Arg | Asn | Gly | Ser | Asp |
| | | | 100 | | | | | 105 | | | | | | 110 | |
| Met | Ile | Val | Ser | Phe | Pro | Ala | Ser | Glu | Asp | Thr | Leu | Lys | Pro | His | Lys |
| | | | 115 | | | | | 120 | | | | | | 125 | |
| Ser | Lys | Leu | Arg | Gly | Gln | Arg | Ser | Ser | Arg | Ser | Ser | His | Lys | Thr | Met |
| | | | 130 | | | | | 135 | | | | | | 140 | |

Ser Arg Ser Leu Ser Ser Asp Ser Gln Ser Lys Ser Ser Gly Phe Thr
145 150 155 160
Pro Pro Glu Asn Met Lys Val Asp Leu Ser Lys Leu Glu Met Pro Ala
165 170 175
Leu Leu Asn Tyr Trp Arg His Phe Asn Leu Val Asp Ala Ile Pro Asn
180 185 190
Pro Ser Lys Glu Gln Leu Ile Asp Ile Val Gln Arg His Phe Met Ser
195 200 205
Gln Gln Met Asp Glu Leu Gln Val Ile Val Gly Phe Val Gln Ala Ala
210 215 220
Lys Arg Met Lys Lys Ala Cys Lys Phe Gln Ser Lys Glu Ser Arg Asn
225 230 235 240
Thr Asp Leu Asn Cys Ile Ser
245

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1482510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

Met Ile Val Ser Phe Pro Ala Ser Glu Asp Thr Leu Lys Pro His Lys
1 5 10 15
Ser Lys Leu Arg Gly Gln Arg Ser Ser Arg Ser Ser His Lys Thr Met
20 25 30
Ser Arg Ser Leu Ser Ser Asp Ser Gln Ser Lys Ser Ser Gly Phe Thr
35 40 45
Pro Pro Glu Asn Met Lys Val Asp Leu Ser Lys Leu Glu Met Pro Ala
50 55 60
Leu Leu Asn Tyr Trp Arg His Phe Asn Leu Val Asp Ala Ile Pro Asn
65 70 75 80
Pro Ser Lys Glu Gln Leu Ile Asp Ile Val Gln Arg His Phe Met Ser
85 90 95
Gln Gln Met Asp Glu Leu Gln Val Ile Val Gly Phe Val Gln Ala Ala
100 105 110
Lys Arg Met Lys Lys Ala Cys Lys Phe Gln Ser Lys Glu Ser Arg Asn
115 120 125
Thr Asp Leu Asn Cys Ile Ser
130 135

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1323

(D) OTHER INFORMATION: / Ceres Seq. ID 1482514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

ccattaccta gaacatccta atcaaaaaat tgatgttgat gataaagtct tatctgtttc 60
aattgatgca ggatgatgga gattgggctg ctattggtgt gaaagatggt caaaaattga 120
tgatgatggg aactgctgat gagatagtga aagctcctga gaaggccatt gtttttgcag 180

| | | | | | | |
|------------|-------------|------------|-------------|-------------|-------------|------|
| agaatctacc | tgaagaagcg | ctagccacta | atctgggtta | cagtgctggc | cttgtcaatc | 240 |
| ttggcaacac | gtgttacatg | aactccacgg | tgcagtgtt | aaaatctgtc | ccagagttga | 300 |
| aatctgcatt | atccaattac | tcacttgctg | cccgaagcaa | tgatgttgac | cagacttctc | 360 |
| acatgctcac | agttgccaca | cgtgagttat | ttggtgagct | tgatagaagt | gtcaatgctg | 420 |
| tttcgccttc | acagttcttg | atggtattac | gaaaaaagta | tcctcagttt | agtcagttgc | 480 |
| agaatggaat | gcacatgcag | caggatgctg | aagaatgttg | gacacaactg | ttatacaccc | 540 |
| tttctcagtc | cctaaaagca | ccaacttcca | gcgaaggtgc | tgatgctgtg | aaagctctat | 600 |
| ttggtgtcaa | tctccagagc | aggttgcatt | gtcaagaaag | tggcgaagaa | agctcagaga | 660 |
| cagaatctgt | atattctcta | aaatgtcata | tatcacatga | agtgaaccac | ttgcatgaag | 720 |
| gattaaaaca | tggactgaaa | ggggaacttg | aaaaaacatc | tcctgctctt | ggccgtactg | 780 |
| cactctacgt | caaggagtca | cttatagatt | ccttgccaag | gtacttgact | gttcagttcg | 840 |
| tgcggttttt | ctggaaaagg | gagagtaatc | agaaagcaaa | gatcctcagg | aaagtggatt | 900 |
| acccgctggg | gttggaatata | tttgaccttt | gctctgagga | tcttcggaag | aaactggaag | 960 |
| ctcctcgcca | gaaacttaga | gaggaggaag | gtaaaaagct | tgggtcttcaa | actagtgtca | 1020 |
| agagtggctc | aaaggacagt | gatgtgaaaa | tgactgatgc | agaggcgtct | gcaaattggaa | 1080 |
| gtggagaatc | atccacagta | aaccacacag | aagggtacttt | gagccactct | tagcactagt | 1140 |
| ttgaagacca | agcctaaaca | atgcttccac | cttgtgttct | ttttggatta | taayccttca | 1200 |
| tgagttaatt | ttggttgaac | ctttggtagt | atatgttgct | ggattgtgca | ccttctgttt | 1260 |
| tcactcctc | ttccaaacta | ctttattttt | gcttatagat | cttaatgttc | tagttttgct | 1320 |
| ttt | | | | | | |

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..366

(D) OTHER INFORMATION: / Ceres Seq. ID 1482515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Met | Ile | Lys | Ser | Tyr | Leu | Phe | Gln | Leu | Met | Gln | Asp | Asp | Gly |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Asp | Trp | Ala | Ala | Ile | Gly | Val | Lys | Asp | Gly | Gln | Lys | Leu | Met | Met | Met |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Gly | Thr | Ala | Asp | Glu | Ile | Val | Lys | Ala | Pro | Glu | Lys | Ala | Ile | Val | Phe |
| | | | 35 | | | | | 40 | | | | | 45 | | |
| Ala | Glu | Asn | Leu | Pro | Glu | Glu | Ala | Leu | Ala | Thr | Asn | Leu | Gly | Tyr | Ser |
| | | | 50 | | | | | 55 | | | | | 60 | | |
| Ala | Gly | Leu | Val | Asn | Leu | Gly | Asn | Thr | Cys | Tyr | Met | Asn | Ser | Thr | Val |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Gln | Cys | Leu | Lys | Ser | Val | Pro | Glu | Leu | Lys | Ser | Ala | Leu | Ser | Asn | Tyr |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Ser | Leu | Ala | Ala | Arg | Ser | Asn | Asp | Val | Asp | Gln | Thr | Ser | His | Met | Leu |
| | | | 100 | | | | | 105 | | | | | | 110 | |
| Thr | Val | Ala | Thr | Arg | Glu | Leu | Phe | Gly | Glu | Leu | Asp | Arg | Ser | Val | Asn |
| | | | 115 | | | | | 120 | | | | | 125 | | |
| Ala | Val | Ser | Pro | Ser | Gln | Phe | Trp | Met | Val | Leu | Arg | Lys | Lys | Tyr | Pro |
| | | | 130 | | | | | 135 | | | | | 140 | | |
| Gln | Phe | Ser | Gln | Leu | Gln | Asn | Gly | Met | His | Met | Gln | Gln | Asp | Ala | Glu |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Glu | Cys | Trp | Thr | Gln | Leu | Leu | Tyr | Thr | Leu | Ser | Gln | Ser | Leu | Lys | Ala |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Pro | Thr | Ser | Ser | Glu | Gly | Ala | Asp | Ala | Val | Lys | Ala | Leu | Phe | Gly | Val |
| | | | 180 | | | | | 185 | | | | | | 190 | |
| Asn | Leu | Gln | Ser | Arg | Leu | His | Cys | Gln | Glu | Ser | Gly | Glu | Glu | Ser | Ser |
| | | | 195 | | | | 200 | | | | | | 205 | | |
| Glu | Thr | Glu | Ser | Val | Tyr | Ser | Leu | Lys | Cys | His | Ile | Ser | His | Glu | Val |

| | | |
|---|---|-----|
| 210 | 215 | 220 |
| Asn His Leu His Glu Gly | Leu Lys His Gly Leu Lys Gly Glu Leu Glu | |
| 225 | 230 | 235 |
| Lys Thr Ser Pro Ala Leu Gly Arg Thr Ala Leu Tyr Val Lys Glu Ser | | 240 |
| | 245 | 250 |
| Leu Ile Asp Ser Leu Pro Arg Tyr Leu Thr Val Gln Phe Val Arg Phe | | 255 |
| | 260 | 265 |
| Phe Trp Lys Arg Glu Ser Asn Gln Lys Ala Lys Ile Leu Arg Lys Val | | 270 |
| | 275 | 280 |
| Asp Tyr Pro Leu Val Leu Asp Ile Phe Asp Leu Cys Ser Glu Asp Leu | | 285 |
| | 290 | 295 |
| Arg Lys Lys Leu Glu Ala Pro Arg Gln Lys Leu Arg Glu Glu Glu Gly | | 300 |
| 305 | 310 | 315 |
| Lys Lys Leu Gly Leu Gln Thr Ser Ala Lys Ser Gly Ser Lys Asp Ser | | 320 |
| | 325 | 330 |
| Asp Val Lys Met Thr Asp Ala Glu Ala Ser Ala Asn Gly Ser Gly Glu | | 335 |
| | 340 | 345 |
| Ser Ser Thr Val Asn Pro Gln Glu Gly Thr Leu Ser His Ser | | 350 |
| | 355 | 360 |
| | | 365 |

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..364
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

| | |
|---|-----|
| Met Ile Lys Ser Tyr Leu Phe Gln Leu Met Gln Asp Asp Gly Asp Trp | |
| 1 | 5 |
| Ala Ala Ile Gly Val Lys Asp Gly Gln Lys Leu Met Met Met Gly Thr | 10 |
| | 20 |
| Ala Asp Glu Ile Val Lys Ala Pro Glu Lys Ala Ile Val Phe Ala Glu | 25 |
| | 30 |
| Asn Leu Pro Glu Glu Ala Leu Ala Thr Asn Leu Gly Tyr Ser Ala Gly | 35 |
| | 40 |
| Leu Val Asn Leu Gly Asn Thr Cys Tyr Met Asn Ser Thr Val Gln Cys | 45 |
| 65 | 50 |
| Leu Lys Ser Val Pro Glu Leu Lys Ser Ala Leu Ser Asn Tyr Ser Leu | 55 |
| | 60 |
| Ala Ala Arg Ser Asn Asp Val Asp Gln Thr Ser His Met Leu Thr Val | 65 |
| | 70 |
| Ala Thr Arg Glu Leu Phe Gly Glu Leu Asp Arg Ser Val Asn Ala Val | 75 |
| | 80 |
| Ser Pro Ser Gln Phe Trp Met Val Leu Arg Lys Lys Tyr Pro Gln Phe | 85 |
| | 90 |
| Ser Gln Leu Gln Asn Gly Met His Met Gln Gln Asp Ala Glu Glu Cys | 95 |
| 145 | 100 |
| Trp Thr Gln Leu Leu Tyr Thr Leu Ser Gln Ser Leu Lys Ala Pro Thr | 105 |
| | 110 |
| Ser Ser Glu Gly Ala Asp Ala Val Lys Ala Leu Phe Gly Val Asn Leu | 115 |
| | 120 |
| Gln Ser Arg Leu His Cys Gln Glu Ser Gly Glu Glu Ser Ser Glu Thr | 125 |
| | 130 |
| Glu Ser Val Tyr Ser Leu Lys Cys His Ile Ser His Glu Val Asn His | 135 |
| | 140 |
| | 145 |
| | 150 |
| | 155 |
| | 160 |
| | 165 |
| | 170 |
| | 175 |
| | 180 |
| | 185 |
| | 190 |
| | 195 |
| | 200 |
| | 205 |
| | 210 |
| | 215 |
| | 220 |

Leu His Glu Gly Leu Lys His Gly Leu Lys Gly Glu Leu Glu Lys Thr
225 230 235 240
Ser Pro Ala Leu Gly Arg Thr Ala Leu Tyr Val Lys Glu Ser Leu Ile
245 250 255
Asp Ser Leu Pro Arg Tyr Leu Thr Val Gln Phe Val Arg Phe Phe Trp
260 265 270
Lys Arg Glu Ser Asn Gln Lys Ala Lys Ile Leu Arg Lys Val Asp Tyr
275 280 285
Pro Leu Val Leu Asp Ile Phe Asp Leu Cys Ser Glu Asp Leu Arg Lys
290 295 300
Lys Leu Glu Ala Pro Arg Gln Lys Leu Arg Glu Glu Glu Gly Lys Lys
305 310 315 320
Leu Gly Leu Gln Thr Ser Ala Lys Ser Gly Ser Lys Asp Ser Asp Val
325 330 335
Lys Met Thr Asp Ala Glu Ala Ser Ala Asn Gly Ser Gly Glu Ser Ser
340 345 350
Thr Val Asn Pro Gln Glu Gly Thr Leu Ser His Ser
355 360

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..355
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

Met Gln Asp Asp Gly Asp Trp Ala Ala Ile Gly Val Lys Asp Gly Gln
1 5 10 15
Lys Leu Met Met Met Gly Thr Ala Asp Glu Ile Val Lys Ala Pro Glu
20 25 30
Lys Ala Ile Val Phe Ala Glu Asn Leu Pro Glu Glu Ala Leu Ala Thr
35 40 45
Asn Leu Gly Tyr Ser Ala Gly Leu Val Asn Leu Gly Asn Thr Cys Tyr
50 55 60
Met Asn Ser Thr Val Gln Cys Leu Lys Ser Val Pro Glu Leu Lys Ser
65 70 75 80
Ala Leu Ser Asn Tyr Ser Leu Ala Ala Arg Ser Asn Asp Val Asp Gln
85 90 95
Thr Ser His Met Leu Thr Val Ala Thr Arg Glu Leu Phe Gly Glu Leu
100 105 110
Asp Arg Ser Val Asn Ala Val Ser Pro Ser Gln Phe Trp Met Val Leu
115 120 125
Arg Lys Lys Tyr Pro Gln Phe Ser Gln Leu Gln Asn Gly Met His Met
130 135 140
Gln Gln Asp Ala Glu Glu Cys Trp Thr Gln Leu Leu Tyr Thr Leu Ser
145 150 155 160
Gln Ser Leu Lys Ala Pro Thr Ser Ser Glu Gly Ala Asp Ala Val Lys
165 170 175
Ala Leu Phe Gly Val Asn Leu Gln Ser Arg Leu His Cys Gln Glu Ser
180 185 190
Gly Glu Glu Ser Ser Glu Thr Glu Ser Val Tyr Ser Leu Lys Cys His
195 200 205
Ile Ser His Glu Val Asn His Leu His Glu Gly Leu Lys His Gly Leu
210 215 220
Lys Gly Glu Leu Glu Lys Thr Ser Pro Ala Leu Gly Arg Thr Ala Leu

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..630
(D) OTHER INFORMATION: / Ceres Seq. ID 1482525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:803: | | | | | | |
|---|------------|------------|-------------|------------|------------|-----|
| aaccttcgca | gctagatctg | gacgcttttt | actgactaga | ctcctgacaa | tatcttcac | 60 |
| acaaatagca | ttacattgat | gagccatgca | tcyaatcctt | ttgctctgac | cttcatttat | 120 |
| ctgcacagta | aaatgctccg | tccaacaatt | attgcaaaag | caatggccac | agwccattct | 180 |
| tgctcatgtga | tcacctggta | aatcctccat | gcaaacatca | caactcatct | gtgaagactg | 240 |
| aggaaaggaa | gagttgccat | attgataatc | gaagacagtg | acaccagctc | cagaaaacaa | 300 |
| rctatmtttt | mctttctmaa | caaacacagc | aaacaacttc | tccacatccc | actggtaatg | 360 |
| aataagaaga | gtccgtgcat | ggtgctcctt | tattgataac | aattscatca | cccttagcaa | 420 |
| atctttctctc | tgtgctgcta | gaagcgattc | ctgagtgatg | acctgagttg | tttgawcytt | 480 |
| tagaggacaa | gaggctgcaa | ttcaagactc | ttcawtatca | attccatcga | aaagaatctt | 540 |
| gactcgagga | gtaataggca | agccctcttc | ctccgcgccta | aaataatcat | ccatcgatca | 600 |
| caattctggt | tttcgattag | gatgttctag | | | | |

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS
- (A) LENGTH: 40 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..40
(D) OTHER INFORMATION: / Ceres Seq. ID 1482526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

| | | | | | | | | | | | | | | | |
|---|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:804. | | | | | | | | | | | | | | | |
| Met | Ser | His | Ala | Xaa | Asn | Pro | Phe | Ala | Leu | Thr | Phe | Ile | Tyr | Leu | His |
| 1 | | | 5 | | | | | | 10 | | | | | 15 | |
| Ser | Lys | Met | Leu | Arg | Pro | Thr | Ile | Ile | Ala | Lys | Ala | Met | Ala | Thr | Xaa |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| His | Ser | Cys | His | Val | Ile | Thr | Trp | | | | | | | | |
| | | 35 | | | | 40 | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:605:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 657 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..657
 (D) OTHER INFORMATION: / Ceres Seq. ID 1482535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

| | |
|--|-----|
| attacctaga acatcctaata caaaaagtat caatggcttc cttcacctgt tcttctccat | 60 |
| cttcgatttt acctattatt gatacgagaa gtgggaattt gcgatgcaca ttccagtctc | 120 |
| aggtttcttg tgggattcag agagatgata atggacgccg tgtttgccgg aggagaacat | 180 |
| tgacgaagaa ggacgatatg ttgcgttaca aaatgcaaag agttccattt gtggaagagc | 240 |
| aagtgaggaa gataagagra gttgggaaag taatgacaat ggacatagag cagcttcttt | 300 |
| tgagggaaga caatcggttt gaatttgtca atagcgtagc agctgaagca acagagtacg | 360 |
| tggacaagaa cagagacgaa tatggagggt ccaaaaaagc tatctttcat gttctaagca | 420 |
| accgtgtgaa cgatctcggc tttgaccgcc ctgaggctta tgtagaagct gatccttaca | 480 |
| aaccgggtcc tggctatttg ttggagtact acacttgata tattataaca aaaagtgtca | 540 |
| atgtacttta cagcttttgt tcttgtatta ccaaaaccaa atcaatgcgt ttcacagctt | 600 |
| tgttgttttc ttggccagat ttcattttat ttatttagat ttactagatg aagacgg | |

(2) INFORMATION FOR SEQ ID NO:606:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 171 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..171
 (D) OTHER INFORMATION: / Ceres Seq. ID 1482536

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Leu | Glu | His | Pro | Asn | Gln | Lys | Val | Ser | Met | Ala | Ser | Phe | Thr | Cys |
| 1 | | | 5 | | | | | | 10 | | | | | 15 | |
| Ser | Ser | Pro | Ser | Ser | Ile | Leu | Pro | Ile | Ile | Asp | Thr | Arg | Ser | Gly | Asn |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Arg | Cys | Thr | Phe | Gln | Ser | Gln | Val | Ser | Cys | Gly | Ile | Gln | Arg | Asp |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Asp | Asn | Gly | Arg | Arg | Val | Trp | Arg | Arg | Arg | Thr | Leu | Thr | Lys | Lys | Asp |
| | | | 50 | | | 55 | | | | 60 | | | | | |
| Asp | Met | Leu | Arg | Tyr | Lys | Met | Gln | Arg | Val | Pro | Phe | Val | Glu | Glu | Gln |
| | | | | | 70 | | | | | 75 | | | | 80 | |
| Val | Arg | Lys | Ile | Arg | Xaa | Val | Gly | Lys | Val | Met | Thr | Met | Asp | Ile | Glu |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Gln | Leu | Leu | Leu | Arg | Glu | Asp | Asn | Arg | Phe | Glu | Phe | Val | Asn | Ser | Val |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ala | Ala | Glu | Ala | Thr | Glu | Tyr | Val | Asp | Lys | Asn | Arg | Asp | Glu | Tyr | Gly |
| | | | 115 | | | | 120 | | | | | 125 | | | |
| Gly | Ser | Lys | Lys | Ala | Ile | Phe | His | Val | Leu | Ser | Asn | Arg | Val | Asn | Asp |
| | | | 130 | | | 135 | | | | | 140 | | | | |
| Leu | Gly | Phe | Asp | Arg | Pro | Glu | Ala | Tyr | Val | Glu | Ala | Asp | Pro | Tyr | Lys |
| | | | | | 150 | | | | | 155 | | | | 160 | |
| Pro | Gly | Pro | Gly | Tyr | Leu | Leu | Glu | Tyr | Tyr | Thr | | | | | |
| | | | | | 165 | | | | | 170 | | | | | |

(2) INFORMATION FOR SEQ ID NO:607:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..161
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482537
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Ser | Phe | Thr | Cys | Ser | Ser | Pro | Ser | Ser | Ile | Leu | Pro | Ile | Ile | |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | | |
| Asp | Thr | Arg | Ser | Gly | Asn | Leu | Arg | Cys | Thr | Phe | Gln | Ser | Gln | Val | Ser | |
| | | | 20 | | | | | 25 | | | | | | 30 | | |
| Cys | Gly | Ile | Gln | Arg | Asp | Asp | Asn | Gly | Arg | Arg | Val | Trp | Arg | Arg | Arg | |
| | | | 35 | | | | 40 | | | | | 45 | | | | |
| Thr | Leu | Thr | Lys | Lys | Asp | Asp | Met | Leu | Arg | Tyr | Lys | Met | Gln | Arg | Val | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Pro | Phe | Val | Glu | Glu | Gln | Val | Arg | Lys | Ile | Arg | Xaa | Val | Gly | Lys | Val | |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | | |
| Met | Thr | Met | Asp | Ile | Glu | Gln | Leu | Leu | Leu | Arg | Glu | Asp | Asn | Arg | Phe | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Glu | Phe | Val | Asn | Ser | Val | Ala | Ala | Glu | Ala | Thr | Glu | Tyr | Val | Asp | Lys | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Asn | Arg | Asp | Glu | Tyr | Gly | Gly | Ser | Lys | Lys | Ala | Ile | Phe | His | Val | Leu | |
| | | 115 | | | | | 120 | | | | | | 125 | | | |
| Ser | Asn | Arg | Val | Asn | Asp | Leu | Gly | Phe | Asp | Arg | Pro | Glu | Ala | Tyr | Val | |
| | 130 | | | | | 135 | | | | 140 | | | | | | |
| Glu | Ala | Asp | Pro | Tyr | Lys | Pro | Gly | Pro | Gly | Tyr | Leu | Leu | Glu | Tyr | Tyr | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Thr | | | | | | | | | | | | | | | | |

- (2) INFORMATION FOR SEQ ID NO:608:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..106
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1482538
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Leu | Arg | Tyr | Lys | Met | Gln | Arg | Val | Pro | Phe | Val | Glu | Glu | Gln | Val | |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | | |
| Arg | Lys | Ile | Arg | Xaa | Val | Gly | Lys | Val | Met | Thr | Met | Asp | Ile | Glu | Gln | |
| | | | 20 | | | | | 25 | | | | | | 30 | | |
| Leu | Leu | Leu | Arg | Glu | Asp | Asn | Arg | Phe | Glu | Phe | Val | Asn | Ser | Val | Ala | |
| | | 35 | | | | 40 | | | | | | 45 | | | | |
| Ala | Glu | Ala | Thr | Glu | Tyr | Val | Asp | Lys | Asn | Arg | Asp | Glu | Tyr | Gly | Gly | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Ser | Lys | Lys | Ala | Ile | Phe | His | Val | Leu | Ser | Asn | Arg | Val | Asn | Asp | Leu | |
| 65 | | | | 70 | | | | | | 75 | | | | 80 | | |
| Gly | Phe | Asp | Arg | Pro | Glu | Ala | Tyr | Val | Glu | Ala | Asp | Pro | Tyr | Lys | Pro | |
| | | | 85 | | | | | 90 | | | | | | 95 | | |
| Gly | Pro | Gly | Tyr | Leu | Leu | Glu | Tyr | Thr | | | | | | | | |
| | | 100 | | | | | 105 | | | | | | | | | |

- (2) INFORMATION FOR SEQ ID NO:609:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..814

(D) OTHER INFORMATION: / Ceres Seq. ID 1482542

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

| | | | | | | |
|-------------|-------------|------------|------------|-------------|-------------|-----|
| agcaccggac | cacacaatct | tcccccaaat | ctcgcttcca | tcgctctctt | ccacggaaat | 60 |
| ctcagcacac | caatcatggg | acttatctct | ctttactttc | aatattttct | cacttttctaa | 120 |
| tcctatcctt | ctaattttat | ttagatgtca | atcattgtga | ataggattat | gagcctgctt | 180 |
| agttgcattg | gactccaatt | gggtgaattg | gctaagaaat | ttcgacatgg | tgcgttcata | 240 |
| taattcgact | gcaacctcta | caaagctgga | aaacatgaat | gaacatacgc | ctctgtggat | 300 |
| tgcacagatc | tctatctgct | tctttttgga | tgaacggagg | gagaaagacc | taggcatact | 360 |
| cagtgtatccc | atgaattttg | tgctcctagg | tacatcattt | ggggctcgta | cagtgtagtt | 420 |
| gtgaatctca | ctaagatgcc | aacgagacct | tccaagaaat | cagttgcata | cctgcttggt | 480 |
| cgtgctccac | ttcttttgaa | cagatggatt | gcatgcagaa | tttcagacac | tatgctctcg | 540 |
| ttgaccagt | ctaaatttaag | agtcagattt | tgatgaggaa | gttttagcaag | taacttggct | 600 |
| gaaacagcat | gcttttctgt | tatttgattt | gcttctactg | ggcactggat | aagattctct | 660 |
| ggctgacctc | tagttttaca | tagtctctct | gatagcgtgt | gaccgatgta | gggggtaagg | 720 |
| gatatcagaa | gttttaatgc | tccaaccctt | aattcgtcac | gaggattggt | gatgagttct | 780 |
| atcatggcaa | agcttgctgc | ggtttctttg | atcg | | | |

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..52

(D) OTHER INFORMATION: / Ceres Seq. ID 1482543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Pro | Asp | His | Thr | Ile | Phe | Pro | Gln | Ile | Ser | Pro | Pro | Ser | Pro | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ser | Thr | Glu | Ile | Ser | Ala | His | Gln | Ser | Trp | Asp | Leu | Ser | Leu | Phe | Thr |
| | | 20 | | | | | 25 | | | | | | 30 | | |
| Phe | Asn | Ile | Phe | Ser | Leu | Ser | Asn | Pro | Ile | Leu | Leu | Ile | Leu | Phe | Arg |
| | | 35 | | | | | 40 | | | | | | 45 | | |
| Cys | Gln | Ser | Leu | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1482544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Arg | Ser | Tyr | Asn | Ser | Thr | Ala | Thr | Ser | Thr | Lys | Leu | Glu | Asn |
| 1 | | | | 5 | | | | | 10 | | | | 15 | | |
| Met | Asn | Glu | His | Thr | Pro | Leu | Trp | Ile | Ala | Gln | Ile | Ser | Ile | Cys | Phe |

20 25 30
Phe Leu Asp Glu Arg Arg Glu Lys Asp Leu Gly Ile Leu Ser Asp Pro
35 40 45
Met Asn Phe Val Leu Leu Gly Thr Ser Phe Gly Ala Arg Thr Val
50 55 60

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

Met Asn Glu His Thr Pro Leu Trp Ile Ala Gln Ile Ser Ile Cys Phe
1 5 10 15
Phe Leu Asp Glu Arg Arg Glu Lys Asp Leu Gly Ile Leu Ser Asp Pro
20 25 30
Met Asn Phe Val Leu Leu Gly Thr Ser Phe Gly Ala Arg Thr Val
35 40 45

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1982 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1982
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

| | | | | | | |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| gataccttgct | acaaaatgtc | gcgtaattct | tctactgatt | tcagctcaat | cgctcaaatt | 60 |
| cgagtttgcg | tttagaaatt | gaagttgact | cttctgttct | tgaatctatc | tccgatcggg | 120 |
| gaactatctc | tcagtagcag | gagattgac | actccttcga | cattgctctt | tgaattcgtc | 180 |
| ctcaagggtg | ttaatgagct | cgtagaagct | accagaaatg | gcgtccatga | gctctgggtg | 240 |
| tgaaagcctt | cgactttgca | tggttgattt | gaggagaggt | caaactgaag | gacaagagtt | 300 |
| agagaaaatt | ttgttctttt | atcctgcccga | tttagacttc | tcgacgcagt | tatcagtgat | 360 |
| cggtctcagt | gaagggtcta | ttacttttac | tagacttttc | tctccggagg | cggcttggtg | 420 |
| agtgatcgaa | gcagaaagac | attcccatgt | tttctatgag | gctgaacctg | atatctggat | 480 |
| ggttatgggt | gtggagaaaa | ataaggagac | aggagcgata | tggaggatcg | atgcattaag | 540 |
| gaggggtgct | aaagaagtgc | actcactctt | tgtgatgttt | cacgggtcaa | ttagggcatt | 600 |
| aatcgaaaaa | gaaccaacag | gaggggttac | ccgatcacta | ttgtaccctg | tcatcacaga | 660 |
| ttatttaagc | acattttcaa | tatggtctct | ctcgggaagac | tgctgctgtg | aattttttgt | 720 |
| tgggaagaaa | cttcagctac | caactttccg | tgaacttttg | agagagcgtg | gaactgttca | 780 |
| aatgcttact | ttagcaaggg | acactgcagt | tgaagttcag | tctcttggtc | aagtactaga | 840 |
| ttcatgtgct | gggagcttac | gatgtcactc | tatgatctta | tttcaagatc | ttttgggttc | 900 |
| aacaaccctc | tcagctgatg | ataccgtcga | cttggtttaca | tttgcggtaa | tgaggttgac | 960 |
| ctcaaaaagc | ttctcctctg | atagcagttc | ttgggtcatat | ctacgtaaaag | ggcctgggtc | 1020 |
| atctgaaatc | tcttctagat | ctaactctggc | accggttgcc | tcaattgatt | ccctacactc | 1080 |
| aagaaacggg | aataacatgc | atcatgttat | taggccacta | caaaatgata | agtggaacaaa | 1140 |
| agggaaagat | gggtttctaa | taaccgatat | ttgggggtctt | gagactggcg | gctcccctga | 1200 |
| ttctgccatc | cctacaattt | ggcttcagca | gacacaagaa | agaatgtatc | tccttgcccta | 1260 |
| tcagcataaa | agtctcacct | tacttcttct | gatgcctaca | aatgccattg | tcaatggaga | 1320 |
| tttaagcatc | tcagccgtga | aacagcaagt | tattgaagat | gcactactga | gaattttgaa | 1380 |
| aattgaagag | aatattttcaa | gaggggtggg | cggtgagaat | gcttaccata | ttagggtta | 1440 |

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|------|
| ccgttactta | gtagttgata | atgacacgaa | agtatccaga | tcttctcctt | caggaaaagt | 1500 |
| aacaacactt | gcaaaggagt | ctctacttgc | actaaacaag | cttagagaag | aagtggattc | 1560 |
| agaaaaaagc | cgtgcaaaag | gacaggagaa | agacatggaa | atatgcatca | gagctaagaa | 1620 |
| caatgtgtgg | gtgatcgccc | gtgtgaccag | aggcaaagag | ctttacatgg | ctttggagaa | 1680 |
| aggcagcgac | actcttcttg | ataccacaga | cgctgttgga | agattcagca | acagggtattg | 1740 |
| cagcggagca | ttcttgatgg | actaagtttt | cggtgttctt | cttctgggtt | tgggaagagg | 1800 |
| gttcttctag | tttcaagtac | gaagtgaaaa | gctcagaaga | agtaatgagc | acttctctct | 1860 |
| cagccattaa | ttttgttttg | tgagaaattg | cagagaggaa | aacgattgtg | ttcttagttg | 1920 |
| gcctgtagat | atgtaacaat | gatattccac | gttggatcag | tgcaaacaaa | tccttttttg | 1980 |

tg

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Met | Ser | Ser | Gly | Asp | Glu | Ser | Leu | Arg | Leu | Cys | Met | Phe |
| 1 | | | 5 | | | | | 10 | | | | | | 15 | |
| Asp | Leu | Arg | Arg | Gly | Gln | Thr | Glu | Gly | Gln | Glu | Leu | Glu | Lys | Ile | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Phe | Phe | Tyr | Pro | Ala | Asp | Leu | Asp | Phe | Ser | Thr | Gln | Leu | Ser | Val | Ile |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Gly | Leu | Ser | Glu | Gly | Leu | Ile | Thr | Phe | Thr | Arg | Leu | Phe | Ser | Pro | Glu |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Ala | Ala | Cys | Glu | Val | Ile | Glu | Ala | Glu | Arg | His | Ser | His | Val | Phe | Tyr |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| Glu | Ala | Glu | Pro | Asp | Ile | Trp | Met | Val | Met | Val | Val | Glu | Lys | Asn | Lys |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Glu | Thr | Gly | Ala | Ile | Trp | Arg | Ile | Asp | Ala | Leu | Arg | Arg | Val | Leu | Lys |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Glu | Val | His | Ser | Leu | Phe | Val | Met | Phe | His | Gly | Ser | Ile | Arg | Ala | Leu |
| | | | 115 | | | | 120 | | | | | 125 | | | |
| Ile | Glu | Lys | Glu | Pro | Thr | Gly | Gly | Leu | Thr | Arg | Ser | Leu | Leu | Tyr | Pro |
| | | | 130 | | | 135 | | | | | 140 | | | | |
| Phe | Ile | Thr | Asp | Tyr | Leu | Ser | Thr | Phe | Gln | Ile | Trp | Ser | Leu | Ser | Glu |
| 145 | | | | 150 | | | | | 155 | | | | | 160 | |
| Asp | Cys | Cys | Cys | Glu | Phe | Phe | Val | Gly | Lys | Lys | Leu | Gln | Leu | Pro | Thr |
| | | | 165 | | | | | 170 | | | | | | 175 | |
| Phe | Arg | Glu | Thr | Leu | Arg | Glu | Arg | Gly | Thr | Val | Gln | Met | Leu | Thr | Leu |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Ala | Arg | Asp | Thr | Ala | Val | Glu | Val | Gln | Ser | Leu | Val | Gln | Val | Leu | Asp |
| | | | 195 | | | | 200 | | | | | 205 | | | |
| Ser | Cys | Ala | Gly | Ser | Leu | Arg | Cys | His | Ser | Met | Ile | Leu | Phe | Gln | Asp |
| | | | 210 | | | 215 | | | | | 220 | | | | |
| Leu | Leu | Val | Ser | Thr | Thr | Leu | Ser | Ala | Asp | Asp | Thr | Val | Asp | Leu | Phe |
| 225 | | | | 230 | | | | | 235 | | | | | 240 | |
| Thr | Phe | Ala | Val | Met | Arg | Leu | Thr | Ser | Lys | Ala | Phe | Ser | Ser | Asp | Thr |
| | | | 245 | | | | | | 250 | | | | | 255 | |
| Ser | Ser | Trp | Ser | Tyr | Leu | Arg | Lys | Gly | Pro | Gly | Ser | Ser | Glu | Ile | Ser |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Ser | Arg | Ser | Asn | Leu | Ala | Pro | Val | Gly | Ser | Ile | Asp | Ser | Leu | His | Ser |
| | | | 275 | | | 280 | | | | | 285 | | | | |
| Arg | Asn | Gly | Asn | Asn | Met | His | His | Val | Ile | Arg | Pro | Leu | Gln | Asn | Asp |

290 295 300
Lys Trp Thr Lys Gly Lys Asp Gly Phe Leu Ile Thr Asp Ile Trp Gly
305 310 315 320
Leu Glu Thr Gly Gly Ser Pro Asp Ser Ala Ile Pro Thr Ile Trp Leu
325 330 335
Gln Gln Thr Gln Glu Arg Met Tyr Leu Leu Ala Tyr Gln His Lys Ser
340 345 350
Leu Thr Leu Leu Leu Met Pro Thr Asn Ala Ile Val Asn Gly Asp
355 360 365
Leu Ser Ile Ser Ala Val Lys Gln Gln Val Ile Glu Asp Ala Ser Leu
370 375 380
Arg Ile Leu Lys Ile Glu Glu Asn Ile Ser Arg Gly Trp Gly Gly Glu
385 390 395 400
Asn Ala Tyr His Ile Lys Gly Tyr Arg Tyr Leu Val Val Asp Asn Asp
405 410 415
Thr Lys Val Ser Arg Ser Ser Pro Ser Gly Lys Val Thr Thr Leu Ala
420 425 430
Lys Glu Ser Leu Leu Ala Leu Asn Lys Leu Arg Glu Glu Val Asp Ser
435 440 445
Glu Lys Ser Arg Ala Lys Gly Gln Glu Lys Asp Met Glu Ile Cys Ile
450 455 460
Arg Ala Lys Asn Asn Val Trp Val Ile Ala Arg Val Thr Arg Gly Lys
465 470 475 480
Glu Leu Tyr Met Ala Leu Glu Lys Gly Ser Asp Thr Leu Leu Asp Thr
485 490 495
Thr Asp Ala Val Gly Arg Phe Ser Asn Arg Tyr Cys Ser Gly Ala Phe
500 505 510
Leu Met Asp
515

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..512

(D) OTHER INFORMATION: / Ceres Seq. ID 1482548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

Met Ser Ser Gly Asp Glu Ser Leu Arg Leu Cys Met Phe Asp Leu Arg
1 5 10 15
Arg Gly Gln Thr Glu Gly Gln Glu Leu Glu Lys Ile Leu Phe Phe Tyr
20 25 30
Pro Ala Asp Leu Asp Phe Ser Thr Gln Leu Ser Val Ile Gly Leu Ser
35 40 45
Glu Gly Leu Ile Thr Phe Thr Arg Leu Phe Ser Pro Glu Ala Ala Cys
50 55 60
Glu Val Ile Glu Ala Glu Arg His Ser His Val Phe Tyr Glu Ala Glu
65 70 75 80
Pro Asp Ile Trp Met Val Met Val Val Glu Lys Asn Lys Glu Thr Gly
85 90 95
Ala Ile Trp Arg Ile Asp Ala Leu Arg Arg Val Leu Lys Glu Val His
100 105 110
Ser Leu Phe Val Met Phe His Gly Ser Ile Arg Ala Leu Ile Glu Lys
115 120 125
Glu Pro Thr Gly Gly Leu Thr Arg Ser Leu Leu Tyr Pro Phe Ile Thr
130 135 140

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asp | Tyr | Leu | Ser | Thr | Phe | Gln | Ile | Trp | Ser | Leu | Ser | Glu | Asp | Cys | Cys | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Cys | Glu | Phe | Phe | Val | Gly | Lys | Lys | Leu | Gln | Leu | Pro | Thr | Phe | Arg | Glu | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Thr | Leu | Arg | Glu | Arg | Gly | Thr | Val | Gln | Met | Leu | Thr | Leu | Ala | Arg | Asp | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Thr | Ala | Val | Glu | Val | Gln | Ser | Leu | Val | Gln | Val | Leu | Asp | Ser | Cys | Ala | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Gly | Ser | Leu | Arg | Cys | His | Ser | Met | Ile | Leu | Phe | Gln | Asp | Leu | Leu | Val | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Ser | Thr | Thr | Leu | Ser | Ala | Asp | Asp | Thr | Val | Asp | Leu | Phe | Thr | Phe | Ala | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Val | Met | Arg | Leu | Thr | Ser | Lys | Ala | Phe | Ser | Ser | Asp | Thr | Ser | Ser | Trp | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Ser | Tyr | Leu | Arg | Lys | Gly | Pro | Gly | Ser | Ser | Glu | Ile | Ser | Ser | Arg | Ser | |
| | | 260 | | | | | 265 | | | | | | 270 | | | |
| Asn | Leu | Ala | Pro | Val | Gly | Ser | Ile | Asp | Ser | Leu | His | Ser | Arg | Asn | Gly | |
| | 275 | | | | | | 280 | | | | | 285 | | | | |
| Asn | Asn | Met | His | His | Val | Ile | Arg | Pro | Leu | Gln | Asn | Asp | Lys | Trp | Thr | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| Lys | Gly | Lys | Asp | Gly | Phe | Leu | Ile | Thr | Asp | Ile | Trp | Gly | Leu | Glu | Thr | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Gly | Gly | Ser | Pro | Asp | Ser | Ala | Ile | Pro | Thr | Ile | Trp | Leu | Gln | Gln | Thr | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| Gln | Glu | Arg | Met | Tyr | Leu | Leu | Ala | Tyr | Gln | His | Lys | Ser | Leu | Thr | Leu | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| Leu | Leu | Leu | Met | Pro | Thr | Asn | Ala | Ile | Val | Asn | Gly | Asp | Leu | Ser | Ile | |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| Ser | Ala | Val | Lys | Gln | Gln | Val | Ile | Glu | Asp | Ala | Ser | Leu | Arg | Ile | Leu | |
| | 370 | | | | | 375 | | | | 380 | | | | | | |
| Lys | Ile | Glu | Glu | Asn | Ile | Ser | Arg | Gly | Trp | Gly | Gly | Glu | Asn | Ala | Tyr | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| His | Ile | Lys | Gly | Tyr | Arg | Tyr | Leu | Val | Val | Asp | Asn | Asp | Thr | Lys | Val | |
| | | | | 405 | | | | | 410 | | | | | 415 | | |
| Ser | Arg | Ser | Ser | Pro | Ser | Gly | Lys | Val | Thr | Thr | Leu | Ala | Lys | Glu | Ser | |
| | | | 420 | | | | | 425 | | | | | 430 | | | |
| Leu | Leu | Ala | Leu | Asn | Lys | Leu | Arg | Glu | Glu | Val | Asp | Ser | Glu | Lys | Ser | |
| | | 435 | | | | | 440 | | | | | 445 | | | | |
| Arg | Ala | Lys | Gly | Gln | Glu | Lys | Asp | Met | Glu | Ile | Cys | Ile | Arg | Ala | Lys | |
| | 450 | | | | | 455 | | | | | 460 | | | | | |
| Asn | Asn | Val | Trp | Val | Ile | Ala | Arg | Val | Thr | Arg | Gly | Lys | Glu | Leu | Tyr | |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 | |
| Met | Ala | Leu | Glu | Lys | Gly | Ser | Asp | Thr | Leu | Leu | Asp | Thr | Thr | Asp | Ala | |
| | | | | 485 | | | | | 490 | | | | | 495 | | |
| Val | Gly | Arg | Phe | Ser | Asn | Arg | Tyr | Cys | Ser | Gly | Ala | Phe | Leu | Met | Asp | |
| | | | 500 | | | | | 505 | | | | | 510 | | | |

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..501
- (D) OTHER INFORMATION: / Ceres Seq. ID 1482549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Asp | Leu | Arg | Arg | Gly | Gln | Thr | Glu | Gly | Gln | Glu | Leu | Glu | Lys |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ile | Leu | Phe | Phe | Tyr | Pro | Ala | Asp | Leu | Asp | Phe | Ser | Thr | Gln | Leu | Ser |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Val | Ile | Gly | Leu | Ser | Glu | Gly | Leu | Ile | Thr | Phe | Thr | Arg | Leu | Phe | Ser |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Pro | Glu | Ala | Ala | Cys | Glu | Val | Ile | Glu | Ala | Glu | Arg | His | Ser | His | Val |
| | 50 | | | | | | 55 | | | | 60 | | | | |
| Phe | Tyr | Glu | Ala | Glu | Pro | Asp | Ile | Trp | Met | Val | Met | Val | Val | Glu | Lys |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Asn | Lys | Glu | Thr | Gly | Ala | Ile | Trp | Arg | Ile | Asp | Ala | Leu | Arg | Arg | Val |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Leu | Lys | Glu | Val | His | Ser | Leu | Phe | Val | Met | Phe | His | Gly | Ser | Ile | Arg |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ala | Leu | Ile | Glu | Lys | Glu | Pro | Thr | Gly | Gly | Leu | Thr | Arg | Ser | Leu | Leu |
| | | 115 | | | | | | 120 | | | | | 125 | | |
| Tyr | Pro | Phe | Ile | Thr | Asp | Tyr | Leu | Ser | Thr | Phe | Gln | Ile | Trp | Ser | Leu |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Ser | Glu | Asp | Cys | Cys | Cys | Glu | Phe | Phe | Val | Gly | Lys | Lys | Leu | Gln | Leu |
| 145 | | | | | 150 | | | | | 155 | | | | 160 | |
| Pro | Thr | Phe | Arg | Glu | Thr | Leu | Arg | Glu | Arg | Gly | Thr | Val | Gln | Met | Leu |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Thr | Leu | Ala | Arg | Asp | Thr | Ala | Val | Glu | Val | Gln | Ser | Leu | Val | Gln | Val |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Leu | Asp | Ser | Cys | Ala | Gly | Ser | Leu | Arg | Cys | His | Ser | Met | Ile | Leu | Phe |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Gln | Asp | Leu | Leu | Val | Ser | Thr | Thr | Leu | Ser | Ala | Asp | Asp | Thr | Val | Asp |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Leu | Phe | Thr | Phe | Ala | Val | Met | Arg | Leu | Thr | Ser | Lys | Ala | Phe | Ser | Ser |
| 225 | | | | | 230 | | | | | 235 | | | | 240 | |
| Asp | Thr | Ser | Ser | Trp | Ser | Tyr | Leu | Arg | Lys | Gly | Pro | Gly | Ser | Ser | Glu |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Ile | Ser | Ser | Arg | Ser | Asn | Leu | Ala | Pro | Val | Gly | Ser | Ile | Asp | Ser | Leu |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| His | Ser | Arg | Asn | Gly | Asn | Asn | Met | His | His | Val | Ile | Arg | Pro | Leu | Gln |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Asn | Asp | Lys | Trp | Thr | Lys | Gly | Lys | Asp | Gly | Phe | Leu | Ile | Thr | Asp | Ile |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Trp | Gly | Leu | Glu | Thr | Gly | Gly | Ser | Pro | Asp | Ser | Ala | Ile | Pro | Thr | Ile |
| 305 | | | | | 310 | | | | | 315 | | | | 320 | |
| Trp | Leu | Gln | Gln | Thr | Gln | Glu | Arg | Met | Tyr | Leu | Leu | Ala | Tyr | Gln | His |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Lys | Ser | Leu | Thr | Leu | Leu | Leu | Leu | Met | Pro | Thr | Asn | Ala | Ile | Val | Asn |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Gly | Asp | Leu | Ser | Ile | Ser | Ala | Val | Lys | Gln | Gln | Val | Ile | Glu | Asp | Ala |
| | 355 | | | | | | 360 | | | | | 365 | | | |
| Ser | Leu | Arg | Ile | Leu | Lys | Ile | Glu | Glu | Asn | Ile | Ser | Arg | Gly | Trp | Gly |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Gly | Glu | Asn | Ala | Tyr | His | Ile | Lys | Gly | Tyr | Arg | Tyr | Leu | Val | Val | Asp |
| 385 | | | | | 390 | | | | | 395 | | | | 400 | |
| Asn | Asp | Thr | Lys | Val | Ser | Arg | Ser | Ser | Pro | Ser | Gly | Lys | Val | Thr | Thr |
| | | | 405 | | | | | | 410 | | | | | 415 | |
| Leu | Ala | Lys | Glu | Ser | Leu | Leu | Ala | Leu | Asn | Lys | Leu | Arg | Glu | Glu | Val |
| | | | 420 | | | | | 425 | | | | | 430 | | |
| Asp | Ser | Glu | Lys | Ser | Arg | Ala | Lys | Gly | Gln | Glu | Lys | Asp | Met | Glu | Ile |
| | | 435 | | | | | 440 | | | | | 445 | | | |
| Cys | Ile | Arg | Ala | Lys | Asn | Asn | Val | Trp | Val | Ile | Ala | Arg | Val | Thr | Arg |
| | 450 | | | | | 455 | | | | | | 460 | | | |

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[illegible]